

Asn Val Glu Phe Val Asp Val Arg Phe Thr Asp Leu Pro Gly Thr Glu  
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 Gln His Phe Ser Ile Pro Ala Ala Ser Phe Asp Ala Asp Thr Il Glu  
 35 40 45  
 Glu Gly Leu Ala Phe Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile  
 50 55 60  
 Asp Glu Ser Asp Met Asn Leu Leu Pro Asp Leu Gly Thr Ala Thr Leu  
 65 70 75 80  
 Asp Pro Phe Arg Lys Ala Lys Thr Leu Asn Val Lys Phe Phe Val His  
 85 90 95  
 Asp Pro Phe Thr Arg Glu Ala Phe Ser Arg Asp Pro Arg Asn Val Ala  
 100 105 110  
 Arg Lys Ala Glu Gln Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys  
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 Asn Phe Gly Ala Glu Ala Glu Phe Tyr Leu Phe Asp Ser Val Arg Tyr  
 130 135 140  
 Ser Thr Glu Met Asn Ser Gly Phe Tyr Glu Val Asp Thr Glu Glu Gly  
 145 150 155 160  
 Trp Trp Asn Arg Gly Lys Glu Thr Asn Leu Asp Gly Thr Pro Asn Leu  
 165 170 175  
 Gly Ala Lys Asn Arg Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr  
 180 185 190  
 Asp Gln Thr Val Asp Val Arg Asp Asp Met Val Arg Asn Leu Ala Ala  
 195 200 205  
 Ser Gly Phe Ala Leu Glu Arg Phe His His Glu Val Gly Gly Gly Gln  
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 Gln Glu Ile Asn Tyr Arg Phe Asn Thr Met Leu His Ala Ala Asp Asp  
 225 230 235 240  
 Ile Gln Thr Phe Lys Tyr Ile Ile Lys Asn Thr Ala Arg Leu His Gly  
 245 250 255  
 Lys Ala Ala Thr Phe Met Pro Lys Pro Leu Ala Gly Asp Asn Gly Ser  
 260 265 270  
 Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Lys Pro Leu Phe  
 275 280 285  
 His Asp Glu Ser Gly Tyr Ala Gly Leu Ser Asp Ile Ala Arg Tyr Tyr  
 290 295 300  
 Ile Gly Gly Ile Leu His His Ala Gly Ala Val Leu Ala Phe Thr Asn  
 305 310 315 320  
 Ala Thr Leu Asn Ser Tyr His Arg Leu Val Pro Gly Phe Glu Ala Pro  
 325 330 335  
 Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Val Arg Ile

340	345	350
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355	360	365
Pro Asp Pro Ser Gly Asn Pro Tyr Leu Gly Phe Ala Ala Met Met Met		
370	375	380
Ala Gly Leu Asp Gly Ile Lys Asn Arg Ile Glu Pro His Ala Pro Val		
385	390	395
Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile Pro		
	405	410
Gln Ala Pro Thr Ser Leu Glu Ala Ser Leu Lys Ala Leu Gln Glu Asp		
	420	425
Thr Asp Phe Leu Thr Glu Ser Asp Val Phe Thr Glu Asp Leu Ile Glu		
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Ala Tyr Ile Gln Tyr Lys Tyr Asp Asn Glu Ile Ser Pro Val Arg Leu		
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Arg Pro Thr Pro Gln Glu Phe Glu Leu Tyr Phe Asp Cys		
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 Met Ser Gly Pro Leu  
 1 5  
 aga agt gaa cgt aaa gtc gtt ggc ttt gtc aga gac cca ctg cca aaa 163  
 Arg Ser Glu Arg Lys Val Val Gly Phe Val Arg Asp Pro Leu Pro Lys  
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 gtt ggt tct tta tcg ctg aaa tct gag cat gcc caa gca gat cta gag 211  
 Val Gly Ser Leu Ser Leu Lys Ser Glu His Ala Gln Ala Asp Leu Glu  
 25 30 35  
 cat ttg ggt tgg cgc aat gtt gag tct ttg gat ttg ttg tgg ggc ttg 259  
 His Leu Gly Trp Arg Asn Val Glu Ser Leu Asp Leu Leu Trp Gly Leu  
 40 45 50  
 tca ggt gca ggc gat ccc gat gtc gcg ctg aac ctt ctt att cgg ctg 307  
 Ser Gly Ala Gly Asp Pro Asp Val Ala Leu Asn Leu Leu Ile Arg Leu  
 55 60 65  
 tat cag gca ctt gaa gca atc ggc gag gat gct cga aac gag ctt gat 355



Tyr 70	Gln	Ala	Leu	Glu	Ala 75	Ile	Gly	Glu	Asp	Ala 80	Arg	Asn	Glu	Leu	Asp 85		
caa	gag	att	cgc	cag	gat	gaa	aaa	cta	cga	gtc	cgc	ctt	ttt	gca	ttg	403	
Gln	Glu	Ile	Arg	Gln 90	Asp	Glu	Lys	Leu	Arg 95	Val	Arg	Leu	Phe	Ala 100	Leu		
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Leu	Gly	Gly	Ser 105	Ser	Ala	Val	Gly	Asp 110	His	Leu	Val	Ala	Asn 115	Pro	Leu		
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Gln	Trp	Lys 120	Leu	Leu	Lys	Leu	Asp 125	Ala	Pro	Ser	Arg	Glu 130	Glu	Met	Phe		
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Gln	Ala 135	Leu	Leu	Glu	Ser	Val 140	Lys	Ala	Gln	Pro	Ala 145	Val	Leu	Glu	Val		
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Glu	Asp	Phe	Ser	Asp	Ala 155	His	Asn	Ile	Ala 160	Arg	Asp	Asp	Leu	Ser	Thr 165		
cct	ggt	ttt	tac	acg	gct	agt	gtt	acc	ggg	cct	gaa	gca	gag	cga	gtc	643	
Pro	Gly	Phe	Tyr 170	Thr	Ala	Ser	Val	Thr 175	Gly	Pro	Glu	Ala	Glu	Arg 180	Val		
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Leu	Lys	Trp	Thr 185	Tyr	Arg	Thr	Leu	Leu 190	Thr	Arg	Ile	Ala	Ala 195	His	Asp		
tta	gcg	ggt	acc	tat	ccc	acc	gac	atg	cgg	aga	aaa	ggt	ggc	gat	cct	739	
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gtt	ccg	ttt	agc	aca	gtg	acc	atg	cag	ctc	agc	gac	cta	gct	gat	gct	787	
Val	Pro 215	Phe	Ser	Thr	Val	Thr 220	Met	Gln	Leu	Ser	Asp 225	Leu	Ala	Asp	Ala		
gct	ttg	act	gct	gct	tta	gct	gtg	gca	att	gcc	aat	gtt	tat	ggt	gaa	835	
Ala	Leu	Thr	Ala	Ala	Leu 235	Ala	Val	Ala	Ile 240	Ala	Asn	Val	Tyr	Gly 245	Glu		
aag	ccg	gtt	gat	tca	gct	tta	tct	gtc	atc	gcg	atg	ggc	aaa	tgt	ggc	883	
Lys	Pro	Val	Asp 250	Ser	Ala	Leu	Ser	Val 255	Ile	Ala	Met	Gly	Lys	Cys 260	Gly		
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Ala	Gln	Glu	Leu 265	Asn	Tyr	Ile	Ser	Asp 270	Val	Asp	Val	Val	Phe 275	Val	Ala		
gag	ccg	gca	aac	tct	aaa	tca	aca	cgc	acc	gca	gca	gag	ctc	att	cgc	979	
Glu	Pro 280	Ala	Asn	Ser	Lys	Ser	Thr 285	Arg	Thr	Ala	Ala	Glu 290	Leu	Ile	Arg		
atc	ggt	agc	aac	tcg	ttc	ttt	gag	gtg	gat	gca	gca	ctt	cgc	cca	gaa	1027	
Ile	Gly	Ser	Asn	Ser	Phe	Phe 300	Glu	Val	Asp	Ala	Ala 305	Leu	Arg	Pro	Glu		

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1075

Gly Lys Ser Gly Ala Leu Val Arg Ser Leu Asp Ser His Met Ala Tyr  
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tac aag cgc tgg gcg gaa acc tgg gag ttt cag gca ctg ctg aaa gct  
1123

Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln Ala Leu Leu Lys Ala  
330 335 340

cgt ccc atg acg ggt gat att aac ctt ggg cag tcc tat gtg gat gct  
1171

Arg Pro Met Thr Gly Asp Ile Asn Leu Gly Gln Ser Tyr Val Asp Ala  
345 350 355

ctt tca ccg ttg att tgg acg gct agc cag cgg gaa tca ttt gtc aca  
1219

Leu Ser Pro Leu Ile Trp Thr Ala Ser Gln Arg Glu Ser Phe Val Thr  
360 365 370

gat gtc caa gct atg cgc cgt cga gtg ttg gac aat gtt ccg gaa gac  
1267

Asp Val Gln Ala Met Arg Arg Arg Val Leu Asp Asn Val Pro Glu Asp  
375 380 385

ttg cgt gat cgt gag ctg aag ctt ggt cgc ggt ggt ttg agg gat gtg  
1315

Leu Arg Asp Arg Glu Leu Lys Leu Gly Arg Gly Gly Leu Arg Asp Val  
390 395 400 405

gag ttt gct gtc cag ctc ctt cag atg gtg cat ggt cgc att gat gag  
1363

Glu Phe Ala Val Gln Leu Leu Gln Met Val His Gly Arg Ile Asp Glu  
410 415 420

acg ttg cgg gtt cgg tca acg gta aat gct ttg cat gtg ttg gtt gat  
1411

Thr Leu Arg Val Arg Ser Thr Val Asn Ala Leu His Val Leu Val Asp  
425 430 435

cag gga tat gtg ggt cgt gaa gac ggg cat aat ctc att gag tcg tat  
1459

Gln Gly Tyr Val Gly Arg Glu Asp Gly His Asn Leu Ile Glu Ser Tyr  
440 445 450

gag ttt ttg cgt ctg ttg gag cat cgc ctt caa ttg gag cgg atc aag  
1507

Glu Phe Leu Arg Leu Leu Glu His Arg Leu Gln Leu Glu Arg Ile Lys  
455 460 465

cgc act cac ttg tta ccg aaa cct gat gac cga atg aat atg cgc tgg  
1555

Arg Thr His Leu Leu Pro Lys Pro Asp Asp Arg Met Asn Met Arg Trp  
470 475 480 485

ttg gcg cgc gct tct ggg ttt act ggt tcg atg gag caa agt tcg gcc  
1603

Leu Ala Arg Ala Ser Gly Phe Thr Gly Ser Met Glu Gln Ser Ser Ala  
490 495 500

aaa gct atg gaa cgg cat ttg cgt aag gtt cgt ttg cag att cag tcg  
1651

Lys Ala Met Glu Arg His Leu Arg Lys Val Arg Leu Gln Ile Gln Ser  
505 510 515

ttg cat agt cag ctg ttt tat cgg cca ctg ctg aac tct gtg gtc aac  
1699

Leu His Ser Gln Leu Phe Tyr Arg Pro Leu Leu Asn Ser Val Val Asn  
520 525 530

ttg agc gcg gat gcc atc agg ttg tct ccg gat gct gca aag cta caa  
1747

Leu Ser Ala Asp Ala Ile Arg Leu Ser Pro Asp Ala Ala Lys Leu Gln  
535 540 545

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1795

Leu Ala Ala Leu Gly Tyr Leu His Pro Ser Arg Ala Tyr Glu His Leu  
550 555 560 565

act gct ctt gca tca gga gct agc cgt aaa gcc aag att cag gcg atg  
1843

Thr Ala Leu Ala Ser Gly Ala Ser Arg Lys Ala Lys Ile Gln Ala Met  
570 575 580

ttg ctg ccc acg ttg atg gag tgg ctg tct caa aca gct gaa cca gat  
1891

Leu Leu Pro Thr Leu Met Glu Trp Leu Ser Gln Thr Ala Glu Pro Asp  
585 590 595

gcg gga ttg ctg aat tac cgc aag ctt tct gat gct tcc tat gat cgc  
1939

Ala Gly Leu Leu Asn Tyr Arg Lys Leu Ser Asp Ala Ser Tyr Asp Arg  
600 605 610

agc tgg ttt ttg cgc atg ctg cgt gat gag ggc gta gtg ggg cag cgg  
1987

Ser Trp Phe Leu Arg Met Leu Arg Asp Glu Gly Val Val Gly Gln Arg  
615 620 625

ttg atg cgt att ttg gga aat tct ccc tat att tct gaa ctg att atc  
2035

Leu Met Arg Ile Leu Gly Asn Ser Pro Tyr Ile Ser Glu Leu Ile Ile  
630 635 640 645

tcc act ccg gac ttt atg aaa cag ctg ggt gat gcg gcg tct ggt cct  
2083

Ser Thr Pro Asp Phe Met Lys Gln Leu Gly Asp Ala Ala Ser Gly Pro  
650 655 660

aaa ttg ctt gct act gca ccg act cag gtt gtg aaa gca atc aag gca  
2131

Lys Leu Leu Ala Thr Ala Pro Thr Gln Val Val Lys Ala Ile Lys Ala  
665 670 675

acg gtg tcg cgt cat gag tca cct gat cgg gcg atc cag gct gca cga  
2179

Thr Val Ser Arg His Glu Ser Pro Asp Arg Ala Ile Gln Ala Ala Arg  
680 685 690

tcg ctg agg agg cag gag ctg gca cgc att gcc tct gct gat ttg ctc  
2227

Ser Leu Arg Arg Gln Glu Leu Ala Arg Ile Ala Ser Ala Asp Leu Leu  
695 700 705

aac atg ctc act gtt cag gaa gta tgc caa agc ttg tca cta gtc tgg  
2275

Asn Met Leu Thr Val Gln Glu Val Cys Gln Ser Leu Ser Leu Val Trp  
710 715 720 725

gat gcg gtg ttg gat gct gcc ttg gat gcg gaa atc cgt gct gca ctt  
2323

Asp Ala Val Leu Asp Ala Ala Leu Asp Ala Glu Ile Arg Ala Ala Leu  
730 735 740

aac gat cca cag aaa cca gat cag cct ctg gcc aat att tct gtg atc  
2371

Asn Asp Pro Gln Lys Pro Asp Gln Pro Leu Ala Asn Ile Ser Val Ile  
745 750 755

ggc atg ggc cgt ttg ggt gga gca gaa ctt gga tac ggt tct gat gcc  
2419

Gly Met Gly Arg Leu Gly Gly Ala Glu Leu Gly Tyr Gly Ser Asp Ala  
760 765 770

gat gtg atg ttt gta tgc gag ccg gta gcc ggt gtg gaa gag cat gag  
2467

Asp Val Met Phe Val Cys Glu Pro Val Ala Gly Val Glu Glu His Glu  
775 780 785

gcc gtc aca tgg tct att gct atc tgt gat tcc atg cgg tcg agg ctt  
2515

Ala Val Thr Trp Ser Ile Ala Ile Cys Asp Ser Met Arg Ser Arg Leu  
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gcg cag cct tcc ggt gat cca cct ttg gag gtg gat ctg ggg ctg cgt  
2563

Ala Gln Pro Ser Gly Asp Pro Pro Leu Glu Val Asp Leu Gly Leu Arg  
810 815 820

cct gaa ggg aga tct ggt gcg att gtg cgc acc gtt gat tcc tat gtg  
2611

Pro Glu Gly Arg Ser Gly Ala Ile Val Arg Thr Val Asp Ser Tyr Val  
825 830 835

aag tac tac gaa aag tgg ggt gaa act tgg gag att cag gcg ctg ctg  
2659

Lys Tyr Tyr Glu Lys Trp Gly Glu Thr Trp Glu Ile Gln Ala Leu Leu  
840 845 850

agg gct gcg tgg gtt gct ggt gat cgt gag ctg ggt att aag ttc ttg  
2707

Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu Gly Ile Lys Phe Leu  
855 860 865

gag tcg att gat cgt ttc cgc tac cca gtt gac ggg gca acg cag gcg  
2755

Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp Gly Ala Thr Gln Ala  
870 875 880 885

cag ctt cgt gaa gtt cgt cga att aag gcg agg gtg gat aat gag agg  
 2803  
 Gln Leu Arg Glu Val Arg Arg Ile Lys Ala Arg Val Asp Asn Glu Arg  
 890 895 900

ctt ccg cgc ggg gct gat cga aat acc cat acc aag ctg ggt cgg gga  
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 Leu Pro Arg Gly Ala Asp Arg Asn Thr His Thr Lys Leu Gly Arg Gly  
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gcg tta act gac atc gag tgg act gtg cag ttg ttg acc atg atg cat  
 2899  
 Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu Leu Thr Met Met His  
 920 925 930

gct cat gag att ccg gag ctg cac aat acg tcg acg ttg gaa gtt ctt  
 2947  
 Ala His Glu Ile Pro Glu Leu His Asn Thr Ser Thr Leu Glu Val Leu  
 935 940 945

gaa gtg ctg gaa aag cat cag att att aac cct gtg cag gtg cag acg  
 2995  
 Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro Val Gln Val Gln Thr  
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 3139  
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 Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg Lys Ser Arg Gln Val  
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 3258

&lt;210&gt; 100

&lt;211&gt; 1045

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 100

Met Ser Gly Pro Leu Arg Ser Glu Arg Lys Val Val Gly Phe Val Arg

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Gln Ala Asp Leu Glu His Leu Gly Trp Arg Asn Val Glu Ser Leu Asp	35	40	45
Leu Leu Trp Gly Leu Ser Gly Ala Gly Asp Pro Asp Val Ala Leu Asn	50	55	60
Leu Leu Ile Arg Leu Tyr Gln Ala Leu Glu Ala Ile Gly Glu Asp Ala	65	70	75
Arg Asn Glu Leu Asp Gln Glu Ile Arg Gln Asp Glu Lys Leu Arg Val	85	90	95
Arg Leu Phe Ala Leu Leu Gly Gly Ser Ser Ala Val Gly Asp His Leu	100	105	110
Val Ala Asn Pro Leu Gln Trp Lys Leu Leu Lys Leu Asp Ala Pro Ser	115	120	125
Arg Glu Glu Met Phe Gln Ala Leu Leu Glu Ser Val Lys Ala Gln Pro	130	135	140
Ala Val Leu Glu Val Glu Asp Phe Ser Asp Ala His Asn Ile Ala Arg	145	150	155
Asp Asp Leu Ser Thr Pro Gly Phe Tyr Thr Ala Ser Val Thr Gly Pro	165	170	175
Glu Ala Glu Arg Val Leu Lys Trp Thr Tyr Arg Thr Leu Leu Thr Arg	180	185	190
Ile Ala Ala His Asp Leu Ala Gly Thr Tyr Pro Thr Asp Met Arg Arg	195	200	205
Lys Gly Gly Asp Pro Val Pro Phe Ser Thr Val Thr Met Gln Leu Ser	210	215	220
Asp Leu Ala Asp Ala Ala Leu Thr Ala Ala Leu Ala Val Ala Ile Ala	225	230	235
Asn Val Tyr Gly Glu Lys Pro Val Asp Ser Ala Leu Ser Val Ile Ala	245	250	255
Met Gly Lys Cys Gly Ala Gln Glu Leu Asn Tyr Ile Ser Asp Val Asp	260	265	270
Val Val Phe Val Ala Glu Pro Ala Asn Ser Lys Ser Thr Arg Thr Ala	275	280	285
Ala Glu Leu Ile Arg Ile Gly Ser Asn Ser Phe Phe Glu Val Asp Ala	290	295	300
Ala Leu Arg Pro Glu Gly Lys Ser Gly Ala Leu Val Arg Ser Leu Asp	305	310	315
Ser His Met Ala Tyr Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln	325	330	335

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Ser	Tyr	Val	Asp	Ala	Leu	Ser	Pro	Leu	Ile	Trp	Thr	Ala	Ser	Gln	Arg	355	360	365	
Glu	Ser	Phe	Val	Thr	Asp	Val	Gln	Ala	Met	Arg	Arg	Arg	Val	Leu	Asp	370	375	380	
Asn	Val	Pro	Glu	Asp	Leu	Arg	Asp	Arg	Glu	Leu	Lys	Leu	Gly	Arg	Gly	385	390	395	400
Gly	Leu	Arg	Asp	Val	Glu	Phe	Ala	Val	Gln	Leu	Leu	Gln	Met	Val	His	405	410	415	
Gly	Arg	Ile	Asp	Glu	Thr	Leu	Arg	Val	Arg	Ser	Thr	Val	Asn	Ala	Leu	420	425	430	
His	Val	Leu	Val	Asp	Gln	Gly	Tyr	Val	Gly	Arg	Glu	Asp	Gly	His	Asn	435	440	445	
Leu	Ile	Glu	Ser	Tyr	Glu	Phe	Leu	Arg	Leu	Leu	Glu	His	Arg	Leu	Gln	450	455	460	
Leu	Glu	Arg	Ile	Lys	Arg	Thr	His	Leu	Leu	Pro	Lys	Pro	Asp	Asp	Arg	465	470	475	480
Met	Asn	Met	Arg	Trp	Leu	Ala	Arg	Ala	Ser	Gly	Phe	Thr	Gly	Ser	Met	485	490	495	
Glu	Gln	Ser	Ser	Ala	Lys	Ala	Met	Glu	Arg	His	Leu	Arg	Lys	Val	Arg	500	505	510	
Leu	Gln	Ile	Gln	Ser	Leu	His	Ser	Gln	Leu	Phe	Tyr	Arg	Pro	Leu	Leu	515	520	525	
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Ala	Ala	Lys	Leu	Gln	Leu	Ala	Ala	Leu	Gly	Tyr	Leu	His	Pro	Ser	Arg	545	550	555	560
Ala	Tyr	Glu	His	Leu	Thr	Ala	Leu	Ala	Ser	Gly	Ala	Ser	Arg	Lys	Ala	565	570	575	
Lys	Ile	Gln	Ala	Met	Leu	Leu	Pro	Thr	Leu	Met	Glu	Trp	Leu	Ser	Gln	580	585	590	
Thr	Ala	Glu	Pro	Asp	Ala	Gly	Leu	Leu	Asn	Tyr	Arg	Lys	Leu	Ser	Asp	595	600	605	
Ala	Ser	Tyr	Asp	Arg	Ser	Trp	Phe	Leu	Arg	Met	Leu	Arg	Asp	Glu	Gly	610	615	620	
Val	Val	Gly	Gln	Arg	Leu	Met	Arg	Ile	Leu	Gly	Asn	Ser	Pro	Tyr	Ile	625	630	635	640
Ser	Glu	Leu	Ile	Ile	Ser	Thr	Pro	Asp	Phe	Met	Lys	Gln	Leu	Gly	Asp	645	650	655	

Ala Ala Ser Gly Pro Lys Leu Leu Ala Thr Ala Pro Thr Gln Val Val  
 660 665 670  
 Lys Ala Ile Lys Ala Thr Val Ser Arg His Glu Ser Pro Asp Arg Ala  
 675 680 685  
 Ile Gln Ala Ala Arg Ser Leu Arg Arg Gln Glu Leu Ala Arg Ile Ala  
 690 695 700  
 Ser Ala Asp Leu Leu Asn Met Leu Thr Val Gln Glu Val Cys Gln Ser  
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 Leu Ser Leu Val Trp Asp Ala Val Leu Asp Ala Ala Leu Asp Ala Glu  
 725 730 735  
 Ile Arg Ala Ala Leu Asn Asp Pro Gln Lys Pro Asp Gln Pro Leu Ala  
 740 745 750  
 Asn Ile Ser Val Ile Gly Met Gly Arg Leu Gly Gly Ala Glu Leu Gly  
 755 760 765  
 Tyr Gly Ser Asp Ala Asp Val Met Phe Val Cys Glu Pro Val Ala Gly  
 770 775 780  
 Val Glu Glu His Glu Ala Val Thr Trp Ser Ile Ala Ile Cys Asp Ser  
 785 790 795 800  
 Met Arg Ser Arg Leu Ala Gln Pro Ser Gly Asp Pro Pro Leu Glu Val  
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 Asp Leu Gly Leu Arg Pro Glu Gly Arg Ser Gly Ala Ile Val Arg Thr  
 820 825 830  
 Val Asp Ser Tyr Val Lys Tyr Tyr Glu Lys Trp Gly Glu Thr Trp Glu  
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 Ile Gln Ala Leu Leu Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu  
 850 855 860  
 Gly Ile Lys Phe Leu Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp  
 865 870 875 880  
 Gly Ala Thr Gln Ala Gln Leu Arg Glu Val Arg Arg Ile Lys Ala Arg  
 885 890 895  
 Val Asp Asn Glu Arg Leu Pro Arg Gly Ala Asp Arg Asn Thr His Thr  
 900 905 910  
 Lys Leu Gly Arg Gly Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu  
 915 920 925  
 Leu Thr Met Met His Ala His Glu Ile Pro Glu Leu His Asn Thr Ser  
 930 935 940  
 Thr Leu Glu Val Leu Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro  
 945 950 955 960  
 Val Gln Val Gln Thr Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Ala  
 965 970 975  
 Arg Asn Ala Leu Val Leu Val Arg Gly Lys Arg Leu Asp Gln Leu Pro



980			985			990										
Thr	Pro	Gly	Pro	His	Leu	Ala	Gln	Val	Ala	Gly	Ala	Ser	Gly	Trp	Asp	
995						1000						1005				
Pro	Asn	Glu	Tyr	Gln	Glu	Tyr	Leu	Glu	Asn	Tyr	Leu	Lys	Val	Thr	Arg	
1010						1015						1020				
Lys	Ser	Arg	Gln	Val	Val	Asp	Glu	Val	Phe	Trp	Gly	Val	Asp	Ser	Met	
1025						1030						1035			1040	
Glu	Gln	Arg	Glu	Phe												
1045																

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<210> 101
<211> 861
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (1)..(861)
<223> RXN03176
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<400> 101																
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Glu	Leu	Ala	Asp	Tyr	Ile	Pro	Glu	Leu	Lys	Ser	Ala	Asp	Pro	Asn	Pro	
1				5					10					15		
ctg	gca	gta	gcc	ctg	tgc	acc	gtt	aac	gga	cac	atc	tac	agc	gca	ggc	96
Leu	Ala	Val	Ala	Leu	Cys	Thr	Val	Asn	Gly	His	Ile	Tyr	Ser	Ala	Gly	
			20					25					30			
gat	gac	gac	atc	gaa	ttc	acc	atg	caa	agt	att	tcc	aag	cca	ttt	gcc	144
Asp	Asp	Asp	Ile	Glu	Phe	Thr	Met	Gln	Ser	Ile	Ser	Lys	Pro	Phe	Ala	
		35					40					45				
tac	gca	ctc	gca	ctc	caa	gaa	tgc	ggc	ttt	gat	gag	gtc	tct	gca	tcc	192
Tyr	Ala	Leu	Ala	Leu	Gln	Glu	Cys	Gly	Phe	Asp	Glu	Val	Ser	Ala	Ser	
	50					55					60					
gtg	gcc	ttg	gag	ccc	tcc	ggc	gag	gcc	ttc	aac	gaa	ctt	tcc	ctc	gac	240
Val	Ala	Leu	Glu	Pro	Ser	Gly	Glu	Ala	Phe	Asn	Glu	Leu	Ser	Leu	Asp	
65					70					75					80	
ggc	gaa	aac	cgc	ccc	atg	aac	ccc	atg	atc	aac	gcc	ggc	gcg	atc	gcc	288
Gly	Glu	Asn	Arg	Pro	Met	Asn	Pro	Met	Ile	Asn	Ala	Gly	Ala	Ile	Ala	
				85					90					95		
atc	aac	cag	ctg	atc	aac	ggc	tcc	gat	tcc	acc	gtg	gaa	gac	cgc	gtg	336
Ile	Asn	Gln	Leu	Ile	Asn	Gly	Ser	Asp	Ser	Thr	Val	Glu	Asp	Arg	Val	
			100					105					110			
gaa	aaa	atc	cga	cac	tac	ttc	tct	gaa	ctt	gct	gga	cgc	gaa	ctc	acc	384
Glu	Lys	Ile	Arg	His	Tyr	Phe	Ser	Glu	Leu	Ala	Gly	Arg	Glu	Leu	Thr	
		115					120					125				
atc	gac	cgc	gtg	ctt	gcc	gaa	tcc	gaa	ctc	gcc	ggc	gcc	gac	cgc	aac	432
Ile	Asp	Arg	Val	Leu	Ala	Glu	Ser	Glu	Leu	Ala	Gly	Ala	Asp	Arg	Asn	
	130					135					140					

ctc tcc atc gcc cac atg ctg cgc aat tac ggc gtc atc gaa gac gaa 480  
 Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu  
 145 150 155 160  
  
 gcc cac gac gcc gtc ctc agc tac acg ctg caa tgc gcc atc aaa gta 528  
 Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val  
 165 170 175  
  
 acc acg cgc gac ctc gca gtc atg acc gcc acg ctc gcc gcc ggc ggc 576  
 Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly  
 180 185 190  
  
 aca cac cca att acc ggc aag aag ctt ctc gac gcc cgc gtc tgc cgc 624  
 Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg  
 195 200 205  
  
 ctc acc ctc tcc gtc atg gct tca gca ggc atg tac gac gag gca ggg 672  
 Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly  
 210 215 220  
  
 cag tgg ctc tcc acc gta ggc atc ccc gcg aaa tca gga gtc gcc ggc 720  
 Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly  
 225 230 235 240  
  
 gga ctc atc ggc att ctg cca ggt cag ctg ggc atc gcc aca ttt tcc 768  
 Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser  
 245 250 255  
  
 cca cgc ctg aac ccc aaa ggc aac agc gtg cgc ggc gta aaa ata ttc 816  
 Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe  
 260 265 270  
  
 aaa cag ctt tcc gac gac atg ggc ctc cac ctc atg tcc acc gag 861  
 Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu  
 275 280 285

&lt;210&gt; 102

&lt;211&gt; 287

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 102

Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro  
 1 5 10 15  
  
 Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly  
 20 25 30  
  
 Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala  
 35 40 45  
  
 Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser  
 50 55 60  
  
 Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp  
 65 70 75 80  
  
 Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala  
 85 90 95

Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val  
 100 105 110  
 Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr  
 115 120 125  
 Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn  
 130 135 140  
 Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu  
 145 150 155 160  
 Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val  
 165 170 175  
 Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly  
 180 185 190  
 Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg  
 195 200 205  
 Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly  
 210 215 220  
 Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly  
 225 230 235 240  
 Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser  
 245 250 255  
 Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe  
 260 265 270  
 Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu  
 275 280 285

&lt;210&gt; 103

&lt;211&gt; 861

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(861)

&lt;223&gt; FRXA02879

&lt;400&gt; 103

gag ttg gcc gat tac atc ccg gaa cta aaa tct gcg gac cca aac ccg 48  
 Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro  
 1 5 10 15

ctg gca gta gcc ctg tgc acc gtt aac gga cac atc tac agc gca ggc 96  
 Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly  
 20 25 30

gat gac gac atc gaa ttc acc atg caa agt att tcc aag cca ttt gcc 144  
 Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala  
 35 40 45

tac gca ctc gca ctc caa gaa tgc ggc ttt gat gag gtc tct gca tcc	192
Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser	
50 55 60	
gtg gcc ttg gag ccc tcc ggt gag gcc ttc aac gaa ctt tcc ctc gac	240
Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp	
65 70 75 80	
ggc gaa aac cgc ccc atg aac ccc atg atc aac gcc ggc gcg atc gcc	288
Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala	
85 90 95	
atc aac cag ctg atc aac ggc tcc gat tcc acc gtg gaa gac cgc gtg	336
Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val	
100 105 110	
gaa aaa atc cga cac tac ttc tct gaa ctt gct gga cgc gaa ctc acc	384
Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr	
115 120 125	
atc gac cgc gtg ctt gcc gaa tcc gaa ctc gcc ggc gcc gac cgc aac	432
Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn	
130 135 140	
ctc tcc atc gcc cac atg ctg cgc aat tac ggc gtc atc gaa gac gaa	480
Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu	
145 150 155 160	
gcc cac gac gcc gtc ctc agc tac acg ctg caa tgc gcc atc aaa gta	528
Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val	
165 170 175	
acc acg cgc gac ctc gca gtc atg acc gcc acg ctc gcc gcc ggc ggc	576
Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly	
180 185 190	
aca cac cca att acc ggc aag aag ctt ctc gac gcc cgc gtc tgc cgc	624
Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg	
195 200 205	
ctc acc ctc tcc gtc atg gct tca gca ggc atg tac gac gag gca ggg	672
Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly	
210 215 220	
cag tgg ctc tcc acc gta ggc atc ccc gcg aaa tca gga gtc gcc ggc	720
Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly	
225 230 235 240	
gga ctc atc ggc att ctg cca ggt cag ctg ggc atc gcc aca ttt tcc	768
Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser	
245 250 255	
cca cgc ctg aac ccc aaa ggc aac agc gtg cgc ggc gta aaa ata ttc	816
Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe	
260 265 270	
aaa cag ctt tcc gac gac atg ggc ctc cac ctc atg tcc acc gag	861
Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu	
275 280 285	

<210> 104  
 <211> 287  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 104

Glu	Leu	Ala	Asp	Tyr	Ile	Pro	Glu	Leu	Lys	Ser	Ala	Asp	Pro	Asn	Pro
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Leu	Ala	Val	Ala	Leu	Cys	Thr	Val	Asn	Gly	His	Ile	Tyr	Ser	Ala	Gly
			20					25					30		
Asp	Asp	Asp	Ile	Glu	Phe	Thr	Met	Gln	Ser	Ile	Ser	Lys	Pro	Phe	Ala
		35					40					45			
Tyr	Ala	Leu	Ala	Leu	Gln	Glu	Cys	Gly	Phe	Asp	Glu	Val	Ser	Ala	Ser
	50					55					60				
Val	Ala	Leu	Glu	Pro	Ser	Gly	Glu	Ala	Phe	Asn	Glu	Leu	Ser	Leu	Asp
65					70					75					80
Gly	Glu	Asn	Arg	Pro	Met	Asn	Pro	Met	Ile	Asn	Ala	Gly	Ala	Ile	Ala
				85					90					95	
Ile	Asn	Gln	Leu	Ile	Asn	Gly	Ser	Asp	Ser	Thr	Val	Glu	Asp	Arg	Val
			100					105					110		
Glu	Lys	Ile	Arg	His	Tyr	Phe	Ser	Glu	Leu	Ala	Gly	Arg	Glu	Leu	Thr
		115					120					125			
Ile	Asp	Arg	Val	Leu	Ala	Glu	Ser	Glu	Leu	Ala	Gly	Ala	Asp	Arg	Asn
	130					135					140				
Leu	Ser	Ile	Ala	His	Met	Leu	Arg	Asn	Tyr	Gly	Val	Ile	Glu	Asp	Glu
145					150					155					160
Ala	His	Asp	Ala	Val	Leu	Ser	Tyr	Thr	Leu	Gln	Cys	Ala	Ile	Lys	Val
				165					170					175	
Thr	Thr	Arg	Asp	Leu	Ala	Val	Met	Thr	Ala	Thr	Leu	Ala	Ala	Gly	Gly
			180					185					190		
Thr	His	Pro	Ile	Thr	Gly	Lys	Lys	Leu	Leu	Asp	Ala	Arg	Val	Cys	Arg
		195					200					205			
Leu	Thr	Leu	Ser	Val	Met	Ala	Ser	Ala	Gly	Met	Tyr	Asp	Glu	Ala	Gly
	210					215					220				
Gln	Trp	Leu	Ser	Thr	Val	Gly	Ile	Pro	Ala	Lys	Ser	Gly	Val	Ala	Gly
225					230					235					240
Gly	Leu	Ile	Gly	Ile	Leu	Pro	Gly	Gln	Leu	Gly	Ile	Ala	Thr	Phe	Ser
				245				250						255	
Pro	Arg	Leu	Asn	Pro	Lys	Gly	Asn	Ser	Val	Arg	Gly	Val	Lys	Ile	Phe
			260					265					270		
Lys	Gln	Leu	Ser	Asp	Asp	Met	Gly	Leu	His	Leu	Met	Ser	Thr	Glu	
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<210> 105
<211> 1155
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1132)
<223> RXA00278
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gtgggtcggc atccgcccc gtttgcagga gtacttataa atg cac gct ttt cga																163
Met His Ala Phe Arg																211
1 5																259
cgc ccc cct cca ctc acc acg cga gtc ggc gct gca ttg ctg gcc gca																307
Arg Pro Pro Pro Leu Thr Thr Arg Val Gly Ala Ala Leu Leu Ala Ala																355
10 15 20																403
acg ctg ctt gct tcc tgc act cca aca cct gtg gaa ccg gca gaa acc																451
Thr Leu Leu Ala Ser Cys Thr Pro Thr Pro Val Glu Pro Ala Glu Thr																499
25 30 35																547
ttg act gct ttg gat ccc gat gcc ggt cca cca ctg cca ccg gat tct																595
Leu Thr Ala Leu Asp Pro Asp Ala Gly Pro Pro Leu Pro Pro Asp Ser																643
40 45 50																
tcg att gaa gct ccc ggt gaa aaa gag ccc att gtg gaa gta ata gag																
Ser Ile Glu Ala Pro Gly Glu Lys Glu Pro Ile Val Glu Val Ile Glu																
55 60 65																
aat tgg cca ggt tct tta cgc ccg gat gat ctg acc cct gag gag cgg																
Asn Trp Pro Gly Ser Leu Arg Pro Asp Asp Leu Thr Pro Glu Glu Arg																
70 75 80 85																
gta cct ggc atc gtc aac cgg ggt cgc atc att gtg ggt gtg gat caa																
Val Pro Gly Ile Val Asn Arg Gly Arg Ile Ile Val Gly Val Asp Gln																
90 95 100																
tcg caa aac ttg ctc agt ttc cgt gat ccg gtg act ggt gag ctg cgc																
Ser Gln Asn Leu Leu Ser Phe Arg Asp Pro Val Thr Gly Glu Leu Arg																
105 110 115																
ggt ttt gaa gtg gaa tta gcg agg gaa att tcc cgc gac att ttc ggt																
Gly Phe Glu Val Glu Leu Ala Arg Glu Ile Ser Arg Asp Ile Phe Gly																
120 125 130																
gac ccc aat aag gtg gat ttc cga ttc gtc ggc tcg tcc gac cgt ctg																
Asp Pro Asn Lys Val Asp Phe Arg Phe Val Gly Ser Ser Asp Arg Leu																
135 140 145																
cgt tcc ctt gac caa ggt gat gta gat att gtg att cgt tcc gtc acg																
Arg Ser Leu Asp Gln Gly Asp Val Asp Ile Val Ile Arg Ser Val Thr																
150 155 160 165																
atc acc gac gaa cgc gcc aaa ttg gtg gaa ttt tcc aca ccg tac ctg																
Ile Thr Asp Glu Arg Ala Lys Leu Val Glu Phe Ser Thr Pro Tyr Leu																
170 175 180																

cgc acc caa acc cgc atg ttg acc atg gaa tct tca gga atc acg tcc 691  
 Arg Thr Gln Thr Arg Met Leu Thr Met Glu Ser Ser Gly Ile Thr Ser  
                   185                                  190                                  195

atc gca gat cta ccc ggc cac acc att tgt gtc acc gat ggc tcc act 739  
 Ile Ala Asp Leu Pro Gly His Thr Ile Cys Val Thr Asp Gly Ser Thr  
                   200                                  205                                  210

tca ttg cag cga gcc cgc acc att gcg ccg gag gcc tca atc tta aaa 787  
 Ser Leu Gln Arg Ala Arg Thr Ile Ala Pro Glu Ala Ser Ile Leu Lys  
                   215                                  220                                  225

act cgc aat tgg tcc gat tgt ctc atg gcg ttg cag cag cat cag gct 835  
 Thr Arg Asn Trp Ser Asp Cys Leu Met Ala Leu Gln Gln His Gln Ala  
 230                                  235                                  240                                  245

cag gtc att ttg ggc gat gat gtc att ttg tcc ggc atc gca gca cag 883  
 Gln Val Ile Leu Gly Asp Asp Val Ile Leu Ser Gly Ile Ala Ala Gln  
                                   250                                  255                                  260

gat ccc tac acc gag att ctt gat acc tcc ctc gat tcc cat tcc tat 931  
 Asp Pro Tyr Thr Glu Ile Leu Asp Thr Ser Leu Asp Ser His Ser Tyr  
                                   265                                  270                                  275

gga gtg gca gcg gca tcg acc act gct gaa aca gac tct tcg ggg ttg 979  
 Gly Val Ala Ala Ala Ser Thr Thr Ala Glu Thr Asp Ser Ser Gly Leu  
                   280                                  285                                  290

att cgg cag gta aac tac aca att gaa cgg atc cgc aca gac cgc atg  
 1027  
 Ile Arg Gln Val Asn Tyr Thr Ile Glu Arg Ile Arg Thr Asp Arg Met  
                   295                                  300                                  305

tgg tgg aca atg ttc gac gat tgg ttc gga cct tat ctc tgg tcc tac  
 1075  
 Trp Trp Thr Met Phe Asp Asp Trp Phe Gly Pro Tyr Leu Trp Ser Tyr  
 310                                  315                                  320                                  325

ggt cca cca cag ctg cag tac atg cca gag gaa gaa ggg aca gaa aac  
 1123  
 Gly Pro Pro Gln Leu Gln Tyr Met Pro Glu Glu Glu Gly Thr Glu Asn  
                                   330                                  335                                  340

gat gaa gga taatgaagat ttcgatccag att  
 1155  
 Asp Glu Gly

<210> 106  
 <211> 344  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 106  
 Met His Ala Phe Arg Arg Pro Pro Pro Leu Thr Thr Arg Val Gly Ala  
   1                                  5                                  10                                  15

Ala Leu Leu Ala Ala Thr Leu Leu Ala Ser Cys Thr Pro Thr Pro Val  
                   20                                  25                                  30

Glu Pro Ala Glu Thr Leu Thr Ala Leu Asp Pro Asp Ala Gly Pro Pro  
 35 40 45  
 Leu Pro Pro Asp Ser Ser Ile Glu Ala Pro Gly Glu Lys Glu Pro Ile  
 50 55 60  
 Val Glu Val Ile Glu Asn Trp Pro Gly Ser Leu Arg Pro Asp Asp Leu  
 65 70 75 80  
 Thr Pro Glu Glu Arg Val Pro Gly Ile Val Asn Arg Gly Arg Ile Ile  
 85 90 95  
 Val Gly Val Asp Gln Ser Gln Asn Leu Leu Ser Phe Arg Asp Pro Val  
 100 105 110  
 Thr Gly Glu Leu Arg Gly Phe Glu Val Glu Leu Ala Arg Glu Ile Ser  
 115 120 125  
 Arg Asp Ile Phe Gly Asp Pro Asn Lys Val Asp Phe Arg Phe Val Gly  
 130 135 140  
 Ser Ser Asp Arg Leu Arg Ser Leu Asp Gln Gly Asp Val Asp Ile Val  
 145 150 155 160  
 Ile Arg Ser Val Thr Ile Thr Asp Glu Arg Ala Lys Leu Val Glu Phe  
 165 170 175  
 Ser Thr Pro Tyr Leu Arg Thr Gln Thr Arg Met Leu Thr Met Glu Ser  
 180 185 190  
 Ser Gly Ile Thr Ser Ile Ala Asp Leu Pro Gly His Thr Ile Cys Val  
 195 200 205  
 Thr Asp Gly Ser Thr Ser Leu Gln Arg Ala Arg Thr Ile Ala Pro Glu  
 210 215 220  
 Ala Ser Ile Leu Lys Thr Arg Asn Trp Ser Asp Cys Leu Met Ala Leu  
 225 230 235 240  
 Gln Gln His Gln Ala Gln Val Ile Leu Gly Asp Asp Val Ile Leu Ser  
 245 250 255  
 Gly Ile Ala Ala Gln Asp Pro Tyr Thr Glu Ile Leu Asp Thr Ser Leu  
 260 265 270  
 Asp Ser His Ser Tyr Gly Val Ala Ala Ala Ser Thr Thr Ala Glu Thr  
 275 280 285  
 Asp Ser Ser Gly Leu Ile Arg Gln Val Asn Tyr Thr Ile Glu Arg Ile  
 290 295 300  
 Arg Thr Asp Arg Met Trp Trp Thr Met Phe Asp Asp Trp Phe Gly Pro  
 305 310 315 320  
 Tyr Leu Trp Ser Tyr Gly Pro Pro Gln Leu Gln Tyr Met Pro Glu Glu  
 325 330 335  
 Glu Gly Thr Glu Asn Asp Glu Gly  
 340



<210> 107  
 <211> 1035  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1012)  
 <223> RXA00727

<400> 107  
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 Leu Arg Phe Pro Lys  
 1 5  
 atc ccc aag cgc gct gta gcg gcg acc gtc ggc atc gtg gca acc tca 163  
 Ile Pro Lys Arg Ala Val Ala Ala Thr Val Gly Ile Val Ala Thr Ser  
 10 15 20  
 ttc acc ttg gct tct tgt gtc acc aat gag gag cag ggc aac cca gat 211  
 Phe Thr Leu Ala Ser Cys Val Thr Asn Glu Glu Gln Gly Asn Pro Asp  
 25 30 35  
 ggc tgg gag cag atc gtt cca gat cct gta ccg gag att cag gcg atg 259  
 Gly Trp Glu Gln Ile Val Pro Asp Pro Val Pro Glu Ile Gln Ala Met  
 40 45 50  
 gtt ccc gaa gct ctg gct cag cgc ggt gtg ctc acc gcc ggt gcc aac 307  
 Val Pro Glu Ala Leu Ala Gln Arg Gly Val Leu Thr Ala Gly Ala Asn  
 55 60 65  
 cca cct ttc cca ccg ttt gag ttt aaa gat tcc gat ggt cag att atc 355  
 Pro Pro Phe Pro Pro Phe Glu Phe Lys Asp Ser Asp Gly Gln Ile Ile  
 70 75 80 85  
 ggt gtg gaa atg gac ctc gtg cgt gca atg gcg ggg gtg atg ggc ttg 403  
 Gly Val Glu Met Asp Leu Val Arg Ala Met Ala Gly Val Met Gly Leu  
 90 95 100  
 gag ttc agc cct cag gag cag gat ttc tcc ctc atc ctt cca tcg gtt 451  
 Glu Phe Ser Pro Gln Glu Gln Asp Phe Ser Leu Ile Leu Pro Ser Val  
 105 110 115  
 caa gct ggc acc ctt gat atc gga gcc tct ggc ttc act gac aac gag 499  
 Gln Ala Gly Thr Leu Asp Ile Gly Ala Ser Gly Phe Thr Asp Asn Glu  
 120 125 130  
 gaa cgc cgc gag aac ttt gat ttc atc gat ttc ctc ttc gca ggt gtg 547  
 Glu Arg Arg Glu Asn Phe Asp Phe Ile Asp Phe Leu Phe Ala Gly Val  
 135 140 145  
 cag tgg gcg cag gca act gat cgt gaa acc cca atc gat ccg gaa aac 595  
 Gln Trp Ala Gln Ala Thr Asp Arg Glu Thr Pro Ile Asp Pro Glu Asn  
 150 155 160 165  
 gcc tgt ggt ctc acc gtt gct gta cag cgc aca acc gtg gca gag acc 643  
 Ala Cys Gly Leu Thr Val Ala Val Gln Arg Thr Thr Val Ala Glu Thr  
 170 175 180

gac gat gtc cgt cct cgc tca gct caa tgt gaa gcc gaa ggc aaa gag 691  
 Asp Asp Val Arg Pro Arg Ser Ala Gln Cys Glu Ala Glu Gly Lys Glu  
 185 190 195

ccg atc acc att ttg tct tat gaa acc gca gat act gca gct acc gca 739  
 Pro Ile Thr Ile Leu Ser Tyr Glu Thr Ala Asp Thr Ala Ala Thr Ala  
 200 205 210

ttg atc ctg gga cgc gca gac gca ctt gct gcg gac tcc cct gtt tca 787  
 Leu Ile Leu Gly Arg Ala Asp Ala Leu Ala Ala Asp Ser Pro Val Ser  
 215 220 225

gct tgg gct gca gag cgc tcc gaa ggc cgc atc gaa gtt gtg ggc gat 835  
 Ala Trp Ala Ala Glu Arg Ser Glu Gly Arg Ile Glu Val Val Gly Asp  
 230 235 240 245

atg tac ttg gct gcg cca ttt ggt ttc gca ttc ccg ttg gaa tct gac 883  
 Met Tyr Leu Ala Ala Pro Phe Gly Phe Ala Phe Pro Leu Glu Ser Asp  
 250 255 260

ctc acc cca gca gca gct gcg gcg ttc caa cac ttg att gac acc ggc 931  
 Leu Thr Pro Ala Ala Ala Ala Ala Phe Gln His Leu Ile Asp Thr Gly  
 265 270 275

gat tac cag cgc atc atg gcg caa tgg ggc att gaa gaa ggc ctt ctt 979  
 Asp Tyr Gln Arg Ile Met Ala Gln Trp Gly Ile Glu Glu Gly Leu Leu  
 280 285 290

gat gag gcc ctg atc aac gaa cag cca ctc aac tagagccttc cagcaactaa  
 1032  
 Asp Glu Ala Leu Ile Asn Glu Gln Pro Leu Asn  
 295 300

aaa  
 1035

<210> 108  
 <211> 304  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 108  
 Leu Arg Phe Pro Lys Ile Pro Lys Arg Ala Val Ala Ala Thr Val Gly  
 1 5 10 15  
 Ile Val Ala Thr Ser Phe Thr Leu Ala Ser Cys Val Thr Asn Glu Glu  
 20 25 30  
 Gln Gly Asn Pro Asp Gly Trp Glu Gln Ile Val Pro Asp Pro Val Pro  
 35 40 45  
 Glu Ile Gln Ala Met Val Pro Glu Ala Leu Ala Gln Arg Gly Val Leu  
 50 55 60  
 Thr Ala Gly Ala Asn Pro Pro Phe Pro Pro Phe Glu Phe Lys Asp Ser  
 65 70 75 80  
 Asp Gly Gln Ile Ile Gly Val Glu Met Asp Leu Val Arg Ala Met Ala  
 85 90 95

Gly Val Met Gly Leu Glu Phe Ser Pro Gln Glu Gln Asp Phe Ser Leu  
 100 105 110  
 Ile Leu Pro Ser Val Gln Ala Gly Thr Leu Asp Ile Gly Ala Ser Gly  
 115 120 125  
 Phe Thr Asp Asn Glu Glu Arg Arg Glu Asn Phe Asp Phe Ile Asp Phe  
 130 135 140  
 Leu Phe Ala Gly Val Gln Trp Ala Gln Ala Thr Asp Arg Glu Thr Pro  
 145 150 155 160  
 Ile Asp Pro Glu Asn Ala Cys Gly Leu Thr Val Ala Val Gln Arg Thr  
 165 170 175  
 Thr Val Ala Glu Thr Asp Asp Val Arg Pro Arg Ser Ala Gln Cys Glu  
 180 185 190  
 Ala Glu Gly Lys Glu Pro Ile Thr Ile Leu Ser Tyr Glu Thr Ala Asp  
 195 200 205  
 Thr Ala Ala Thr Ala Leu Ile Leu Gly Arg Ala Asp Ala Leu Ala Ala  
 210 215 220  
 Asp Ser Pro Val Ser Ala Trp Ala Ala Glu Arg Ser Glu Gly Arg Ile  
 225 230 235 240  
 Glu Val Val Gly Asp Met Tyr Leu Ala Ala Pro Phe Gly Phe Ala Phe  
 245 250 255  
 Pro Leu Glu Ser Asp Leu Thr Pro Ala Ala Ala Ala Phe Gln His  
 260 265 270  
 Leu Ile Asp Thr Gly Asp Tyr Gln Arg Ile Met Ala Gln Trp Gly Ile  
 275 280 285  
 Glu Glu Gly Leu Leu Asp Glu Ala Leu Ile Asn Glu Gln Pro Leu Asn  
 290 295 300

<210> 109  
 <211> 1962  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1939)  
 <223> RXA02139

<400> 109  
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 Met Arg His Arg Gly  
 1 5  
 cct gac gat gcc ggc act tgg cat gac gcc gat gca gcg ttt gga ttc 163

Pro	Asp	Asp	Ala	Gly	Thr	Trp	His	Asp	Ala	Asp	Ala	Ala	Phe	Gly	Phe		
				10					15					20			
aac	cgc	ctc	tcc	atc	att	gat	att	gca	cac	tcc	cac	caa	cca	ctg	cgt	211	
Asn	Arg	Leu	Ser	Ile	Ile	Asp	Ile	Ala	His	Ser	His	Gln	Pro	Leu	Arg		
			25					30					35				
tgg	gga	cct	gcg	gat	gaa	ccc	gac	cgc	tac	gca	atg	act	ttc	aac	ggt	259	
Trp	Gly	Pro	Ala	Asp	Glu	Pro	Asp	Arg	Tyr	Ala	Met	Thr	Phe	Asn	Gly		
		40					45					50					
gag	atc	tac	aac	tac	gtt	gag	ctg	cgt	aaa	gag	ctc	tcg	gat	ttg	gga	307	
Glu	Ile	Tyr	Asn	Tyr	Val	Glu	Leu	Arg	Lys	Glu	Leu	Ser	Asp	Leu	Gly		
	55					60					65						
tat	gcc	ttt	aat	act	tct	ggc	gat	ggc	gag	cca	att	gtt	gtc	ggt	ttc	355	
Tyr	Ala	Phe	Asn	Thr	Ser	Gly	Asp	Gly	Glu	Pro	Ile	Val	Val	Gly	Phe		
	70				75					80					85		
cac	cac	tgg	ggc	gag	tcc	gtg	gtc	gag	cat	ctc	cgc	gga	atg	ttc	ggc	403	
His	His	Trp	Gly	Glu	Ser	Val	Val	Glu	His	Leu	Arg	Gly	Met	Phe	Gly		
				90					95					100			
att	gcc	att	tgg	gat	aca	aag	gaa	aag	tcg	ctt	ttc	ctt	gcg	cgt	gat	451	
Ile	Ala	Ile	Trp	Asp	Thr	Lys	Glu	Lys	Ser	Leu	Phe	Leu	Ala	Arg	Asp		
			105					110					115				
cag	ttc	ggc	att	aag	cca	ctg	ttc	tac	gca	acc	acc	gag	cat	ggc	acc	499	
Gln	Phe	Gly	Ile	Lys	Pro	Leu	Phe	Tyr	Ala	Thr	Thr	Glu	His	Gly	Thr		
		120					125					130					
gtg	ttc	tcc	tca	gag	aag	aag	acc	atc	ttg	gag	atg	gcc	gag	gag	atg	547	
Val	Phe	Ser	Ser	Glu	Lys	Lys	Thr	Ile	Leu	Glu	Met	Ala	Glu	Glu	Met		
	135					140					145						
aat	cta	gat	ctg	ggc	ctt	gat	aag	cgc	acc	att	gag	cac	tac	gtg	gac	595	
Asn	Leu	Asp	Leu	Gly	Leu	Asp	Lys	Arg	Thr	Ile	Glu	His	Tyr	Val	Asp		
	150				155					160					165		
ttg	cag	tac	gtg	ccc	gag	cca	gat	acc	ctt	cac	gcg	cag	att	tcc	cgc	643	
Leu	Gln	Tyr	Val	Pro	Glu	Pro	Asp	Thr	Leu	His	Ala	Gln	Ile	Ser	Arg		
				170					175					180			
ttg	gag	tca	ggc	tgc	acc	gca	aca	gtt	cgt	ccg	ggc	ggc	aag	ctg	gaa	691	
Leu	Glu	Ser	Gly	Cys	Thr	Ala	Thr	Val	Arg	Pro	Gly	Gly	Lys	Leu	Glu		
			185					190					195				
cag	aag	cgt	tac	ttc	aag	cct	cag	ttc	cca	gta	cag	aag	gtc	gta	aag	739	
Gln	Lys	Arg	Tyr	Phe	Lys	Pro	Gln	Phe	Pro	Val	Gln	Lys	Val	Val	Lys		
		200					205					210					
ggt	aag	gag	cag	gac	ctc	ttc	gat	cgc	att	gcc	cag	gtg	ttg	gag	gat	787	
Gly	Lys	Glu	Gln	Asp	Leu	Phe	Asp	Arg	Ile	Ala	Gln	Val	Leu	Glu	Asp		
	215					220					225						
agc	gtc	gaa	aag	cat	atg	cgt	gcc	gac	gtg	acc	gta	ggc	tcg	ttc	ctt	835	
Ser	Val	Glu	Lys	His	Met	Arg	Ala	Asp	Val	Thr	Val	Gly	Ser	Phe	Leu		
	230				235					240					245		
ttc	ggc	ggc	att	gac	tca	acc	gca	att	gcg	gcg	ctt	gca	aag	cgc	cac	883	
Phe	Gly	Gly	Ile	Asp	Ser	Thr	Ala	Ile	Ala	Ala	Leu	Ala	Lys	Arg	His		

250										255					260					
aac	cct	gac	ctg	ctc	acc	ttc	acc	acc	ggc	ttc	gag	cgt	gaa	ggc	tac	931				
Asn	Pro	Asp	Leu	Leu	Thr	Phe	Thr	Thr	Gly	Phe	Glu	Arg	Glu	Gly	Tyr					
			265						270				275							
tcg	gag	gtc	gat	gtg	gct	gcg	gag	tcc	gcc	gct	gcg	att	ggc	gct	gag	979				
Ser	Glu	Val	Asp	Val	Ala	Ala	Glu	Ser	Ala	Ala	Ala	Ile	Gly	Ala	Glu					
		280					285					290								
cac	atc	gtg	aag	att	gtc	tcg	cct	gag	gaa	tac	gcc	aac	gcg	att	cct					
1027																				
His	Ile	Val	Lys	Ile	Val	Ser	Pro	Glu	Glu	Tyr	Ala	Asn	Ala	Ile	Pro					
	295					300					305									
aag	atc	atg	tgg	tac	ttg	gat	gat	cct	gta	gct	gac	cca	tca	ttg	gtc					
1075																				
Lys	Ile	Met	Trp	Tyr	Leu	Asp	Asp	Pro	Val	Ala	Asp	Pro	Ser	Leu	Val					
310					315					320					325					
ccg	ctg	tac	ttc	gtg	gca	gcg	gaa	gca	cgt	aag	cac	gtc	aag	gtt	gtg					
1123																				
Pro	Leu	Tyr	Phe	Val	Ala	Ala	Glu	Ala	Arg	Lys	His	Val	Lys	Val	Val					
			330						335					340						
ctg	tct	ggc	gag	ggc	gca	gat	gag	ctg	ttc	ggc	gga	tac	acc	att	tac					
1171																				
Leu	Ser	Gly	Glu	Gly	Ala	Asp	Glu	Leu	Phe	Gly	Gly	Tyr	Thr	Ile	Tyr					
		345					350						355							
aag	gag	ccg	cta	tcg	ctt	gct	cca	ttt	gag	aag	atc	cct	tcc	cca	cta					
1219																				
Lys	Glu	Pro	Leu	Ser	Leu	Ala	Pro	Phe	Glu	Lys	Ile	Pro	Ser	Pro	Leu					
	360						365					370								
cgt	aaa	ggc	ctg	gga	aag	ctc	agc	aag	gtt	ctg	cca	gac	ggc	atg	aag					
1267																				
Arg	Lys	Gly	Leu	Gly	Lys	Leu	Ser	Lys	Val	Leu	Pro	Asp	Gly	Met	Lys					
	375					380					385									
ggc	aag	tcc	ctt	ctt	gag	cgt	ggc	tcc	atg	acc	atg	gaa	gag	cgc	tac					
1315																				
Gly	Lys	Ser	Leu	Leu	Glu	Arg	Gly	Ser	Met	Thr	Met	Glu	Glu	Arg	Tyr					
390					395				400						405					
tac	ggc	aac	gct	cgc	tcc	ttc	aat	ttc	gag	cag	atg	caa	cgc	gtt	att					
1363																				
Tyr	Gly	Asn	Ala	Arg	Ser	Phe	Asn	Phe	Glu	Gln	Met	Gln	Arg	Val	Ile					
			410						415					420						
cca	tgg	gca	aag	cgc	gaa	tgg	gac	cac	cgc	gaa	gtc	act	gcg	ccg	atc					
1411																				
Pro	Trp	Ala	Lys	Arg	Glu	Trp	Asp	His	Arg	Glu	Val	Thr	Ala	Pro	Ile					
		425					430						435							
tac	gca	cag	tcc	cgc	aac	ttt	gat	cca	gta	gcc	cgc	atg	caa	cac	ctg					
1459																				
Tyr	Ala	Gln	Ser	Arg	Asn	Phe	Asp	Pro	Val	Ala	Arg	Met	Gln	His	Leu					
	440						445					450								

gat ctg ttc acc tgg atg cgc ggc gac atc ctg gtc aag gct gac aag  
1507

Asp Leu Phe Thr Trp Met Arg Gly Asp Ile Leu Val Lys Ala Asp Lys  
455 460 465

atc aac atg gcg aac tcc ctt gag ctg cga gtt cca ttc ttg gat aag  
1555

Ile Asn Met Ala Asn Ser Leu Glu Leu Arg Val Pro Phe Leu Asp Lys  
470 475 480 485

gaa gtt ttc aag gtt gca gag acc att cct tac gac ctg aag att gcc  
1603

Glu Val Phe Lys Val Ala Glu Thr Ile Pro Tyr Asp Leu Lys Ile Ala  
490 495 500

aac ggt acc acc aag tac gcg ctg cgc agg gca ctc gag cag att gtt  
1651

Asn Gly Thr Thr Lys Tyr Ala Leu Arg Arg Ala Leu Glu Gln Ile Val  
505 510 515

ccg cct cac gtt ttg cac cgc aag aag ctg ggc ttc cct gtt ccc atg  
1699

Pro Pro His Val Leu His Arg Lys Lys Leu Gly Phe Pro Val Pro Met  
520 525 530

cgc cac tgg ctt gcc ggc gat gag ctg ttc ggt tgg gcg cag gac acc  
1747

Arg His Trp Leu Ala Gly Asp Glu Leu Phe Gly Trp Ala Gln Asp Thr  
535 540 545

atc aag gaa tcc ggt act gaa gat atc ttc aac aag cag gct gtg ctg  
1795

Ile Lys Glu Ser Gly Thr Glu Asp Ile Phe Asn Lys Gln Ala Val Leu  
550 555 560 565

gat atg ctg aac gag cac cgc gat ggc gtg tca gat cat tcc cgt cga  
1843

Asp Met Leu Asn Glu His Arg Asp Gly Val Ser Asp His Ser Arg Arg  
570 575 580

ctg tgg act gtt ctg tca ttt atg gtg tgg cac ggc att ttt gtg gaa  
1891

Leu Trp Thr Val Leu Ser Phe Met Val Trp His Gly Ile Phe Val Glu  
585 590 595

aac cgc att gat cca cag att gag gac cgc tcc tac cca gtc gag ctt  
1939

Asn Arg Ile Asp Pro Gln Ile Glu Asp Arg Ser Tyr Pro Val Glu Leu  
600 605 610

taagtcttaa agcctaaacc ccc  
1962

<210> 110

<211> 613

<212> PRT

<213> Corynebacterium glutamicum

<400> 110

Met Arg His Arg Gly Pro Asp Asp Ala Gly Thr Trp His Asp Ala Asp

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Ala Ala Phe Gly Phe Asn Arg Leu Ser Ile Ile Asp Ile Ala His Ser	20	25	30
His Gln Pro Leu Arg Trp Gly Pro Ala Asp Glu Pro Asp Arg Tyr Ala	35	40	45
Met Thr Phe Asn Gly Glu Ile Tyr Asn Tyr Val Glu Leu Arg Lys Glu	50	55	60
Leu Ser Asp Leu Gly Tyr Ala Phe Asn Thr Ser Gly Asp Gly Glu Pro	65	70	75
Ile Val Val Gly Phe His His Trp Gly Glu Ser Val Val Glu His Leu	85	90	95
Arg Gly Met Phe Gly Ile Ala Ile Trp Asp Thr Lys Glu Lys Ser Leu	100	105	110
Phe Leu Ala Arg Asp Gln Phe Gly Ile Lys Pro Leu Phe Tyr Ala Thr	115	120	125
Thr Glu His Gly Thr Val Phe Ser Ser Glu Lys Lys Thr Ile Leu Glu	130	135	140
Met Ala Glu Glu Met Asn Leu Asp Leu Gly Leu Asp Lys Arg Thr Ile	145	150	155
Glu His Tyr Val Asp Leu Gln Tyr Val Pro Glu Pro Asp Thr Leu His	165	170	175
Ala Gln Ile Ser Arg Leu Glu Ser Gly Cys Thr Ala Thr Val Arg Pro	180	185	190
Gly Gly Lys Leu Glu Gln Lys Arg Tyr Phe Lys Pro Gln Phe Pro Val	195	200	205
Gln Lys Val Val Lys Gly Lys Glu Gln Asp Leu Phe Asp Arg Ile Ala	210	215	220
Gln Val Leu Glu Asp Ser Val Glu Lys His Met Arg Ala Asp Val Thr	225	230	235
Val Gly Ser Phe Leu Phe Gly Gly Ile Asp Ser Thr Ala Ile Ala Ala	245	250	255
Leu Ala Lys Arg His Asn Pro Asp Leu Leu Thr Phe Thr Thr Gly Phe	260	265	270
Glu Arg Glu Gly Tyr Ser Glu Val Asp Val Ala Ala Glu Ser Ala Ala	275	280	285
Ala Ile Gly Ala Glu His Ile Val Lys Ile Val Ser Pro Glu Glu Tyr	290	295	300
Ala Asn Ala Ile Pro Lys Ile Met Trp Tyr Leu Asp Asp Pro Val Ala	305	310	315
Asp Pro Ser Leu Val Pro Leu Tyr Phe Val Ala Ala Glu Ala Arg Lys	325	330	335

His Val Lys Val Val Leu Ser Gly Glu Gly Ala Asp Glu Leu Phe Gly  
 340 345 350  
 Gly Tyr Thr Ile Tyr Lys Glu Pro Leu Ser Leu Ala Pro Phe Glu Lys  
 355 360 365  
 Ile Pro Ser Pro Leu Arg Lys Gly Leu Gly Lys Leu Ser Lys Val Leu  
 370 375 380  
 Pro Asp Gly Met Lys Gly Lys Ser Leu Leu Glu Arg Gly Ser Met Thr  
 385 390 395 400  
 Met Glu Glu Arg Tyr Tyr Gly Asn Ala Arg Ser Phe Asn Phe Glu Gln  
 405 410 415  
 Met Gln Arg Val Ile Pro Trp Ala Lys Arg Glu Trp Asp His Arg Glu  
 420 425 430  
 Val Thr Ala Pro Ile Tyr Ala Gln Ser Arg Asn Phe Asp Pro Val Ala  
 435 440 445  
 Arg Met Gln His Leu Asp Leu Phe Thr Trp Met Arg Gly Asp Ile Leu  
 450 455 460  
 Val Lys Ala Asp Lys Ile Asn Met Ala Asn Ser Leu Glu Leu Arg Val  
 465 470 475 480  
 Pro Phe Leu Asp Lys Glu Val Phe Lys Val Ala Glu Thr Ile Pro Tyr  
 485 490 495  
 Asp Leu Lys Ile Ala Asn Gly Thr Thr Lys Tyr Ala Leu Arg Arg Ala  
 500 505 510  
 Leu Glu Gln Ile Val Pro Pro His Val Leu His Arg Lys Lys Leu Gly  
 515 520 525  
 Phe Pro Val Pro Met Arg His Trp Leu Ala Gly Asp Glu Leu Phe Gly  
 530 535 540  
 Trp Ala Gln Asp Thr Ile Lys Glu Ser Gly Thr Glu Asp Ile Phe Asn  
 545 550 555 560  
 Lys Gln Ala Val Leu Asp Met Leu Asn Glu His Arg Asp Gly Val Ser  
 565 570 575  
 Asp His Ser Arg Arg Leu Trp Thr Val Leu Ser Phe Met Val Trp His  
 580 585 590  
 Gly Ile Phe Val Glu Asn Arg Ile Asp Pro Gln Ile Glu Asp Arg Ser  
 595 600 605  
 Tyr Pro Val Glu Leu  
 610

&lt;210&gt; 111

&lt;211&gt; 1284

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1261)

&lt;223&gt; RXN00116

&lt;400&gt; 111

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tttgcgcacc aatcaatggg ggatcaaata tagtagctgc atg agt aat gac ttc 115  
Met Ser Asn Asp Phe  
1 5

gtc gtt tct agg ctt aga ccc ttt ggt gaa acg att ttt gca acc atg 163  
Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr Ile Phe Ala Thr Met  
10 15 20

acc cag cga gct gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt 211  
Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe  
25 30 35

cct gat gag gat ggt cct cgt cgg atg tta gag atc gcg tcg gag cag 259  
Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln  
40 45 50

att ctc ggg gga aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg 307  
Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser  
55 60 65

ttg agg gca gct gtg gct cgt gat cat ttg gag agg ttt gat ctg gag 355  
Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu  
70 75 80 85

tac aac cct gat tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg 403  
Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala  
90 95 100

att acg gcg act gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc 451  
Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile  
105 110 115

gtt ttg gaa ccg tat tac gat gcg tat gcg gcg gct att gcg ttg gcg 499  
Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala  
120 125 130

ggg gcg acg ccg gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg 547  
Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp  
135 140 145

gat gtg gat gtc gat aag ttg cat gcg gcg gtg act aag aag acg ccg 595  
Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg  
150 155 160 165

atg att atc gtt aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct 643  
Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser  
170 175 180

aag aag gcg ttg aag cag ttg gcg ggt gtt gct cgt gcg tat gac ttg 691  
Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala Arg Ala Tyr Asp Leu  
185 190 195

ttg gtg ttg tca gat gag gtg tat gag cat ctt gtt ttt gat gat cag 739

Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu Val Phe Asp Asp Gln  
 200 205 210  
 aag cat gtg agt gtc gcg aag ctg ccc ggt atg tgg gat cgc acg gtg 787  
 Lys His Val Ser Val Ala Lys Leu Pro Gly Met Trp Asp Arg Thr Val  
 215 220 225  
 acg gtg tcg tcg gcg gcg aaa acg ttc aat gtg act ggt tgg aag acg 835  
 Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val Thr Gly Trp Lys Thr  
 230 235 240 245  
 ggg tgg gcg ttg gca ccg gag ccg ttg ttg gag gcg gtg ttg aag gcg 883  
 Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu Ala Val Leu Lys Ala  
 250 255 260  
 aag cag ttt atg tct tat gtg ggg gct aca cct ttt cag ccg gct gtg 931  
 Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro Phe Gln Pro Ala Val  
 265 270 275  
 gcg cat gcg att gaa cat gag cag aag tgg gtg tca aag atg tct aag 979  
 Ala His Ala Ile Glu His Glu Gln Lys Trp Val Ser Lys Met Ser Lys  
 280 285 290  
 ggg ctt gag ctc aag cgg gat att ttg cgt act gcg tta gat aag gcg  
 1027  
 Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr Ala Leu Asp Lys Ala  
 295 300 305  
 ggg ctg aag act cat gac agt atg ggc acg tat ttc atc gtt gcg gat  
 1075  
 Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr Phe Ile Val Ala Asp  
 310 315 320 325  
 att ggg gat cgt gat ggt gcg gag ttc tgt ttt gag ttg att gag aag  
 1123  
 Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe Glu Leu Ile Glu Lys  
 330 335 340  
 gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag  
 1171  
 Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys  
 345 350 355  
 aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg  
 1219  
 Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr  
 360 365 370  
 ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta  
 1261  
 Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu  
 375 380 385  
 tagtttgaac aggttggttg ggg  
 1284

&lt;210&gt; 112

&lt;211&gt; 387

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 112

Met	Ser	Asn	Asp	Phe	Val	Val	Ser	Arg	Leu	Arg	Pro	Phe	Gly	Glu	Thr
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Ile	Phe	Ala	Thr	Met	Thr	Gln	Arg	Ala	Val	Glu	Ala	Gly	Ala	Ile	Asn
			20					25					30		
Leu	Gly	Gln	Gly	Phe	Pro	Asp	Glu	Asp	Gly	Pro	Arg	Arg	Met	Leu	Glu
		35					40					45			
Ile	Ala	Ser	Glu	Gln	Ile	Leu	Gly	Gly	Asn	Asn	Gln	Tyr	Ser	Ala	Gly
	50					55					60				
Arg	Gly	Asp	Ala	Ser	Leu	Arg	Ala	Ala	Val	Ala	Arg	Asp	His	Leu	Glu
65					70					75					80
Arg	Phe	Asp	Leu	Glu	Tyr	Asn	Pro	Asp	Ser	Glu	Val	Leu	Ile	Thr	Val
			85						90					95	
Gly	Ala	Thr	Glu	Ala	Ile	Thr	Ala	Thr	Val	Leu	Gly	Leu	Val	Glu	Pro
			100					105					110		
Gly	Asp	Glu	Val	Ile	Val	Leu	Glu	Pro	Tyr	Tyr	Asp	Ala	Tyr	Ala	Ala
		115					120					125			
Ala	Ile	Ala	Leu	Ala	Gly	Ala	Thr	Arg	Val	Ala	Val	Pro	Leu	Gln	Glu
	130					135					140				
Val	Glu	Asn	Ser	Trp	Asp	Val	Asp	Val	Asp	Lys	Leu	His	Ala	Ala	Val
145					150					155					160
Thr	Lys	Lys	Thr	Arg	Met	Ile	Ile	Val	Asn	Ser	Pro	His	Asn	Pro	Thr
				165					170					175	
Gly	Ser	Val	Phe	Ser	Lys	Lys	Ala	Leu	Lys	Gln	Leu	Ala	Gly	Val	Ala
			180					185					190		
Arg	Ala	Tyr	Asp	Leu	Leu	Val	Leu	Ser	Asp	Glu	Val	Tyr	Glu	His	Leu
		195					200					205			
Val	Phe	Asp	Asp	Gln	Lys	His	Val	Ser	Val	Ala	Lys	Leu	Pro	Gly	Met
	210					215					220				
Trp	Asp	Arg	Thr	Val	Thr	Val	Ser	Ser	Ala	Ala	Lys	Thr	Phe	Asn	Val
225					230					235					240
Thr	Gly	Trp	Lys	Thr	Gly	Trp	Ala	Leu	Ala	Pro	Glu	Pro	Leu	Leu	Glu
				245					250					255	
Ala	Val	Leu	Lys	Ala	Lys	Gln	Phe	Met	Ser	Tyr	Val	Gly	Ala	Thr	Pro
			260					265					270		
Phe	Gln	Pro	Ala	Val	Ala	His	Ala	Ile	Glu	His	Glu	Gln	Lys	Trp	Val
		275					280					285			
Ser	Lys	Met	Ser	Lys	Gly	Leu	Glu	Leu	Lys	Arg	Asp	Ile	Leu	Arg	Thr
		290				295					300				
Ala	Leu	Asp	Lys	Ala	Gly	Leu	Lys	Thr	His	Asp	Ser	Met	Gly	Thr	Tyr
305					310					315					320

Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe  
 325 330 335

Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe  
 340 345 350

Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys  
 355 360 365

Lys Lys Glu Glu Thr Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile  
 370 375 380

Lys Lys Leu  
 385

<210> 113

<211> 607

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(607)

<223> FRXA00116

<400> 113

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ttctaggctt agaccctttg gtgaaacgat ttttgcaacc atg acc cag cga gct 115  
 Met Thr Gln Arg Ala  
 1 5

gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt cct gat gag gat 163  
 Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp  
 10 15 20

ggt cct cgt cgg atg tta gag atc gcg tcg gag cag att ctc ggg gga 211  
 Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly  
 25 30 35

aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg ttg agg gca gct 259  
 Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala  
 40 45 50

gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat 307  
 Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp  
 55 60 65

tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act 355  
 Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr  
 70 75 80 85

gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg 403  
 Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro  
 90 95 100

tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg ccg 451  
 Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg  
 105 110 115

gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg gat gtg gat gtc 499  
 Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val  
           120                          125                          130

gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt 547  
 Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val  
           135                          140                          145

aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg 595  
 Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu  
           150                          155                          160                          165

aag cag ttg gcg 607  
 Lys Gln Leu Ala

<210> 114  
 <211> 169  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 114  
 Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly  
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Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu  
           20                          25                          30

Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala  
           35                          40                          45

Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu  
           50                          55                          60

Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu  
           65                          70                          75                          80

Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val  
           85                          90                          95

Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu  
           100                          105                          110

Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser  
           115                          120                          125

Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr  
           130                          135                          140

Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe  
           145                          150                          155                          160

Ser Lys Lys Ala Leu Lys Gln Leu Ala  
           165

<210> 115  
 <211> 1230  
 <212> DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1207)

&lt;223&gt; RXN00618

&lt;400&gt; 115

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gaagccaagc actagaagca atgttcagcc gtttcgcgctc atg cag atg ttg gac 115  
Met Gln Met Leu Asp  
1 5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163  
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys  
10 15 20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211  
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala  
25 30 35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259  
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly  
40 45 50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307  
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr  
55 60 65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355  
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser  
70 75 80 85

ggt gga ttc gtg gca tcg ttt atc gcc acc ttg gat cac ggg gat tat 403  
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu Asp His Gly Asp Tyr  
90 95 100

gtg gca atg cct acc ccg ggg tac ccg gca tat cgc aat att ctg gaa 451  
Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr Arg Asn Ile Leu Glu  
105 110 115

tct ttg ggg gcg aag gtt ctg aac ctg cgc tgt act gca gag act cgt 499  
Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys Thr Ala Glu Thr Arg  
120 125 130

ttc cag cca acc gct caa atg ttg gag gaa ctg cca cac aag ccg aag 547  
Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu Pro His Lys Pro Lys  
135 140 145

gct gtt att gtc acc agc cca gga aac cca acg ggc acc atc att gat 595  
Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr Gly Thr Ile Ile Asp  
150 155 160 165

ccg gaa gag cta gag cgc atc gcc aag tgg tgc gat gac aat gat gct 643  
Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys Asp Asp Asn Asp Ala  
170 175 180

gtt ctt atc tct gat gag gac tac cac ggc atg agc ttt ggt cgt ccg 691  
Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met Ser Phe Gly Arg Pro  
185 190 195

ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt acc 739  
 Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly Thr  
 200 205 210

ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc atc 787  
 Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile Ile  
 215 220 225

gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct ctt 835  
 Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser Leu  
 230 235 240 245

tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc ttc 883  
 Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala Phe  
 250 255 260

act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat cgc 931  
 Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr Arg  
 265 270 275

gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt ggc 979  
 Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu Gly  
 280 285 290

act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt tct  
 1027  
 Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val Ser  
 295 300 305

gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat gaa  
 1075  
 Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp Glu  
 310 315 320 325

gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa ggc  
 1123  
 Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu Gly  
 330 335 340

cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc att  
 1171  
 His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile  
 345 350 355

gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac  
 1217  
 Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys  
 360 365

taggttagtt tcg  
 1230

&lt;210&gt; 116

&lt;211&gt; 369

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 116

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp

1	5	10	15												
Thr	Leu	Met	Phe	Cys	Ala	Gly	Gln	Pro	Ser	Thr	Gly	Ala	Pro	Glu	Ala
			20					25					30		
Val	Ile	Glu	Glu	Ala	Glu	Ile	Ala	Leu	Arg	Ser	Gly	Pro	Leu	Gly	Tyr
		35					40					45			
Thr	Glu	Val	Ile	Gly	Asp	Arg	Glu	Phe	Arg	Glu	Arg	Ile	Ala	Asp	Trp
	50					55					60				
His	Ser	Ala	Thr	Tyr	Asp	Val	Asp	Thr	Asn	Pro	Asp	Asn	Val	Ile	Val
	65				70					75					80
Thr	Thr	Gly	Ser	Ser	Gly	Gly	Phe	Val	Ala	Ser	Phe	Ile	Ala	Thr	Leu
				85					90					95	
Asp	His	Gly	Asp	Tyr	Val	Ala	Met	Pro	Thr	Pro	Gly	Tyr	Pro	Ala	Tyr
			100					105					110		
Arg	Asn	Ile	Leu	Glu	Ser	Leu	Gly	Ala	Lys	Val	Leu	Asn	Leu	Arg	Cys
		115					120					125			
Thr	Ala	Glu	Thr	Arg	Phe	Gln	Pro	Thr	Ala	Gln	Met	Leu	Glu	Glu	Leu
	130					135					140				
Pro	His	Lys	Pro	Lys	Ala	Val	Ile	Val	Thr	Ser	Pro	Gly	Asn	Pro	Thr
	145				150					155					160
Gly	Thr	Ile	Ile	Asp	Pro	Glu	Glu	Leu	Glu	Arg	Ile	Ala	Lys	Trp	Cys
				165					170					175	
Asp	Asp	Asn	Asp	Ala	Val	Leu	Ile	Ser	Asp	Glu	Asp	Tyr	His	Gly	Met
			180					185					190		
Ser	Phe	Gly	Arg	Pro	Leu	Ala	Thr	Ala	His	Gln	Phe	Ser	Lys	Asn	Ala
		195					200					205			
Ile	Val	Val	Gly	Thr	Leu	Ser	Lys	Tyr	Phe	Ser	Met	Thr	Gly	Trp	Arg
	210					215					220				
Val	Gly	Trp	Ile	Ile	Val	Pro	Asp	Glu	Leu	Val	Thr	Pro	Ile	Glu	Asn
	225				230					235					240
Leu	Gln	Ala	Ser	Leu	Ser	Leu	Cys	Ala	Pro	Ala	Ile	Gly	Gln	Ala	Ala
				245					250					255	
Gly	Arg	Ala	Ala	Phe	Thr	Leu	Glu	Ala	Gly	Ala	Glu	Leu	Asp	Ala	His
			260					265					270		
Val	Glu	Ala	Tyr	Arg	Glu	Ala	Arg	Glu	Val	Phe	Val	Asp	Lys	Leu	Pro
		275					280					285			
Glu	Ile	Gly	Leu	Gly	Thr	Phe	Ala	Asp	Pro	Asp	Gly	Gly	Leu	Tyr	Leu
	290					295					300				
Trp	Val	Asp	Val	Ser	Ala	Tyr	Thr	Asp	Asp	Ser	Glu	Glu	Trp	Ala	Leu
	305				310					315					320
Arg	Leu	Leu	Asp	Glu	Ala	Gly	Val	Ala	Val	Ala	Pro	Gly	Val	Asp	Phe
				325					330					335	



Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser  
                   340                                  345                                  350

Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys  
                   355                                  360                                  365

Lys

<210> 117

<211> 657

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(634)

<223> FRXA00618

<400> 117

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caatgatgct gttcttatct ctgatgagga ctaccacggc atg agc ttt ggt cgt 115  
   Met Ser Phe Gly Arg  
   1                                  5

ccg ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt 163  
  Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly  
                                   10                                  15                                  20

acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc 211  
  Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile  
                                   25                                  30                                  35

atc gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct 259  
  Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser  
                                   40                                  45                                  50

ctt tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc 307  
  Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala  
                                   55                                  60                                  65

ttc act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat 355  
  Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr  
   70                                  75                                  80                                  85

cgc gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt 403  
  Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu  
                                   90                                  95                                  100

ggc act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt 451  
  Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val  
                                   105                                  110                                  115

tct gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat 499  
  Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp  
                                   120                                  125                                  130

gaa gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa 547

Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu  
 135 140 145

ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595  
 Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr  
 150 155 160 165

att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644  
 Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys  
 170 175

taggttagtt tcg 657

<210> 118  
 <211> 178  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 118  
 Met Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn  
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Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp  
 20 25 30

Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu  
 35 40 45

Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala  
 50 55 60

Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala  
 65 70 75 80

His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu  
 85 90 95

Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr  
 100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala  
 115 120 125

Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp  
 130 135 140

Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala  
 145 150 155 160

Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile  
 165 170 175

Lys Lys

<210> 119  
 <211> 385  
 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(385)

&lt;223&gt; FRXA00627

&lt;400&gt; 119

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 Met Gln Met Leu Asp  
 1 5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163  
 Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys  
 10 15 20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211  
 Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala  
 25 30 35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259  
 Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly  
 40 45 50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307  
 Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr  
 55 60 65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355  
 Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser  
 70 75 80 85

ggt gga ttc gtg gca tcg ttt atc gcc acc 385  
 Gly Gly Phe Val Ala Ser Phe Ile Ala Thr  
 90 95

&lt;210&gt; 120

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 120

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp  
 1 5 10 15

Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala  
 20 25 30

Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr  
 35 40 45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp  
 50 55 60

His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val  
 65 70 75 80

Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr  
 85 90 95

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<210> 121
<211> 1434
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1411)
<223> RXA02550
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<400> 121															
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tagctttcaa ctacgcacac aaagtggcaa cattgagcgg gtg act aca gac aag 115															
Val Thr Thr Asp Lys 1 5															
cgc aaa acc tct aag acc acc gac acc gcc aac aag gct gtg ggc gcg 163															
Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn Lys Ala Val Gly Ala 10 15 20															
gat cag gca gcg cgt ccc act cgg cga aca act cgc cgc atc ttc gat 211															
Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr Arg Arg Ile Phe Asp 25 30 35															
cag tcg gag aag atg aag gac gtg ctg tac gag atc cgt ggc ccg gtg 259															
Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu Ile Arg Gly Pro Val 40 45 50															
gcc gcg gag gcg gaa cgc atg gag ctt gat ggg cat aac atc tta aag 307															
Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly His Asn Ile Leu Lys 55 60 65															
ctc aac acg gga aat cca gcc gtg ttc gga ttc gat gcc ccc gac gtg 355															
Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe Asp Ala Pro Asp Val 70 75 80 85															
att atg cgt gac atg atc gcc aac ctt cca act tcc caa ggg tat tcc 403															
Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr Ser Gln Gly Tyr Ser 90 95 100															
acc tcc aaa ggc att att ccg gcc cgg cga gca gtg gtc acc cgc tac 451															
Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala Val Val Thr Arg Tyr 105 110 115															
gaa gtt gtg ccc gga ttc ccc cac ttc gat gtt gat gat gtg ttc tta 499															
Glu Val Val Pro Gly Phe Pro His Phe Asp Val Asp Asp Val Phe Leu 120 125 130															
ggc aac ggt gtc tca gaa cta atc acc atg acc acc caa gca ctc ctc 547															
Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr Thr Gln Ala Leu Leu 135 140 145															
aac gac ggc gat gaa gtt ctt atc ccc gca ccg gac tac cca ctg tgg 595															
Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro Asp Tyr Pro Leu Trp 150 155 160 165															
act gcc gca acc tcc ctg gct ggt ggt aag cct gtg cac tac ctc tgt 643															
Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro Val His Tyr Leu Cys															

170						175						180						
gat	gag	gaa	gat	gac	tgg	aac	cca	tcc	atc	gaa	gac	atc	aag	tcc	aaa	691		
Asp	Glu	Glu	Asp	Asp	Trp	Asn	Pro	Ser	Ile	Glu	Asp	Ile	Lys	Ser	Lys			
			185					190					195					
atc	tca	gag	aaa	acc	aaa	gct	att	gtg	gtg	atc	aac	ccc	aac	aac	ccc	739		
Ile	Ser	Glu	Lys	Thr	Lys	Ala	Ile	Val	Val	Ile	Asn	Pro	Asn	Asn	Pro			
		200					205					210						
acg	gga	gct	gtc	tac	ccg	cgc	cgg	gtg	ttg	gaa	caa	atc	gtc	gag	att	787		
Thr	Gly	Ala	Val	Tyr	Pro	Arg	Arg	Val	Leu	Glu	Gln	Ile	Val	Glu	Ile			
	215					220					225							
gca	cgc	gag	cat	gac	ctg	ctg	att	ttg	gcc	gat	gaa	atc	tac	gac	cgc	835		
Ala	Arg	Glu	His	Asp	Leu	Leu	Ile	Leu	Ala	Asp	Glu	Ile	Tyr	Asp	Arg			
	230				235					240					245			
att	ctc	tac	gat	gat	gcc	gag	cac	atc	agc	ctg	gca	acc	ctt	gca	cca	883		
Ile	Leu	Tyr	Asp	Asp	Ala	Glu	His	Ile	Ser	Leu	Ala	Thr	Leu	Ala	Pro			
			250					255						260				
gat	ctc	ctt	tgc	atc	aca	tac	aac	ggt	cta	tcc	aag	gca	tac	cgc	gtc	931		
Asp	Leu	Leu	Cys	Ile	Thr	Tyr	Asn	Gly	Leu	Ser	Lys	Ala	Tyr	Arg	Val			
			265					270					275					
gca	gga	tac	cga	gct	ggc	tgg	atg	gta	ttg	act	gga	cca	aag	caa	tac	979		
Ala	Gly	Tyr	Arg	Ala	Gly	Trp	Met	Val	Leu	Thr	Gly	Pro	Lys	Gln	Tyr			
		280					285					290						
gca	cgt	gga	ttt	att	gag	ggc	ctc	gaa	ctc	ctc	gca	ggc	act	cga	ctc			
1027																		
Ala	Arg	Gly	Phe	Ile	Glu	Gly	Leu	Glu	Leu	Leu	Ala	Gly	Thr	Arg	Leu			
	295					300					305							
tgc	cca	aat	gtc	cca	gct	cag	cac	gct	att	cag	gta	gct	ctg	ggt	gga			
1075																		
Cys	Pro	Asn	Val	Pro	Ala	Gln	His	Ala	Ile	Gln	Val	Ala	Leu	Gly	Gly			
310					315					320				325				
cgc	cag	tcc	atc	tac	gac	ctc	act	ggc	gaa	cac	ggc	cga	ctc	ctg	gaa			
1123																		
Arg	Gln	Ser	Ile	Tyr	Asp	Leu	Thr	Gly	Glu	His	Gly	Arg	Leu	Leu	Glu			
			330					335					340					
cag	cgc	aac	atg	gca	tgg	acg	aaa	ctc	aac	gaa	atc	cca	ggt	gtc	agc			
1171																		
Gln	Arg	Asn	Met	Ala	Trp	Thr	Lys	Leu	Asn	Glu	Ile	Pro	Gly	Val	Ser			
			345					350					355					
tgt	gtg	aaa	cca	atg	gga	gct	cta	tac	gcg	ttc	ccc	aag	ctc	gac	ccc			
1219																		
Cys	Val	Lys	Pro	Met	Gly	Ala	Leu	Tyr	Ala	Phe	Pro	Lys	Leu	Asp	Pro			
		360				365					370							
aac	gtg	tac	gaa	atc	cac	gac	gac	acc	caa	ctc	atg	ctg	gat	ctt	ctc			
1267																		
Asn	Val	Tyr	Glu	Ile	His	Asp	Asp	Thr	Gln	Leu	Met	Leu	Asp	Leu	Leu			
		375				380					385							

cgt gcc gag aaa atc ctc atg gtt cag ggc act ggc ttc aac tgg cca  
 1315  
 Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro  
 390 395 400 405

cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg  
 1363  
 His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu  
 410 415 420

gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag  
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 Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu Ser Thr Tyr Lys Gln  
 425 430 435

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 1434

<210> 122  
 <211> 437  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 122  
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 1 5 10 15

Lys Ala Val Gly Ala Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr  
 20 25 30

Arg Arg Ile Phe Asp Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu  
 35 40 45

Ile Arg Gly Pro Val Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly  
 50 55 60

His Asn Ile Leu Lys Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe  
 65 70 75 80

Asp Ala Pro Asp Val Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr  
 85 90 95

Ser Gln Gly Tyr Ser Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala  
 100 105 110

Val Val Thr Arg Tyr Glu Val Val Pro Gly Phe Pro His Phe Asp Val  
 115 120 125

Asp Asp Val Phe Leu Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr  
 130 135 140

Thr Gln Ala Leu Leu Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro  
 145 150 155 160

Asp Tyr Pro Leu Trp Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro  
 165 170 175

Val His Tyr Leu Cys Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu  
 180 185 190

Asp Ile Lys Ser Lys Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile  
 195 200 205  
 Asn Pro Asn Asn Pro Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu  
 210 215 220  
 Gln Ile Val Glu Ile Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp  
 225 230 235 240  
 Glu Ile Tyr Asp Arg Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu  
 245 250 255  
 Ala Thr Leu Ala Pro Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser  
 260 265 270  
 Lys Ala Tyr Arg Val Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr  
 275 280 285  
 Gly Pro Lys Gln Tyr Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu  
 290 295 300  
 Ala Gly Thr Arg Leu Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln  
 305 310 315 320  
 Val Ala Leu Gly Gly Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His  
 325 330 335  
 Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu  
 340 345 350  
 Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe  
 355 360 365  
 Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu  
 370 375 380  
 Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr  
 385 390 395 400  
 Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro  
 405 410 415  
 Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu  
 420 425 430  
 Ser Thr Tyr Lys Gln  
 435

&lt;210&gt; 123

&lt;211&gt; 1701

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1678)

&lt;223&gt; RXA02193

&lt;400&gt; 123

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agcaccattg tgatttcctt caacttgtga gaggcagtac	atg	tct	aag	acg	agc	115
	Met	Ser	Lys	Thr	Ser	
	1				5	
aac aag tct tca gca gac tca aag aat gac gca aaa gcc gaa gac att	163					
Asn Lys Ser Ser Ala Asp Ser Lys Asn Asp Ala Lys Ala Glu Asp Ile						
	10	15	20			
gtg aac ggc gag aac caa atc gcc acg aat gag tcg cag tct tca gac	211					
Val Asn Gly Glu Asn Gln Ile Ala Thr Asn Glu Ser Gln Ser Ser Asp						
	25	30	35			
agc gct gca gtt tcg gaa cgt gtc gtc gaa cca aaa acc acg gtt cag	259					
Ser Ala Ala Val Ser Glu Arg Val Val Glu Pro Lys Thr Thr Val Gln						
	40	45	50			
aaa aag ttc cga atc gaa tcg gat ctg ctt ggt gaa ctt cag atc cca	307					
Lys Lys Phe Arg Ile Glu Ser Asp Leu Leu Gly Glu Leu Gln Ile Pro						
	55	60	65			
tcc cac gca tat tac ggg gtg cac acc ctt cgt gcg gtg gac aac ttc	355					
Ser His Ala Tyr Tyr Gly Val His Thr Leu Arg Ala Val Asp Asn Phe						
	70	75	80	85		
caa atc tca cga acc acc atc aac cac gtc cca gat ttc att cgc ggc	403					
Gln Ile Ser Arg Thr Thr Ile Asn His Val Pro Asp Phe Ile Arg Gly						
	90	95	100			
atg gtc cag gtg aaa aag gcc gca gct tta gca aac cgc cga ctg cac	451					
Met Val Gln Val Lys Lys Ala Ala Ala Leu Ala Asn Arg Arg Leu His						
	105	110	115			
aca ctt cca gca caa aaa gca gaa gca att gtc tgg gct tgt gat cag	499					
Thr Leu Pro Ala Gln Lys Ala Glu Ala Ile Val Trp Ala Cys Asp Gln						
	120	125	130			
atc ctc att gag gaa cgc tgt atg gat cag ttc ccc atc gat gtg ttc	547					
Ile Leu Ile Glu Glu Arg Cys Met Asp Gln Phe Pro Ile Asp Val Phe						
	135	140	145			
cag ggt ggc gca ggt acc tca ctg aac atg aac acc aac gag gtt gtt	595					
Gln Gly Gly Ala Gly Thr Ser Leu Asn Met Asn Thr Asn Glu Val Val						
	150	155	160	165		
gcc aac ctt gca ctt gag ttc tta ggc cat gaa aag ggc gag tac cac	643					
Ala Asn Leu Ala Leu Glu Phe Leu Gly His Glu Lys Gly Glu Tyr His						
	170	175	180			
atc ctg cac ccc atg gat gat gtg aac atg tcc cag tcc acc aac gat	691					
Ile Leu His Pro Met Asp Asp Val Asn Met Ser Gln Ser Thr Asn Asp						
	185	190	195			
tcc tac cca act ggt ttc cgc ctg ggc att tac gct gga ctg cag acc	739					
Ser Tyr Pro Thr Gly Phe Arg Leu Gly Ile Tyr Ala Gly Leu Gln Thr						
	200	205	210			
ctc atc gct gaa att gat gag ctt cag gtt gcg ttc cgc cac aag ggc	787					
Leu Ile Ala Glu Ile Asp Glu Leu Gln Val Ala Phe Arg His Lys Gly						
	215	220	225			



aat gag ttt gtc gac atc atc aag atg ggc cgc acc cag ttg cag gat	835
Asn Glu Phe Val Asp Ile Ile Lys Met Gly Arg Thr Gln Leu Gln Asp	
230 235 240 245	
gct gtt ccc atg agc ttg ggc gaa gag ttc cga gca ttc gcg cac aac	883
Ala Val Pro Met Ser Leu Gly Glu Glu Phe Arg Ala Phe Ala His Asn	
250 255 260	
ctc gca gaa gag cag acc gtg ctg cgt gaa gct gcc aac cgt ctc ctc	931
Leu Ala Glu Glu Gln Thr Val Leu Arg Glu Ala Ala Asn Arg Leu Leu	
265 270 275	
gag gtc aat ctt ggt gca acc gca atc ggt act ggt gtg aac act cca	979
Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Val Asn Thr Pro	
280 285 290	
gca ggc tac cgc cac cag gtt gtc gct gct ctg tct gag gtc acc gga	
1027 Ala Gly Tyr Arg His Gln Val Val Ala Ala Leu Ser Glu Val Thr Gly	
295 300 305	
ctg gaa cta aag tcc gca cgt gat ctc atc gag gct acc tct gac acc	
1075 Leu Glu Leu Lys Ser Ala Arg Asp Leu Ile Glu Ala Thr Ser Asp Thr	
310 315 320 325	
ggt gca tat gtt cat gcg cac tcc gca atc aag cgt gca gcc atg aaa	
1123 Gly Ala Tyr Val His Ala His Ser Ala Ile Lys Arg Ala Ala Met Lys	
330 335 340	
ctg tcc aag atc tgt aac gat cta cgt ctg ctg tct tct ggt cct cgt	
1171 Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg	
345 350 355	
gct ggc ttg aac gaa atc aac ctg cca cca cgc cag gct ggt tcc tcc	
1219 Ala Gly Leu Asn Glu Ile Asn Leu Pro Pro Arg Gln Ala Gly Ser Ser	
360 365 370	
atc atg cca gcc aag gtc aac cca gtg atc cca gaa gtg gtc aac cag	
1267 Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln	
375 380 385	
gtc tgc ttc aag gtc ttc ggt aac gat ctc acc gtc acc atg gct gcg	
1315 Val Cys Phe Lys Val Phe Gly Asn Asp Leu Thr Val Thr Met Ala Ala	
390 395 400 405	
gaa gct ggc cag ttg cag ctc aac gtc atg gag cca gtc att ggc gaa	
1363 Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly Glu	
410 415 420	
tcc ctc ttc cag tca ctg cgc atc ctg ggc aat gca gcc aag act ttg	
1411 Ser Leu Phe Gln Ser Leu Arg Ile Leu Gly Asn Ala Ala Lys Thr Leu	
425 430 435	

cgt gag aag tgc gtc gta gga atc acc gcc aac gct gat gtt tgc cgt  
1459  
Arg Glu Lys Cys Val Val Gly Ile Thr Ala Asn Ala Asp Val Cys Arg  
440 445 450

gct tac gtt gat aac tcc atc ggg att atc act tac ctg aac cca ttc  
1507  
Ala Tyr Val Asp Asn Ser Ile Gly Ile Ile Thr Tyr Leu Asn Pro Phe  
455 460 465

ctg ggc cac gac att gga gat cag atc ggt aag gaa gca gcc gaa act  
1555  
Leu Gly His Asp Ile Gly Asp Gln Ile Gly Lys Glu Ala Ala Glu Thr  
470 475 480 485

ggt cga cca gtg cgt gaa ctc atc ctg gaa aag aag ctc atg gat gaa  
1603  
Gly Arg Pro Val Arg Glu Leu Ile Leu Glu Lys Lys Leu Met Asp Glu  
490 495 500

aag acg ctc gag gca gtc ctg tcc aag gag aac ctc atg cac cca atg  
1651  
Lys Thr Leu Glu Ala Val Leu Ser Lys Glu Asn Leu Met His Pro Met  
505 510 515

ttc cgc gga agg ctc tac ttg gag aac taatccaaga tctcgtctga  
1698  
Phe Arg Gly Arg Leu Tyr Leu Glu Asn  
520 525

tac  
1701

<210> 124  
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<213> Corynebacterium glutamicum

<400> 124  
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Ser Gln Ser Ser Asp Ser Ala Ala Val Ser Glu Arg Val Val Glu Pro  
35 40 45  
Lys Thr Thr Val Gln Lys Lys Phe Arg Ile Glu Ser Asp Leu Leu Gly  
50 55 60  
Glu Leu Gln Ile Pro Ser His Ala Tyr Tyr Gly Val His Thr Leu Arg  
65 70 75 80  
Ala Val Asp Asn Phe Gln Ile Ser Arg Thr Thr Ile Asn His Val Pro  
85 90 95  
Asp Phe Ile Arg Gly Met Val Gln Val Lys Lys Ala Ala Ala Leu Ala  
100 105 110

Asn Arg Arg Leu His Thr Leu Pro Ala Gln Lys Ala Glu Ala Ile Val  
 115 120 125  
 Trp Ala Cys Asp Gln Ile Leu Ile Glu Glu Arg Cys Met Asp Gln Phe  
 130 135 140  
 Pro Ile Asp Val Phe Gln Gly Gly Ala Gly Thr Ser Leu Asn Met Asn  
 145 150 155 160  
 Thr Asn Glu Val Val Ala Asn Leu Ala Leu Glu Phe Leu Gly His Glu  
 165 170 175  
 Lys Gly Glu Tyr His Ile Leu His Pro Met Asp Asp Val Asn Met Ser  
 180 185 190  
 Gln Ser Thr Asn Asp Ser Tyr Pro Thr Gly Phe Arg Leu Gly Ile Tyr  
 195 200 205  
 Ala Gly Leu Gln Thr Leu Ile Ala Glu Ile Asp Glu Leu Gln Val Ala  
 210 215 220  
 Phe Arg His Lys Gly Asn Glu Phe Val Asp Ile Ile Lys Met Gly Arg  
 225 230 235 240  
 Thr Gln Leu Gln Asp Ala Val Pro Met Ser Leu Gly Glu Glu Phe Arg  
 245 250 255  
 Ala Phe Ala His Asn Leu Ala Glu Glu Gln Thr Val Leu Arg Glu Ala  
 260 265 270  
 Ala Asn Arg Leu Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr  
 275 280 285  
 Gly Val Asn Thr Pro Ala Gly Tyr Arg His Gln Val Val Ala Ala Leu  
 290 295 300  
 Ser Glu Val Thr Gly Leu Glu Leu Lys Ser Ala Arg Asp Leu Ile Glu  
 305 310 315 320  
 Ala Thr Ser Asp Thr Gly Ala Tyr Val His Ala His Ser Ala Ile Lys  
 325 330 335  
 Arg Ala Ala Met Lys Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu  
 340 345 350  
 Ser Ser Gly Pro Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Pro Arg  
 355 360 365  
 Gln Ala Gly Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro  
 370 375 380  
 Glu Val Val Asn Gln Val Cys Phe Lys Val Phe Gly Asn Asp Leu Thr  
 385 390 395 400  
 Val Thr Met Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu  
 405 410 415  
 Pro Val Ile Gly Glu Ser Leu Phe Gln Ser Leu Arg Ile Leu Gly Asn  
 420 425 430  
 Ala Ala Lys Thr Leu Arg Glu Lys Cys Val Val Gly Ile Thr Ala Asn

435	440	445
Ala Asp Val Cys Arg Ala Tyr Val Asp Asn Ser Ile Gly Ile Ile Thr		
450	455	460
Tyr Leu Asn Pro Phe Leu Gly His Asp Ile Gly Asp Gln Ile Gly Lys		
465	470	475
Glu Ala Ala Glu Thr Gly Arg Pro Val Arg Glu Leu Ile Leu Glu Lys		
	485	490
Lys Leu Met Asp Glu Lys Thr Leu Glu Ala Val Leu Ser Lys Glu Asn		
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Leu Met His Pro Met Phe Arg Gly Arg Leu Tyr Leu Glu Asn		
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		525

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1075)  
 <223> RXA02432

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 Met Ser Lys Gln His  
 1 5  
 tcc aca cca tta aac aat gat gaa gaa cac act tcc gct cct caa aag 163  
 Ser Thr Pro Leu Asn Asn Asp Glu Glu His Thr Ser Ala Pro Gln Lys  
 10 15 20  
 gtt gcg gta atc acc acg ggc gga acc atc gcc tgt act tcc gac gca 211  
 Val Ala Val Ile Thr Thr Gly Gly Thr Ile Ala Cys Thr Ser Asp Ala  
 25 30 35  
 aat ggg cat ctg ctt ccc acc gtc agc ggt gca gac ctg ctt gcg cca 259  
 Asn Gly His Leu Leu Pro Thr Val Ser Gly Ala Asp Leu Leu Ala Pro  
 40 45 50  
 atc gca cca cgg ttc aat gga gcg cag atc gct ttc gaa atc cac gaa 307  
 Ile Ala Pro Arg Phe Asn Gly Ala Gln Ile Ala Phe Glu Ile His Glu  
 55 60 65  
 atc aac cgc ctt gat tcc tcc tcc atg acg ttt gag gat ctc gat tcc 355  
 Ile Asn Arg Leu Asp Ser Ser Ser Met Thr Phe Glu Asp Leu Asp Ser  
 70 75 80 85  
 atc atc gcc acg gtt cat aag gtg ttg gag gat ccg gat gtt gtt ggc 403  
 Ile Ile Ala Thr Val His Lys Val Leu Glu Asp Pro Asp Val Val Gly  
 90 95 100  
 gta gta gtt acc cac ggc acc gat tcc atg gaa gag tcc gcc atc gcc 451  
 Val Val Val Thr His Gly Thr Asp Ser Met Glu Glu Ser Ala Ile Ala

105						110						115						
gta	gac	acc	ttc	ctt	gat	gat	ccc	cgc	cca	gtc	att	ttc	acc	ggc	gcc	499		
Val	Asp	Thr	Phe	Leu	Asp	Asp	Pro	Arg	Pro	Val	Ile	Phe	Thr	Gly	Ala			
		120					125					130						
caa	aaa	ccc	ttc	gat	cat	ccc	gaa	gcc	gac	ggc	cca	aac	aac	ctt	ttc	547		
Gln	Lys	Pro	Phe	Asp	His	Pro	Glu	Ala	Asp	Gly	Pro	Asn	Asn	Leu	Phe			
		135					140				145							
gaa	gcc	tgc	ctc	atc	gca	tcc	gac	ccc	tcc	gct	cgc	gga	att	ggc	gca	595		
Glu	Ala	Cys	Leu	Ile	Ala	Ser	Asp	Pro	Ser	Ala	Arg	Gly	Ile	Gly	Ala			
150					155					160					165			
ctc	att	gtc	ttc	ggc	cac	gcc	gtc	atc	cct	gct	cgc	ggc	tgc	gtt	aaa	643		
Leu	Ile	Val	Phe	Gly	His	Ala	Val	Ile	Pro	Ala	Arg	Gly	Cys	Val	Lys			
				170					175					180				
tgg	cac	acc	tct	gat	gag	ctg	gcg	ttt	gca	acc	aac	ggc	cct	gaa	gaa	691		
Trp	His	Thr	Ser	Asp	Glu	Leu	Ala	Phe	Ala	Thr	Asn	Gly	Pro	Glu	Glu			
			185					190					195					
cca	gag	cgc	ccc	gat	gcg	ctg	ccc	gta	gct	aaa	ttg	gcg	gat	gtc	tct	739		
Pro	Glu	Arg	Pro	Asp	Ala	Leu	Pro	Val	Ala	Lys	Leu	Ala	Asp	Val	Ser			
		200					205						210					
gtc	gaa	atc	atc	ccc	gca	tac	cct	ggc	gcc	acc	ggc	gca	atg	gtg	gaa	787		
Val	Glu	Ile	Ile	Pro	Ala	Tyr	Pro	Gly	Ala	Thr	Gly	Ala	Met	Val	Glu			
		215				220					225							
gct	gcc	atc	gct	gcc	ggc	gct	caa	gga	ctt	gta	gtg	gaa	gca	atg	gga	835		
Ala	Ala	Ile	Ala	Ala	Gly	Ala	Gln	Gly	Leu	Val	Val	Glu	Ala	Met	Gly			
230					235					240					245			
tca	ggc	aat	gtt	ggc	tcc	cgc	atg	ggc	gat	gcc	cta	ggc	aaa	gca	ctt	883		
Ser	Gly	Asn	Val	Gly	Ser	Arg	Met	Gly	Asp	Ala	Leu	Gly	Lys	Ala	Leu			
				250					255					260				
gac	gct	gga	att	ccc	gtg	gtg	atg	agc	act	agg	gtt	cct	cgt	ggc	gaa	931		
Asp	Ala	Gly	Ile	Pro	Val	Val	Met	Ser	Thr	Arg	Val	Pro	Arg	Gly	Glu			
			265					270					275					
gta	tcc	gga	gtg	tat	ggc	ggc	gca	ggc	gga	ggc	gcg	act	ttg	gct	gcg	979		
Val	Ser	Gly	Val	Tyr	Gly	Gly	Ala	Gly	Gly	Gly	Ala	Thr	Leu	Ala	Ala			
		280					285						290					
aag	ggc	gct	gtg	gga	tct	cgc	tac	ttc	aga	gct	ggc	cag	gca	cgt	att			
1027																		
Lys	Gly	Ala	Val	Gly	Ser	Arg	Tyr	Phe	Arg	Ala	Gly	Gln	Ala	Arg	Ile			
		295					300				305							
ttg	ctc	gcg	att	gcc	att	gcg	acg	ggc	gca	cat	ccg	gtg	acg	ctt	tac			
1075																		
Leu	Leu	Ala	Ile	Ala	Ile	Ala	Thr	Gly	Ala	His	Pro	Val	Thr	Leu	Tyr			
310					315					320					325			
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1098																		

&lt;210&gt; 126

&lt;211&gt; 325

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 126

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Ser	Ala	Pro	Gln	Lys	Val	Ala	Val	Ile	Thr	Thr	Gly	Gly	Thr	Ile	Ala	20	25	30	
Cys	Thr	Ser	Asp	Ala	Asn	Gly	His	Leu	Leu	Pro	Thr	Val	Ser	Gly	Ala	35	40	45	
Asp	Leu	Leu	Ala	Pro	Ile	Ala	Pro	Arg	Phe	Asn	Gly	Ala	Gln	Ile	Ala	50	55	60	
Phe	Glu	Ile	His	Glu	Ile	Asn	Arg	Leu	Asp	Ser	Ser	Ser	Met	Thr	Phe	65	70	75	80
Glu	Asp	Leu	Asp	Ser	Ile	Ile	Ala	Thr	Val	His	Lys	Val	Leu	Glu	Asp	85	90	95	
Pro	Asp	Val	Val	Gly	Val	Val	Val	Thr	His	Gly	Thr	Asp	Ser	Met	Glu	100	105	110	
Glu	Ser	Ala	Ile	Ala	Val	Asp	Thr	Phe	Leu	Asp	Asp	Pro	Arg	Pro	Val	115	120	125	
Ile	Phe	Thr	Gly	Ala	Gln	Lys	Pro	Phe	Asp	His	Pro	Glu	Ala	Asp	Gly	130	135	140	
Pro	Asn	Asn	Leu	Phe	Glu	Ala	Cys	Leu	Ile	Ala	Ser	Asp	Pro	Ser	Ala	145	150	155	160
Arg	Gly	Ile	Gly	Ala	Leu	Ile	Val	Phe	Gly	His	Ala	Val	Ile	Pro	Ala	165	170	175	
Arg	Gly	Cys	Val	Lys	Trp	His	Thr	Ser	Asp	Glu	Leu	Ala	Phe	Ala	Thr	180	185	190	
Asn	Gly	Pro	Glu	Glu	Pro	Glu	Arg	Pro	Asp	Ala	Leu	Pro	Val	Ala	Lys	195	200	205	
Leu	Ala	Asp	Val	Ser	Val	Glu	Ile	Ile	Pro	Ala	Tyr	Pro	Gly	Ala	Thr	210	215	220	
Gly	Ala	Met	Val	Glu	Ala	Ala	Ile	Ala	Ala	Gly	Ala	Gln	Gly	Leu	Val	225	230	235	240
Val	Glu	Ala	Met	Gly	Ser	Gly	Asn	Val	Gly	Ser	Arg	Met	Gly	Asp	Ala	245	250	255	
Leu	Gly	Lys	Ala	Leu	Asp	Ala	Gly	Ile	Pro	Val	Val	Met	Ser	Thr	Arg	260	265	270	
Val	Pro	Arg	Gly	Glu	Val	Ser	Gly	Val	Tyr	Gly	Gly	Ala	Gly	Gly	Gly	275	280	285	
Ala	Thr	Leu	Ala	Ala	Lys	Gly	Ala	Val	Gly	Ser	Arg	Tyr	Phe	Arg	Ala	290	295	300	

Gly Gln Ala Arg Ile Leu Leu Ala Ile Ala Ile Ala Thr Gly Ala His  
 305 310 315 320

Pro Val Thr Leu Tyr  
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<210> 127

<211> 775

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> RXN03003

<400> 127

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caatgatcgc tgcgctgccg cctcaggcat aatctaacgc atg acc tct cgc acc 115  
 Met Thr Ser Arg Thr  
 1 5

ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tcg ctc gct tcc 163  
 Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser  
 10 15 20

gca aaa gcc aaa gct gcg tct cac ccg gat ggg atc gtg aat ctt tct 211  
 Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser  
 25 30 35

gtt ggc act ccg gtt gat ccg gtc gcg ccc agc att cag atc gcg ttg 259  
 Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser Ile Gln Ile Ala Leu  
 40 45 50

gca gaa gca gcg ggg ttt tcg ggt tac cct caa acc atc ggc acc ccg 307  
 Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln Thr Ile Gly Thr Pro  
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gaa ctc cgc gca gcc atc agg ggc gcg ctt gag cgg cgc tac aac atg 355  
 Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu Arg Arg Tyr Asn Met  
 70 75 80 85

aca aag ctt gtc gac gcc tcc ctc ctc ccc gtc gtg ggt acc aag gag 403  
 Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val Val Gly Thr Lys Glu  
 90 95 100

gca att gcc ctt ctt cca ttc gcg ttg ggt att tcc ggc acc gtt gtc 451  
 Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile Ser Gly Thr Val Val  
 105 110 115

atc cca gag att gcg tac cca acc tac gaa gtc gct gtc gtg gcc gca 499  
 Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val Ala Val Val Ala Ala  
 120 125 130

gga tgc acc gtg ttg cgt tct gat tcg ctg ttt aag ctc ggc ccg cag 547  
 Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln  
 135 140 145

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 Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys  
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 gtt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643  
 Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu  
 170 175 180  
  
 aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691.  
 Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp  
 185 190 195  
  
 gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat 739  
 Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp  
 200 205 210  
  
 ggc gac cac acc aac ttg atc gcc att cac tcg ctg 775  
 Gly Asp His Thr Asn Leu Ile Ala Ile His Ser Leu  
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&lt;210&gt; 128

&lt;211&gt; 225

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 128

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 Asp Ser Leu Ala Ser Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly  
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 Ile Val Asn Leu Ser Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser  
 35 40 45  
  
 Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln  
 50 55 60  
  
 Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu  
 65 70 75 80  
  
 Arg Arg Tyr Asn Met Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val  
 85 90 95  
  
 Val Gly Thr Lys Glu Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile  
 100 105 110  
  
 Ser Gly Thr Val Val Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val  
 115 120 125  
  
 Ala Val Val Ala Ala Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe  
 130 135 140  
  
 Lys Leu Gly Pro Gln Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser  
 145 150 155 160  
  
 Asn Pro Thr Gly Lys Val Leu Gly Ile Pro His Leu Arg Lys Val Val  
 165 170 175  
  
 Lys Trp Ala Gln Glu Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr



180										185					190					
Leu	Gly	Leu	Gly	Trp	Asp	Asp	Glu	Asn	Pro	Pro	Ile	Ser	Ile	Leu	Asp					
195							200			205										
Pro	Arg	Val	Cys	Asp	Gly	Asp	His	Thr	Asn	Leu	Ile	Ala	Ile	His	Ser					
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Met Asn Leu Leu Thr 5																				
1																				
acc aaa att gac ctg gat gcc atc gcc cat aac acg agg gtg ctt aaa 163																				
Thr Lys Ile Asp Leu Asp Ala Ile Ala His Asn Thr Arg Val Leu Lys 20																				
10																				
15																				
caa atg gcg ggt ccg gcg aag ctg atg gcg gtg gtg aag gcg aat gca 211																				
Gln Met Ala Gly Pro Ala Lys Leu Met Ala Val Val Lys Ala Asn Ala 35																				
25																				
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tat aac cat ggc gta gag aag gtc gct ccg gtt att gct gct cat ggt 259																				
Tyr Asn His Gly Val Glu Lys Val Ala Pro Val Ile Ala Ala His Gly 50																				
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Ala Asp Ala Phe Gly Val Ala Thr Leu Ala Glu Ala Met Gln Leu Arg 65																				
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Asp Ile Gly Ile Ser Gln Glu Val Leu Cys Trp Ile Trp Thr Pro Glu 85																				
70																				
75																				
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Gln Asp Phe Arg Ala Ala Ile Asp Arg Asn Ile Asp Leu Ala Val Ile 100																				
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Ser Pro Ala His Ala Lys Ala Leu Ile Glu Thr Asp Ala Glu His Ile 115																				
105																				
110																				
115																				
cgg gtg tcc atc aag att gat tct ggg ttg cat cgt tcg ggt gtg gat 499																				
Arg Val Ser Ile Lys Ile Asp Ser Gly Leu His Arg Ser Gly Val Asp 130																				
120																				
125																				
130																				

gag cag gag tgg gag ggc gtg ttc agc gcg ttg gct gct gcc ccg cac	547
Glu Gln Glu Trp Glu Gly Val Phe Ser Ala Leu Ala Ala Pro His	
135 140 145	
att gag gtc acg ggc atg ttc acg cac ttg gcg tgc gcg gat gag cca	595
Ile Glu Val Thr Gly Met Phe Thr His Leu Ala Cys Ala Asp Glu Pro	
150 155 160 165	
gag aat ccg gaa act gat cgc caa att att gct ttt cga cgc gcc ctt	643
Glu Asn Pro Glu Thr Asp Arg Gln Ile Ile Ala Phe Arg Arg Ala Leu	
170 175 180	
gcg ctc gcc cgc aag cac ggg ctt gag tgc ccg gtc aac cac gta tgc	691
Ala Leu Ala Arg Lys His Gly Leu Glu Cys Pro Val Asn His Val Cys	
185 190 195	
aac tca cct gca ttc ttg act cga tct gat tta cac atg gag atg gtc	739
Asn Ser Pro Ala Phe Leu Thr Arg Ser Asp Leu His Met Glu Met Val	
200 205 210	
cga ccg ggt ttg gcc ttt tat ggg ttg gaa ccc gtg gcg gga ctg gag	787
Arg Pro Gly Leu Ala Phe Tyr Gly Leu Glu Pro Val Ala Gly Leu Glu	
215 220 225	
cat ggt ttg aag ccg gcg atg acg tgg gag gcg aag gtg agc gtc gta	835
His Gly Leu Lys Pro Ala Met Thr Trp Glu Ala Lys Val Ser Val Val	
230 235 240 245	
aag caa att gaa gct gga caa ggc act tcc tat ggc ctg acc tgg cgc	883
Lys Gln Ile Glu Ala Gly Gln Gly Thr Ser Tyr Gly Leu Thr Trp Arg	
250 255 260	
gct gag gat cgc ggc ttt gtg gct gtg gtg cct gcg ggc tat gcc gat	931
Ala Glu Asp Arg Gly Phe Val Ala Val Val Pro Ala Gly Tyr Ala Asp	
265 270 275	
ggc atg ccg cgg cat gcc cag ggg aaa ttc tcc gtc acg att gat ggc	979
Gly Met Pro Arg His Ala Gln Gly Lys Phe Ser Val Thr Ile Asp Gly	
280 285 290	
ctg gac tat ccg cag gtt ggg cgc gta tgc atg gat cag ttc gtt att	
1027	
Leu Asp Tyr Pro Gln Val Gly Arg Val Cys Met Asp Gln Phe Val Ile	
295 300 305	
tct ttg ggc gac aat cca cac ggc gtg gaa gct ggg gcg aag gcc gtg	
1075	
Ser Leu Gly Asp Asn Pro His Gly Val Glu Ala Gly Ala Lys Ala Val	
310 315 320 325	
ata ttc ggt gag aat ggg cat gac gca act gat ttt gcg gag cgt tta	
1123	
Ile Phe Gly Glu Asn Gly His Asp Ala Thr Asp Phe Ala Glu Arg Leu	
330 335 340	
gac acc att aac tat gag gta gtg tgc cga cca acc ggc cga act gtc	
1171	
Asp Thr Ile Asn Tyr Glu Val Val Cys Arg Pro Thr Gly Arg Thr Val	
345 350 355	

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 Arg Ala Tyr Val  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 130

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			20					25					30		
Val	Lys	Ala	Asn	Ala	Tyr	Asn	His	Gly	Val	Glu	Lys	Val	Ala	Pro	Val
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Ile	Ala	Ala	His	Gly	Ala	Asp	Ala	Phe	Gly	Val	Ala	Thr	Leu	Ala	Glu
	50					55					60				
Ala	Met	Gln	Leu	Arg	Asp	Ile	Gly	Ile	Ser	Gln	Glu	Val	Leu	Cys	Trp
65					70					75					80
Ile	Trp	Thr	Pro	Glu	Gln	Asp	Phe	Arg	Ala	Ala	Ile	Asp	Arg	Asn	Ile
				85					90					95	
Asp	Leu	Ala	Val	Ile	Ser	Pro	Ala	His	Ala	Lys	Ala	Leu	Ile	Glu	Thr
			100					105					110		
Asp	Ala	Glu	His	Ile	Arg	Val	Ser	Ile	Lys	Ile	Asp	Ser	Gly	Leu	His
		115					120					125			
Arg	Ser	Gly	Val	Asp	Glu	Gln	Glu	Trp	Glu	Gly	Val	Phe	Ser	Ala	Leu
	130					135					140				
Ala	Ala	Ala	Pro	His	Ile	Glu	Val	Thr	Gly	Met	Phe	Thr	His	Leu	Ala
145					150					155					160
Cys	Ala	Asp	Glu	Pro	Glu	Asn	Pro	Glu	Thr	Asp	Arg	Gln	Ile	Ile	Ala
				165					170					175	
Phe	Arg	Arg	Ala	Leu	Ala	Leu	Ala	Arg	Lys	His	Gly	Leu	Glu	Cys	Pro
			180					185					190		
Val	Asn	His	Val	Cys	Asn	Ser	Pro	Ala	Phe	Leu	Thr	Arg	Ser	Asp	Leu
		195					200					205			
His	Met	Glu	Met	Val	Arg	Pro	Gly	Leu	Ala	Phe	Tyr	Gly	Leu	Glu	Pro
	210					215					220				
Val	Ala	Gly	Leu	Glu	His	Gly	Leu	Lys	Pro	Ala	Met	Thr	Trp	Glu	Ala
225					230					235					240
Lys	Val	Ser	Val	Val	Lys	Gln	Ile	Glu	Ala	Gly	Gln	Gly	Thr	Ser	Tyr
				245					250					255	
Gly	Leu	Thr	Trp	Arg	Ala	Glu	Asp	Arg	Gly	Phe	Val	Ala	Val	Val	Pro

260	265	270
Ala Gly Tyr Ala Asp Gly Met Pro Arg His Ala Gln Gly Lys Phe Ser		
275	280	285
Val Thr Ile Asp Gly Leu Asp Tyr Pro Gln Val Gly Arg Val Cys Met		
290	295	300
Asp Gln Phe Val Ile Ser Leu Gly Asp Asn Pro His Gly Val Glu Ala		
305	310	315
Gly Ala Lys Ala Val Ile Phe Gly Glu Asn Gly His Asp Ala Thr Asp		
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Phe Ala Glu Arg Leu Asp Thr Ile Asn Tyr Glu Val Val Cys Arg Pro		
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Thr Gly Arg Thr Val Arg Ala Tyr Val		
355	360	

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 Met Met Ile Asp Thr 5  
 1  
 cct gct gtt ctc att gac cgc gag cgc tta act gcc aac att tcc agg 163  
 Pro Ala Val Leu Ile Asp Arg Glu Arg Leu Thr Ala Asn Ile Ser Arg 20  
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 atg gca gct cac gcc ggt gcc cat gag att gcc ctg cgt ccg cat gtg 211  
 Met Ala Ala His Ala Gly Ala His Glu Ile Ala Leu Arg Pro His Val 35  
 25 30  
 aaa acg cac aaa atc att gaa att gcg cag atg cag gtc gac gcc ggt 259  
 Lys Thr His Lys Ile Ile Glu Ile Ala Gln Met Gln Val Asp Ala Gly 50  
 40 45  
 gcc cga ggg atc acc tgc gca acc att ggc gag gcg gaa att ttt gcc 307  
 Ala Arg Gly Ile Thr Cys Ala Thr Ile Gly Glu Ala Glu Ile Phe Ala 65  
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 ggc gca ggt ttt acg gac atc ttt att gca tat ccg ctg tat cta acc 355  
 Gly Ala Gly Phe Thr Asp Ile Phe Ile Ala Tyr Pro Leu Tyr Leu Thr 85  
 70 75 80  
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 Asp His Ala Val Gln Arg Leu Asn Ala Ile Pro Gly Glu Ile Ser Ile 100  
 90 95

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Gly	Val	Asp	Ser	Val	Glu	Met	Ala	Gln	Ala	Thr	Ala	Gly	Leu	Arg	Glu	
			105					110					115			
gat	atc	aag	gct	ctg	att	gaa	gtg	gat	tcg	gga	cat	cgt	aga	agt	gga	499
Asp	Ile	Lys	Ala	Leu	Ile	Glu	Val	Asp	Ser	Gly	His	Arg	Arg	Ser	Gly	
		120					125					130				
gtc	acg	gcg	act	gct	tca	gaa	ttg	agt	cag	atc	cgc	gag	gcg	ctg	ggc	547
Val	Thr	Ala	Thr	Ala	Ser	Glu	Leu	Ser	Gln	Ile	Arg	Glu	Ala	Leu	Gly	
	135					140					145					
agc	agg	tat	gca	gga	gtg	ttt	act	ttt	cct	ggg	cat	tct	tat	ggc	ccg	595
Ser	Arg	Tyr	Ala	Gly	Val	Phe	Thr	Phe	Pro	Gly	His	Ser	Tyr	Gly	Pro	
150					155				160						165	
gga	aat	ggt	gag	cag	gca	gca	gct	gat	gag	ctt	cag	gct	cta	aac	aac	643
Gly	Asn	Gly	Glu	Gln	Ala	Ala	Ala	Asp	Glu	Leu	Gln	Ala	Leu	Asn	Asn	
			170					175						180		
agc	gtc	cag	cga	ctt	gct	ggc	ggc	ctg	act	tct	ggc	ggt	tcc	tcg	ccg	691
Ser	Val	Gln	Arg	Leu	Ala	Gly	Gly	Leu	Thr	Ser	Gly	Gly	Ser	Ser	Pro	
			185					190					195			
tct	gcg	cag	ttt	aca	gac	gca	atc	gat	gag	atg	cga	cca	ggc	gtg	tat	739
Ser	Ala	Gln	Phe	Thr	Asp	Ala	Ile	Asp	Glu	Met	Arg	Pro	Gly	Val	Tyr	
		200					205					210				
gtg	ttt	aac	gat	tcc	cag	cag	atc	acc	tcg	gga	gca	tgc	act	gag	aag	787
Val	Phe	Asn	Asp	Ser	Gln	Gln	Ile	Thr	Ser	Gly	Ala	Cys	Thr	Glu	Lys	
	215					220					225					
cag	gtg	gca	atg	acg	gtg	ctg	tct	act	gtg	gtc	agc	cga	aat	gtg	tca	835
Gln	Val	Ala	Met	Thr	Val	Leu	Ser	Thr	Val	Val	Ser	Arg	Asn	Val	Ser	
230					235				240					245		
gat	cgt	cgg	atc	att	ttg	gat	gcg	gga	tcc	aaa	atc	ctc	agc	act	gat	883
Asp	Arg	Arg	Ile	Ile	Leu	Asp	Ala	Gly	Ser	Lys	Ile	Leu	Ser	Thr	Asp	
			250					255						260		
aaa	cca	gca	tgg	att	gat	ggc	aat	ggt	ttt	gtt	ctg	ggg	aat	cct	gaa	931
Lys	Pro	Ala	Trp	Ile	Asp	Gly	Asn	Gly	Phe	Val	Leu	Gly	Asn	Pro	Glu	
			265				270						275			
gcc	cga	atc	tct	gct	ttg	tcg	gag	cat	cac	gca	acc	att	ttc	tgg	cca	979
Ala	Arg	Ile	Ser	Ala	Leu	Ser	Glu	His	His	Ala	Thr	Ile	Phe	Trp	Pro	
		280					285					290				
gat	aaa	gtg	cta	ctt	cca	gta	atc	ggg	gag	cag	ctc	aac	atc	gtg	ccc	
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310				315				320						325		
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1123																

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 Asn Asn

<210> 132  
 <211> 343  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 132  
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 35 40 45  
 Gln Val Asp Ala Gly Ala Arg Gly Ile Thr Cys Ala Thr Ile Gly Glu  
 50 55 60  
 Ala Glu Ile Phe Ala Gly Ala Gly Phe Thr Asp Ile Phe Ile Ala Tyr  
 65 70 75 80  
 Pro Leu Tyr Leu Thr Asp His Ala Val Gln Arg Leu Asn Ala Ile Pro  
 85 90 95  
 Gly Glu Ile Ser Ile Gly Val Asp Ser Val Glu Met Ala Gln Ala Thr  
 100 105 110  
 Ala Gly Leu Arg Glu Asp Ile Lys Ala Leu Ile Glu Val Asp Ser Gly  
 115 120 125  
 His Arg Arg Ser Gly Val Thr Ala Thr Ala Ser Glu Leu Ser Gln Ile  
 130 135 140  
 Arg Glu Ala Leu Gly Ser Arg Tyr Ala Gly Val Phe Thr Phe Pro Gly  
 145 150 155 160  
 His Ser Tyr Gly Pro Gly Asn Gly Glu Gln Ala Ala Ala Asp Glu Leu  
 165 170 175  
 Gln Ala Leu Asn Asn Ser Val Gln Arg Leu Ala Gly Gly Leu Thr Ser  
 180 185 190  
 Gly Gly Ser Ser Pro Ser Ala Gln Phe Thr Asp Ala Ile Asp Glu Met  
 195 200 205  
 Arg Pro Gly Val Tyr Val Phe Asn Asp Ser Gln Gln Ile Thr Ser Gly  
 210 215 220  
 Ala Cys Thr Glu Lys Gln Val Ala Met Thr Val Leu Ser Thr Val Val  
 225 230 235 240  
 Ser Arg Asn Val Ser Asp Arg Arg Ile Ile Leu Asp Ala Gly Ser Lys

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Ile	Leu	Ser	Thr	Asp	Lys	Pro	Ala	Trp	Ile	Asp	Gly	Asn	Gly	Phe	Val		
			260					265					270				
Leu	Gly	Asn	Pro	Glu	Ala	Arg	Ile	Ser	Ala	Leu	Ser	Glu	His	His	Ala		
		275					280					285					
Thr	Ile	Phe	Trp	Pro	Asp	Lys	Val	Leu	Leu	Pro	Val	Ile	Gly	Glu	Gln		
	290					295					300						
Leu	Asn	Ile	Val	Pro	Asn	His	Ala	Cys	Asn	Val	Ile	Asn	Leu	Val	Asp		
305					310				315						320		
Glu	Val	Tyr	Val	Arg	Glu	Ala	Asp	Gly	Thr	Phe	Arg	Thr	Trp	Lys	Val		
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Val	Ala	Arg	Gly	Arg	Asn	Asn											
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 <223> RXA02536

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 Met Asp Asn Phe Ala  
 1 5  
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 Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu Gln Gly Ala Arg Val  
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 Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe Gly Thr Gly Arg Leu  
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 Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe Ser Thr Ala Val Arg  
 40 45 50  
 aaa tta gcc gat gag ctg gac gtt gtc atc gtt gcg ggc atg ttc acc 307  
 Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val Ala Gly Met Phe Thr  
 55 60 65  
 cct gct gac acc gtg cag cgc ggt gaa aaa acg atc tcg cgc gtc aac 355  
 Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr Ile Ser Arg Val Asn  
 70 75 80 85  
 aac acc gtg ctg att agt ggc gct gga ttg cat cag gga tac aac aaa 403  
 Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His Gln Gly Tyr Asn Lys  
 90 95 100

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 Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu Ser Asp Thr Val Lys  
 105 110 115  
  
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 Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp Asp Ile Lys Phe Gly  
 120 125 130  
  
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 Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu Gln Phe Lys Asp Leu  
 135 140 145  
  
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 Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro Thr Ser Trp Gln Asp  
 150 155 160 165  
  
 ggt cct gga aaa tta gaa caa tgg gaa gtc ctc cct cgc gcg cgt gca 643  
 Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu Pro Arg Ala Arg Ala  
 170 175 180  
  
 ctg gat tcc acc tgc tgg atc gta gcg tgt ggg caa gcg cga ctt cca 691  
 Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly Gln Ala Arg Leu Pro  
 185 190 195  
  
 gaa gaa tta cgc gat gaa cga aaa ggc cct acg ggg att ggt cat tcc 739  
 Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr Gly Ile Gly His Ser  
 200 205 210  
  
 atg gtg aca aac cca cac ggt gaa gta att gct agc gcg ggt tat gag 787  
 Met Val Thr Asn Pro His Gly Glu Val Ile Ala Ser Ala Gly Tyr Glu  
 215 220 225  
  
 cca gaa atg ttg atc gcg gat att gat gtc agc ggt ttg gcc aaa att 835  
 Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser Gly Leu Ala Lys Ile  
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 cgg gag gca ttg cct gtt ctt taaccactgt ctaaggaatc act 879  
 Arg Glu Ala Leu Pro Val Leu  
 250

&lt;210&gt; 134

&lt;211&gt; 252

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 134

Met Asp Asn Phe Ala Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu  
 1 5 10 15  
  
 Gln Gly Ala Arg Val Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe  
 20 25 30  
  
 Gly Thr Gly Arg Leu Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe  
 35 40 45  
  
 Ser Thr Ala Val Arg Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val  
 50 55 60  
  
 Ala Gly Met Phe Thr Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr



65	70	75	80
Ile Ser Arg Val Asn Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His	85	90	95
Gln Gly Tyr Asn Lys Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu	100	105	110
Ser Asp Thr Val Lys Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp	115	120	125
Asp Ile Lys Phe Gly Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu	130	135	140
Gln Phe Lys Asp Leu Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro	145	150	155
Thr Ser Trp Gln Asp Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu	165	170	175
Pro Arg Ala Arg Ala Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly	180	185	190
Gln Ala Arg Leu Pro Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr	195	200	205
Gly Ile Gly His Ser Met Val Thr Asn Pro His Gly Glu Val Ile Ala	210	215	220
Ser Ala Gly Tyr Glu Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser	225	230	235
Gly Leu Ala Lys Ile Arg Glu Ala Leu Pro Val Leu	245	250	

&lt;210&gt; 135

&lt;211&gt; 1635

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1612)

&lt;223&gt; RXS00870

&lt;400&gt; 135

caagacggcg atgtcgccgc cgctgttgat accgcagcgc gacttggtca cacagatatt 60

caacaattca cttcgagag catttaagga atttacacac	atg tct gaa cca caa	115
	Met Ser Glu Pro Gln	
	1 5	

acc atc tcg cac tgg att gac ggc gcg att tcc cca tcc act tcc ggc	163
Thr Ile Ser His Trp Ile Asp Gly Ala Ile Ser Pro Ser Thr Ser Gly	
10 15 20	

aag acc gct cct gtc tac aat cct gca act ggc cag gtc acc gcc aat	211
Lys Thr Ala Pro Val Tyr Asn Pro Ala Thr Gly Gln Val Thr Ala Asn	
25 30 35	

gtt gcg ctg gct agc cag gaa gag atc gat gcc acc atc gct tct gcc	259
Val Ala Leu Ala Ser Gln Glu Glu Ile Asp Ala Thr Ile Ala Ser Ala	
40 45 50	
acc aag gct gct aag acg tgg ggc aac ctg tct atc gct aag cgc caa	307
Thr Lys Ala Ala Lys Thr Trp Gly Asn Leu Ser Ile Ala Lys Arg Gln	
55 60 65	
gct gtg ctt ttc aac ttc cgt gag ctg ctg aat gct cgc aag ggt gag	355
Ala Val Leu Phe Asn Phe Arg Glu Leu Leu Asn Ala Arg Lys Gly Glu	
70 75 80 85	
ctg gcg gag atc atc act gca gag cac ggc aag gtc ttg tcc gat gcc	403
Leu Ala Glu Ile Ile Thr Ala Glu His Gly Lys Val Leu Ser Asp Ala	
90 95 100	
atg ggt gaa atc ctg cgc ggc cag gaa gtc gtg gag ctt gct acc ggt	451
Met Gly Glu Ile Leu Arg Gly Gln Glu Val Val Glu Leu Ala Thr Gly	
105 110 115	
ttc cca cac ctg ctt aaa ggt gcg ttc aac gag aac gtc tcc acc ggc	499
Phe Pro His Leu Leu Lys Gly Ala Phe Asn Glu Asn Val Ser Thr Gly	
120 125 130	
att gat gtg tat tcc ttg aag cag cca ctg ggt gtt gtc ggt atc atc	547
Ile Asp Val Tyr Ser Leu Lys Gln Pro Leu Gly Val Val Gly Ile Ile	
135 140 145	
agc ccg ttc aac ttc cct gcg atg gtg ccg atg tgg ttt ttc cca atc	595
Ser Pro Phe Asn Phe Pro Ala Met Val Pro Met Trp Phe Phe Pro Ile	
150 155 160 165	
gca atc gct gca ggc aac gca gtt att ttg aag cct tca gag aag gat	643
Ala Ile Ala Ala Gly Asn Ala Val Ile Leu Lys Pro Ser Glu Lys Asp	
170 175 180	
cct tcg gca gcg ctg tgg atg gct cag atc tgg aag gaa gct ggt ctt	691
Pro Ser Ala Ala Leu Trp Met Ala Gln Ile Trp Lys Glu Ala Gly Leu	
185 190 195	
cca gac ggc gta ttc aac gtg ctc cag ggc gac aag ctg gct gtt gat	739
Pro Asp Gly Val Phe Asn Val Leu Gln Gly Asp Lys Leu Ala Val Asp	
200 205 210	
ggt ttg ctg aac agc cct gat gtc tct gcg att tcc ttc gtg ggt tcc	787
Gly Leu Leu Asn Ser Pro Asp Val Ser Ala Ile Ser Phe Val Gly Ser	
215 220 225	
acc cca atc gca aag tac atc tac gag act tcc gcg aag aac ggc aag	835
Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser Ala Lys Asn Gly Lys	
230 235 240 245	
cgc gtc cag gcg ttg ggc ggc gcg aag aac cac atg ctg gtg ctg cca	883
Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His Met Leu Val Leu Pro	
250 255 260	
gat gct gat ctg gat ctg gtt gcc gat cag gca atc aac gca ggt tac	931
Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala Ile Asn Ala Gly Tyr	
265 270 275	
ggc gct gcc ggt gag cgt tgc atg gct gtt tct gtg gtc ttg gct att	979

Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser Val Val Leu Ala Ile  
 280 285 290  
 gaa tct gtt gcc gac gag ctc att gag aag atc aag gag cgc atc gac  
 1027  
 Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile Lys Glu Arg Ile Asp  
 295 300 305  
 acc ctg cgc atc ggc aac ggt gcc ggc gac gag cag ggc gag ccg cac  
 1075  
 Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu Gln Gly Glu Pro His  
 310 315 320 325  
 ctg ggc cca cta atc acc gac gtc cac cgc gac aag gtc gct tct tat  
 1123  
 Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp Lys Val Ala Ser Tyr  
 330 335 340  
 gtc gac atc gct gag gcc gac ggc gcc aag atc atc gtg gac ggg cgt  
 1171  
 Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile Ile Val Asp Gly Arg  
 345 350 355  
 aac tgc gcc gta gac ggg cac gag gag ggc ttc ttc ttc ggc cct acg  
 1219  
 Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe Phe Phe Gly Pro Thr  
 360 365 370  
 ctt atc gac gac atc cca ctc acg ttc cgc gcc tac acc gaa gaa atc  
 1267  
 Leu Ile Asp Asp Ile Pro Leu Thr Phe Arg Ala Tyr Thr Glu Glu Ile  
 375 380 385  
 ttc ggc ccg gtc ctc tct gtc gtt cgt gtc gca tcc ttc gac gag gca  
 1315  
 Phe Gly Pro Val Leu Ser Val Val Arg Val Ala Ser Phe Asp Glu Ala  
 390 395 400 405  
 att gag ctg atc aac tcc ggt gaa ttc ggc aac gga acc gca atc ttc  
 1363  
 Ile Glu Leu Ile Asn Ser Gly Glu Phe Gly Asn Gly Thr Ala Ile Phe  
 410 415 420  
 acc aac gat ggt gga gcg gca cgc cgc ttc cag cat gag atc gaa gtg  
 1411  
 Thr Asn Asp Gly Gly Ala Ala Arg Arg Phe Gln His Glu Ile Glu Val  
 425 430 435  
 ggc atg atc ggc atc aac gta cca atc cca gtg cct gtt gcg tac cac  
 1459  
 Gly Met Ile Gly Ile Asn Val Pro Ile Pro Val Pro Val Ala Tyr His  
 440 445 450  
 tcc ttc ggt ggt tgg aag aac tcc ctc ttc ggt gac gcc aag gca tat  
 1507  
 Ser Phe Gly Gly Trp Lys Asn Ser Leu Phe Gly Asp Ala Lys Ala Tyr  
 455 460 465  
 ggc act caa ggt ttt gat ttc ttc acc agg gaa aag gcg atc acc agc  
 1555  
 Gly Thr Gln Gly Phe Asp Phe Phe Thr Arg Glu Lys Ala Ile Thr Ser

470					475					480					485
cgt	tgg	ctc	gac	cca	gca	acc	cac	ggt	ggc	att	aac	ctc	ggt	ttc	cca
1603															
Arg	Trp	Leu	Asp	Pro	Ala	Thr	His	Gly	Gly	Ile	Asn	Leu	Gly	Phe	Pro
				490					495					500	

cag aac gat taattgaagg agagcacagg act  
1635  
Gln Asn Asp

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<210> 136
<211> 504
<212> PRT
<213> Corynebacterium glutamicum
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<400> 136															
Met	Ser	Glu	Pro	Gln	Thr	Ile	Ser	His	Trp	Ile	Asp	Gly	Ala	Ile	Ser
1				5					10					15	
Pro	Ser	Thr	Ser	Gly	Lys	Thr	Ala	Pro	Val	Tyr	Asn	Pro	Ala	Thr	Gly
			20					25					30		
Gln	Val	Thr	Ala	Asn	Val	Ala	Leu	Ala	Ser	Gln	Glu	Glu	Ile	Asp	Ala
		35					40					45			
Thr	Ile	Ala	Ser	Ala	Thr	Lys	Ala	Ala	Lys	Thr	Trp	Gly	Asn	Leu	Ser
	50					55					60				
Ile	Ala	Lys	Arg	Gln	Ala	Val	Leu	Phe	Asn	Phe	Arg	Glu	Leu	Leu	Asn
65					70					75					80
Ala	Arg	Lys	Gly	Glu	Leu	Ala	Glu	Ile	Ile	Thr	Ala	Glu	His	Gly	Lys
				85					90					95	
Val	Leu	Ser	Asp	Ala	Met	Gly	Glu	Ile	Leu	Arg	Gly	Gln	Glu	Val	Val
			100					105					110		
Glu	Leu	Ala	Thr	Gly	Phe	Pro	His	Leu	Leu	Lys	Gly	Ala	Phe	Asn	Glu
		115					120					125			
Asn	Val	Ser	Thr	Gly	Ile	Asp	Val	Tyr	Ser	Leu	Lys	Gln	Pro	Leu	Gly
	130					135					140				
Val	Val	Gly	Ile	Ile	Ser	Pro	Phe	Asn	Phe	Pro	Ala	Met	Val	Pro	Met
145					150					155					160
Trp	Phe	Phe	Pro	Ile	Ala	Ile	Ala	Ala	Gly	Asn	Ala	Val	Ile	Leu	Lys
				165					170					175	
Pro	Ser	Glu	Lys	Asp	Pro	Ser	Ala	Ala	Leu	Trp	Met	Ala	Gln	Ile	Trp
			180					185					190		
Lys	Glu	Ala	Gly	Leu	Pro	Asp	Gly	Val	Phe	Asn	Val	Leu	Gln	Gly	Asp
		195					200					205			
Lys	Leu	Ala	Val	Asp	Gly	Leu	Leu	Asn	Ser	Pro	Asp	Val	Ser	Ala	Ile
	210					215					220				

Ser Phe Val Gly Ser Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser  
 225 230 235 240  
 Ala Lys Asn Gly Lys Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His  
 245 250 255  
 Met Leu Val Leu Pro Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala  
 260 265 270  
 Ile Asn Ala Gly Tyr Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser  
 275 280 285  
 Val Val Leu Ala Ile Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile  
 290 295 300  
 Lys Glu Arg Ile Asp Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu  
 305 310 315 320  
 Gln Gly Glu Pro His Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp  
 325 330 335  
 Lys Val Ala Ser Tyr Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile  
 340 345 350  
 Ile Val Asp Gly Arg Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe  
 355 360 365  
 Phe Phe Gly Pro Thr Leu Ile Asp Asp Ile Pro Leu Thr Phe Arg Ala  
 370 375 380  
 Tyr Thr Glu Glu Ile Phe Gly Pro Val Leu Ser Val Val Arg Val Ala  
 385 390 395 400  
 Ser Phe Asp Glu Ala Ile Glu Leu Ile Asn Ser Gly Glu Phe Gly Asn  
 405 410 415  
 Gly Thr Ala Ile Phe Thr Asn Asp Gly Gly Ala Ala Arg Arg Phe Gln  
 420 425 430  
 His Glu Ile Glu Val Gly Met Ile Gly Ile Asn Val Pro Ile Pro Val  
 435 440 445  
 Pro Val Ala Tyr His Ser Phe Gly Gly Trp Lys Asn Ser Leu Phe Gly  
 450 455 460  
 Asp Ala Lys Ala Tyr Gly Thr Gln Gly Phe Asp Phe Phe Thr Arg Glu  
 465 470 475 480  
 Lys Ala Ile Thr Ser Arg Trp Leu Asp Pro Ala Thr His Gly Gly Ile  
 485 490 495  
 Asn Leu Gly Phe Pro Gln Asn Asp  
 500

&lt;210&gt; 137

&lt;211&gt; 531

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(508)

&lt;223&gt; RXS02299

&lt;400&gt; 137

acgcggggggt tggtgccgga tcgaaatatt ccttttccttg tcattctcacg ctatgatttc 60

taaaacttgc	aggacaaccc	ccataaggac	accacaggac	atg	ctg	cgc	acc	atc		115
				Met	Leu	Arg	Thr	Ile		
				1				5		

ctc	gga	agt	aag	att	cac	cga	gcc	act	gtc	act	caa	gct	gat	cta	gat	163
Leu	Gly	Ser	Lys	Ile	His	Arg	Ala	Thr	Val	Thr	Gln	Ala	Asp	Leu	Asp	
				10					15					20		

tat	gtt	ggc	tct	gta	acc	atc	gac	gcc	gac	ctg	gtt	cac	gcc	gcc	gga	211
Tyr	Val	Gly	Ser	Val	Thr	Ile	Asp	Ala	Asp	Leu	Val	His	Ala	Ala	Gly	
			25					30					35			

ttg	atc	gaa	ggc	gaa	aaa	gtt	gcc	atc	gta	gac	atc	acc	aac	ggc	gct	259
Leu	Ile	Glu	Gly	Glu	Lys	Val	Ala	Ile	Val	Asp	Ile	Thr	Asn	Gly	Ala	
		40					45					50				

cgt	ctg	gaa	act	tat	gtc	att	gtg	ggc	gac	gcc	gga	acg	ggc	aat	att	307
Arg	Leu	Glu	Thr	Tyr	Val	Ile	Val	Gly	Asp	Ala	Gly	Thr	Gly	Asn	Ile	
	55					60					65					

tgc	atc	aat	ggc	gcc	gct	gca	cac	ctt	att	aat	cct	ggc	gat	ctt	gtg	355
Cys	Ile	Asn	Gly	Ala	Ala	Ala	His	Leu	Ile	Asn	Pro	Gly	Asp	Leu	Val	
70					75					80					85	

atc	atc	atg	agc	tac	ctt	cag	gca	act	gat	gcg	gaa	gcc	aag	gcg	tat	403
Ile	Ile	Met	Ser	Tyr	Leu	Gln	Ala	Thr	Asp	Ala	Glu	Ala	Lys	Ala	Tyr	
				90					95					100		

gag	cca	aag	att	gtg	cac	gtg	gac	gcc	gac	aac	cgc	atc	gtt	gcg	ctc	451
Glu	Pro	Lys	Ile	Val	His	Val	Asp	Ala	Asp	Asn	Arg	Ile	Val	Ala	Leu	
			105					110						115		

ggc	aac	gat	ctt	gcg	gaa	gca	cta	cct	gga	tcc	ggg	ctt	ttg	acg	tcg	499
Gly	Asn	Asp	Leu	Ala	Glu	Ala	Leu	Pro	Gly	Ser	Gly	Leu	Leu	Thr	Ser	
		120					125					130				

aga	agc	att	tagcgtttta	gctcgccaat	att		531
Arg	Ser	Ile					
		135					

&lt;210&gt; 138

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 138

Met	Leu	Arg	Thr	Ile	Leu	Gly	Ser	Lys	Ile	His	Arg	Ala	Thr	Val	Thr
1				5					10					15	

Gln	Ala	Asp	Leu	Asp	Tyr	Val	Gly	Ser	Val	Thr	Ile	Asp	Ala	Asp	Leu
			20					25					30		

Val	His	Ala	Ala	Gly	Leu	Ile	Glu	Gly	Glu	Lys	Val	Ala	Ile	Val	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
Ile Thr Asn Gly Ala Arg Leu Glu Thr Tyr Val	Ile Val Gly Asp Ala	
50	55	60
Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn		
65	70	75
Pro Gly Asp Leu Val Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala		
85	90	95
Glu Ala Lys Ala Tyr Glu Pro Lys Ile Val His Val Asp Ala Asp Asn		
100	105	110
Arg Ile Val Ala Leu Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser		
115	120	125
Gly Leu Leu Thr Ser Arg Ser Ile		
130	135	

&lt;210&gt; 139

&lt;211&gt; 1053

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1030)

&lt;223&gt; RXA01561

&lt;400&gt; 139

gtgcccagaa attctgcttg cactcaccca agccgttttag caaattgaac ctcacgttca 60

taataatggtt cattttcatc gagttctaga aaacacaggc	atg ctc acc ctc aac	115
	Met Leu Thr Leu Asn	
	1	5

gat gtc atc acc gcc caa caa cga acc gcc cct cat gtt cga cga acg	163
Asp Val Ile Thr Ala Gln Gln Arg Thr Ala Pro His Val Arg Arg Thr	
10	15
20	

cca ctt ttc gaa gca gac ccc atc gac ggc aca caa atc tgg atc aaa	211
Pro Leu Phe Glu Ala Asp Pro Ile Asp Gly Thr Gln Ile Trp Ile Lys	
25	30
35	

gca gag ttc ctc caa aag tgc ggc gtg ttc aaa acg cgt gga gca ttc	259
Ala Glu Phe Leu Gln Lys Cys Gly Val Phe Lys Thr Arg Gly Ala Phe	
40	45
50	

aac cgc cag ctc gca gct tcg gaa aac gga cta ctc gac cca acg gtt	307
Asn Arg Gln Leu Ala Ala Ser Glu Asn Gly Leu Leu Asp Pro Thr Val	
55	60
65	

ggc atc gtc gcg gca tca ggc gga aac gca gga ctc gca aat gct ttt	355
Gly Ile Val Ala Ala Ser Gly Gly Asn Ala Gly Leu Ala Asn Ala Phe	
70	75
80	85

gcc gca gca tcc tta agc gtt ccc gcc acg gta ttg gtg ccc gaa act	403
Ala Ala Ala Ser Leu Ser Val Pro Ala Thr Val Leu Val Pro Glu Thr	
90	95
100	

gcc cca caa gta aaa gtt gat cgc ctc aag caa tac ggt gca acc gtg 451  
 Ala Pro Gln Val Lys Val Asp Arg Leu Lys Gln Tyr Gly Ala Thr Val  
 105 110 115

caa caa atc gga tct gaa tat gcg gaa gca ttt gag gca gct caa acc 499  
 Gln Gln Ile Gly Ser Glu Tyr Ala Glu Ala Phe Glu Ala Ala Gln Thr  
 120 125 130

ttt gag tcg gaa act ggt gct ctg ttt tgc cac gcc tac gac cag ccc 547  
 Phe Glu Ser Glu Thr Gly Ala Leu Phe Cys His Ala Tyr Asp Gln Pro  
 135 140 145

gac atc gca gct gga gca ggc gtc att ggg cta gaa att gtc gaa gat 595  
 Asp Ile Ala Ala Gly Ala Gly Val Ile Gly Leu Glu Ile Val Glu Asp  
 150 155 160 165

ctt ccc gac gtt gac acc atc gtg gtt gct gtc ggt ggc ggt gga ctc 643  
 Leu Pro Asp Val Asp Thr Ile Val Val Ala Val Gly Gly Gly Gly Leu  
 170 175 180

tat gca gga atc gca gcc gtc gta gca gcc cac gac atc aaa gtg gtg 691  
 Tyr Ala Gly Ile Ala Ala Val Val Ala Ala His Asp Ile Lys Val Val  
 185 190 195

gcc gtt gaa ccc tcc aaa att cca acc ctg cac aac tca ctc att gcc 739  
 Ala Val Glu Pro Ser Lys Ile Pro Thr Leu His Asn Ser Leu Ile Ala  
 200 205 210

ggc caa cca gtc gat gtg aac gtt tct ggt atc gcg gca gat tct ttg 787  
 Gly Gln Pro Val Asp Val Asn Val Ser Gly Ile Ala Ala Asp Ser Leu  
 215 220 225

ggg gct cgc caa att gga cga gaa gcc ttt gac atc gca act gcc cat 835  
 Gly Ala Arg Gln Ile Gly Arg Glu Ala Phe Asp Ile Ala Thr Ala His  
 230 235 240 245

ccc cca ata ggc gtc cta gtg gac gat gaa gca atc atc gca gct cga 883  
 Pro Pro Ile Gly Val Leu Val Asp Asp Glu Ala Ile Ile Ala Ala Arg  
 250 255 260

cgc cac ctc tgg gac aac tac cgc atc cct gcc gag cat ggc gct gcc 931  
 Arg His Leu Trp Asp Asn Tyr Arg Ile Pro Ala Glu His Gly Ala Ala  
 265 270 275

gca gca ctc gcc tct ctt acc agt gga gca tac aaa cct gca gca gat 979  
 Ala Ala Leu Ala Ser Leu Thr Ser Gly Ala Tyr Lys Pro Ala Ala Asp  
 280 285 290

gaa aaa gtg gca gtc att gtg tgc gga gcg aac act gac ctc aca aca  
 1027  
 Glu Lys Val Ala Val Ile Val Cys Gly Ala Asn Thr Asp Leu Thr Thr  
 295 300 305

ctg tgatgtgatt tcaaacgata aca  
 1053  
 Leu  
 310

&lt;210&gt; 140



&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 140

Met	Leu	Thr	Leu	Asn	Asp	Val	Ile	Thr	Ala	Gln	Gln	Arg	Thr	Ala	Pro	1	5	10	15
His	Val	Arg	Arg	Thr	Pro	Leu	Phe	Glu	Ala	Asp	Pro	Ile	Asp	Gly	Thr	20	25	30	
Gln	Ile	Trp	Ile	Lys	Ala	Glu	Phe	Leu	Gln	Lys	Cys	Gly	Val	Phe	Lys	35	40	45	
Thr	Arg	Gly	Ala	Phe	Asn	Arg	Gln	Leu	Ala	Ala	Ser	Glu	Asn	Gly	Leu	50	55	60	
Leu	Asp	Pro	Thr	Val	Gly	Ile	Val	Ala	Ala	Ser	Gly	Gly	Asn	Ala	Gly	65	70	75	80
Leu	Ala	Asn	Ala	Phe	Ala	Ala	Ala	Ser	Leu	Ser	Val	Pro	Ala	Thr	Val	85	90	95	
Leu	Val	Pro	Glu	Thr	Ala	Pro	Gln	Val	Lys	Val	Asp	Arg	Leu	Lys	Gln	100	105	110	
Tyr	Gly	Ala	Thr	Val	Gln	Gln	Ile	Gly	Ser	Glu	Tyr	Ala	Glu	Ala	Phe	115	120	125	
Glu	Ala	Ala	Gln	Thr	Phe	Glu	Ser	Glu	Thr	Gly	Ala	Leu	Phe	Cys	His	130	135	140	
Ala	Tyr	Asp	Gln	Pro	Asp	Ile	Ala	Ala	Gly	Ala	Gly	Val	Ile	Gly	Leu	145	150	155	160
Glu	Ile	Val	Glu	Asp	Leu	Pro	Asp	Val	Asp	Thr	Ile	Val	Val	Ala	Val	165	170	175	
Gly	Gly	Gly	Gly	Leu	Tyr	Ala	Gly	Ile	Ala	Ala	Val	Val	Ala	Ala	His	180	185	190	
Asp	Ile	Lys	Val	Val	Ala	Val	Glu	Pro	Ser	Lys	Ile	Pro	Thr	Leu	His	195	200	205	
Asn	Ser	Leu	Ile	Ala	Gly	Gln	Pro	Val	Asp	Val	Asn	Val	Ser	Gly	Ile	210	215	220	
Ala	Ala	Asp	Ser	Leu	Gly	Ala	Arg	Gln	Ile	Gly	Arg	Glu	Ala	Phe	Asp	225	230	235	240
Ile	Ala	Thr	Ala	His	Pro	Pro	Ile	Gly	Val	Leu	Val	Asp	Asp	Glu	Ala	245	250	255	
Ile	Ile	Ala	Ala	Arg	Arg	His	Leu	Trp	Asp	Asn	Tyr	Arg	Ile	Pro	Ala	260	265	270	
Glu	His	Gly	Ala	Ala	Ala	Ala	Leu	Ala	Ser	Leu	Thr	Ser	Gly	Ala	Tyr	275	280	285	
Lys	Pro	Ala	Ala	Asp	Glu	Lys	Val	Ala	Val	Ile	Val	Cys	Gly	Ala	Asn	290	295	300	

Thr Asp Leu Thr Thr Leu  
305 310

<210> 141  
<211> 1470  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
<221> CDS  
<222> (101)..(1447)  
<223> RXA01850

<400> 141  
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tcaccttgta caccaccaga gaaaaggccc accctcagcc atg gct atc agt gtt 115  
Met Ala Ile Ser Val  
1 5

gtt gat cta ttt agc atc ggt atc gga cca tca tcc tca cat acc gtc 163  
Val Asp Leu Phe Ser Ile Gly Ile Gly Pro Ser Ser Ser His Thr Val  
10 15 20

ggc ccc atg aga gcc gcc ctc acg tat atc tct gaa ttt ccc agc tcg 211  
Gly Pro Met Arg Ala Ala Leu Thr Tyr Ile Ser Glu Phe Pro Ser Ser  
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cat gtc gat atc acg ttg cac gga tcc ctt gcc gcc acc ggt aaa ggc 259  
His Val Asp Ile Thr Leu His Gly Ser Leu Ala Ala Thr Gly Lys Gly  
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His Cys Thr Asp Arg Ala Val Leu Leu Gly Leu Val Gly Trp Glu Pro  
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Ala Lys Gly Ser Val Asn Gly Pro Lys Gly Thr Val Ser Tyr Ser Leu  
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acg ttt gat cct cat cct ctt cca gaa cac ccc aat gcc gtt acc ttt 451  
Thr Phe Asp Pro His Pro Leu Pro Glu His Pro Asn Ala Val Thr Phe  
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Lys Gly Ser Thr Thr Arg Thr Tyr Leu Ser Val Gly Gly Gly Phe Ile  
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atg acg ttg gag gat ttc cgg aag ctg gac gat atc gga tca ggt gtg 547  
Met Thr Leu Glu Asp Phe Arg Lys Leu Asp Asp Ile Gly Ser Gly Val  
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tca acc att cat cca gag gca gag gtg cct tgt cct ttt cag aag agt 595  
Ser Thr Ile His Pro Glu Ala Glu Val Pro Cys Pro Phe Gln Lys Ser  
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Ser Gln Leu Leu Ala Tyr Gly Arg Asp Phe Ala Glu Val Met Lys Asp	
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Asn Glu Arg Leu Ile His Gly Asp Leu Gly Thr Val Asp Ala His Leu	
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Asp Arg Val Trp Gln Ile Met Gln Glu Cys Val Ala Gln Gly Ile Ala	
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acg ccg ggg att tta ccg ggt ggg ttg aat gtg caa cgt cgg gcg ccg	787
Thr Pro Gly Ile Leu Pro Gly Gly Leu Asn Val Gln Arg Arg Ala Pro	
215 220 225	
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Gln Val His Ala Leu Ile Ser Asn Gly Asp Thr Cys Glu Leu Gly Ala	
230 235 240 245	
gat ctt gat gct gtg gag tgg gtg aat ctg tac gcc ttg gcg gtg aat	883
Asp Leu Asp Ala Val Glu Trp Val Asn Leu Tyr Ala Leu Ala Val Asn	
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gaa gaa aac gcc gct ggt ggt cgt gtg gtt act gct ccg act aat ggt	931
Glu Glu Asn Ala Ala Gly Gly Arg Val Val Thr Ala Pro Thr Asn Gly	
265 270 275	
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Ala Ala Gly Ile Ile Pro Ala Val Met His Tyr Ala Arg Asp Phe Leu	
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310 315 320 325	
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360 365 370	
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 <213> Corynebacterium glutamicum

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 Glu Phe Pro Ser Ser His Val Asp Ile Thr Leu His Gly Ser Leu Ala  
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 Ala Thr Gly Lys Gly His Cys Thr Asp Arg Ala Val Leu Leu Gly Leu  
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 Val Gly Trp Glu Pro Thr Ile Val Pro Ile Asp Ala Ala Pro Ser Pro  
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 Gly Ala Pro Ile Pro Ala Lys Gly Ser Val Asn Gly Pro Lys Gly Thr  
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 Val Ser Tyr Ser Leu Thr Phe Asp Pro His Pro Leu Pro Glu His Pro  
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 Asn Ala Val Thr Phe Lys Gly Ser Thr Thr Arg Thr Tyr Leu Ser Val  
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 Gly Gly Gly Phe Ile Met Thr Leu Glu Asp Phe Arg Lys Leu Asp Asp  
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 Ile Gly Ser Gly Val Ser Thr Ile His Pro Glu Ala Glu Val Pro Cys  
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Pro Phe Gln Lys Ser Ser Gln Leu Leu Ala Tyr Gly Arg Asp Phe Ala  
 165 170 175  
 Glu Val Met Lys Asp Asn Glu Arg Leu Ile His Gly Asp Leu Gly Thr  
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 Val Asp Ala His Leu Asp Arg Val Trp Gln Ile Met Gln Glu Cys Val  
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 Ala Gln Gly Ile Ala Thr Pro Gly Ile Leu Pro Gly Gly Leu Asn Val  
 210 215 220  
 Gln Arg Arg Ala Pro Gln Val His Ala Leu Ile Ser Asn Gly Asp Thr  
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 Cys Glu Leu Gly Ala Asp Leu Asp Ala Val Glu Trp Val Asn Leu Tyr  
 245 250 255  
 Ala Leu Ala Val Asn Glu Glu Asn Ala Ala Gly Gly Arg Val Val Thr  
 260 265 270  
 Ala Pro Thr Asn Gly Ala Ala Gly Ile Ile Pro Ala Val Met His Tyr  
 275 280 285  
 Ala Arg Asp Phe Leu Thr Gly Phe Gly Ala Glu Gln Ala Arg Thr Phe  
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 305 310 315 320  
 Ile Ser Gly Ala Glu Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ser  
 325 330 335  
 Ala Met Ala Ala Ala Gly Leu Cys Ala Val Leu Gly Gly Ser Pro Gln  
 340 345 350  
 Gln Val Glu Asn Ala Ala Glu Ile Ala Leu Glu His Asn Leu Gly Leu  
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 Thr Cys Asp Pro Val Gly Gly Leu Val Gln Ile Pro Cys Ile Glu Arg  
 370 375 380  
 Asn Ala Ile Ala Ala Met Lys Ser Ile Asn Ala Ala Arg Leu Ala Arg  
 385 390 395 400  
 Ile Gly Asp Gly Asn Asn Arg Val Ser Leu Asp Asp Val Val Val Thr  
 405 410 415  
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 Leu Gly Gly Leu Ala Thr Thr Leu Gly Phe Pro Val Ser Met Thr Glu  
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Cys

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 <211> 1425

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1402)

&lt;223&gt; RXA00580

&lt;400&gt; 143

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                                         Met Thr Asp Ala His
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caa gcg gac gat gtc cgt tac cag cca ctg aac gag ctt gat cct gag 163
Gln Ala Asp Asp Val Arg Tyr Gln Pro Leu Asn Glu Leu Asp Pro Glu
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gtg gct gct gcc atc gct ggg gaa ctt gcc cgt caa cgc gat aca tta 211
Val Ala Ala Ala Ile Ala Gly Glu Leu Ala Arg Gln Arg Asp Thr Leu
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gag atg atc gcg tct gag aac ttc gtt ccc cgt tct gtt ttg cag gcg 259
Glu Met Ile Ala Ser Glu Asn Phe Val Pro Arg Ser Val Leu Gln Ala
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cag ggt tct gtt ctt acc aat aag tat gcc gag ggt tac cct ggc cgc 307
Gln Gly Ser Val Leu Thr Asn Lys Tyr Ala Glu Gly Tyr Pro Gly Arg
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cgt tac tac ggt ggt tgc gaa caa gtt gac atc att gag gat ctt gca 355
Arg Tyr Tyr Gly Gly Cys Glu Gln Val Asp Ile Ile Glu Asp Leu Ala
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cgt gat cgt gcg aag gct ctc ttc ggt gca gag ttc gcc aat gtt cag 403
Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu Phe Ala Asn Val Gln
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Pro His Ser Gly Ala Gln Ala Asn Ala Ala Val Leu Met Thr Leu Ala
                        105                        110                        115

gag cca ggc gac aag atc atg ggt ctg tct ttg gct cat ggt ggt cac 499
Glu Pro Gly Asp Lys Ile Met Gly Leu Ser Leu Ala His Gly Gly His
                        120                        125                        130

ttg acc cac gga atg aag ttg aac ttc tcc gga aag ctg tac gag gtt 547
Leu Thr His Gly Met Lys Leu Asn Phe Ser Gly Lys Leu Tyr Glu Val
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gtt gcg tac ggt gtt gat cct gag acc atg cgt gtt gat atg gat cag 595
Val Ala Tyr Gly Val Asp Pro Glu Thr Met Arg Val Asp Met Asp Gln
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gtt cgt gag att gct ctg aag gag cag cca aag gta att atc gct ggc 643
Val Arg Glu Ile Ala Leu Lys Glu Gln Pro Lys Val Ile Ile Ala Gly
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Trp Ser Ala Tyr Pro Arg His Leu Asp Phe Glu Ala Phe Gln Ser Ile

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ggt	ctt	gtt	gct	gct	ggt	ttg	cac	cca	agc	cca	gtt	cct	tac	tct	gat	787		
Gly	Leu	Val	Ala	Ala	Gly	Leu	His	Pro	Ser	Pro	Val	Pro	Tyr	Ser	Asp			
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Phe	Pro	Gly	Gln	Gln	Gly	Gly	Pro	Leu	Met	His	Ala	Val	Ala	Ala	Lys			
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gct	act	tct	ttg	aag	att	gct	ggc	act	gag	cag	ttc	cgt	gac	cgt	cag	979		
Ala	Thr	Ser	Leu	Lys	Ile	Ala	Gly	Thr	Glu	Gln	Phe	Arg	Asp	Arg	Gln			
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gct	cgc	acg	ttg	gag	ggt	gct	cgc	att	ctt	gct	gag	cgt	ctg	act	gct			
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Ala	Arg	Thr	Leu	Glu	Gly	Ala	Arg	Ile	Leu	Ala	Glu	Arg	Leu	Thr	Ala			
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1075																		
Ser	Asp	Ala	Lys	Ala	Ala	Gly	Val	Asp	Val	Leu	Thr	Gly	Gly	Thr	Asp			
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gcg	gtt	cct	ttc	gat	cct	cgt	cca	cca	atg	gtt	act	tct	ggt	ctg	cgt			
1219																		
Ala	Val	Pro	Phe	Asp	Pro	Arg	Pro	Pro	Met	Val	Thr	Ser	Gly	Leu	Arg			
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Ile	Gly	Thr	Pro	Ala	Leu	Ala	Thr	Arg	Gly	Phe	Asp	Ile	Pro	Ala	Phe			
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1363

Ala Asp Ile Glu Ser Leu Arg Gly Arg Val Ala Lys Leu Ala Ala Asp  
410 415 420

tac cca ctg tat gag ggc ttg gaa gac tgg acc atc gtc taagtttttc  
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<210> 144

<211> 434

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

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Gln Arg Asp Thr Leu Glu Met Ile Ala Ser Glu Asn Phe Val Pro Arg  
35 40 45

Ser Val Leu Gln Ala Gln Gly Ser Val Leu Thr Asn Lys Tyr Ala Glu  
50 55 60

Gly Tyr Pro Gly Arg Arg Tyr Tyr Gly Gly Cys Glu Gln Val Asp Ile  
65 70 75 80

Ile Glu Asp Leu Ala Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu  
85 90 95

Phe Ala Asn Val Gln Pro His Ser Gly Ala Gln Ala Asn Ala Ala Val  
100 105 110

Leu Met Thr Leu Ala Glu Pro Gly Asp Lys Ile Met Gly Leu Ser Leu  
115 120 125

Ala His Gly Gly His Leu Thr His Gly Met Lys Leu Asn Phe Ser Gly  
130 135 140

Lys Leu Tyr Glu Val Val Ala Tyr Gly Val Asp Pro Glu Thr Met Arg  
145 150 155 160

Val Asp Met Asp Gln Val Arg Glu Ile Ala Leu Lys Glu Gln Pro Lys  
165 170 175

Val Ile Ile Ala Gly Trp Ser Ala Tyr Pro Arg His Leu Asp Phe Glu  
180 185 190

Ala Phe Gln Ser Ile Ala Ala Glu Val Gly Ala Lys Leu Trp Val Asp  
195 200 205

Met Ala His Phe Ala Gly Leu Val Ala Ala Gly Leu His Pro Ser Pro  
210 215 220



Val Pro Tyr Ser Asp Val Val Ser Ser Thr Val His Lys Thr Leu Gly  
 225 230 235 240  
 Gly Pro Arg Ser Gly Ile Ile Leu Ala Lys Gln Glu Tyr Ala Lys Lys  
 245 250 255  
 Leu Asn Ser Ser Val Phe Pro Gly Gln Gln Gly Gly Pro Leu Met His  
 260 265 270  
 Ala Val Ala Ala Lys Ala Thr Ser Leu Lys Ile Ala Gly Thr Glu Gln  
 275 280 285  
 Phe Arg Asp Arg Gln Ala Arg Thr Leu Glu Gly Ala Arg Ile Leu Ala  
 290 295 300  
 Glu Arg Leu Thr Ala Ser Asp Ala Lys Ala Ala Gly Val Asp Val Leu  
 305 310 315 320  
 Thr Gly Gly Thr Asp Val His Leu Val Leu Ala Asp Leu Arg Asn Ser  
 325 330 335  
 Gln Met Asp Gly Gln Gln Ala Glu Asp Leu Leu His Glu Val Gly Ile  
 340 345 350  
 Thr Val Asn Arg Asn Ala Val Pro Phe Asp Pro Arg Pro Pro Met Val  
 355 360 365  
 Thr Ser Gly Leu Arg Ile Gly Thr Pro Ala Leu Ala Thr Arg Gly Phe  
 370 375 380  
 Asp Ile Pro Ala Phe Thr Glu Val Ala Asp Ile Ile Gly Thr Ala Leu  
 385 390 395 400  
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 Lys Leu Ala Ala Asp Tyr Pro Leu Tyr Glu Gly Leu Glu Asp Trp Thr  
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Ile Val

<210> 145  
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 <223> RXA01821

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 Thr Ser Ile Glu Asp Asn Gly Asp His Val Val Ile Gln Ala Gly Glu

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Asn	Leu	Pro	Cys	Phe	Ile	Arg	Asp	Arg	Asp	Gly	Phe	His	Val	Phe	Gly	
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Ala	Pro	Cys	Val	Asp	Gly	Tyr	Ser	Ile	Lys	Ile	Ala	Gly	Leu	Asp	Glu	
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Trp	Gly	Val	Pro	Leu	Ser	Leu	Asp	Pro	Pro	Met	Cys	Pro	Arg			
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&lt;210&gt; 146

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 146

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Glu	Thr	Thr	Ile	Val	Asp	Arg	Val	Ile	Val	Thr	Thr	Gly	Ser	Trp	Thr
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Ser	Glu	Leu	Val	Pro	Ser	Ile	Ala	Pro	Leu	Leu	Glu	Val	Arg	Arg	Leu
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Val	Leu	Thr	Trp	Phe	Leu	Pro	Asn	Asn	Pro	Val	Asp	Phe	Gln	Pro	Glu
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Asn	Leu	Pro	Cys	Phe	Ile	Arg	Asp	Arg	Asp	Gly	Phe	His	Val	Phe	Gly
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Ala	Pro	Cys	Val	Asp	Gly	Tyr	Ser	Ile	Lys	Ile	Ala	Gly	Leu	Asp	Glu
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Trp	Gly	Val	Pro	Leu	Ser	Leu	Asp	Pro	Pro	Met	Cys	Pro	Arg
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Gly	Tyr	Gly	Ala	Phe	Thr	Gly	Glu	Ser	Arg	Leu	Phe	Arg	Met	Ala	Tyr		
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cac	gaa	ggc	agc	acc	tac	gtt	ccg	ttg	ctc	aaa	cgc	gca	cga	gca	cta	307	
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Val	Glu	Ser	Val	Glu	Arg	Tyr	Glu	Leu	Pro	His	Glu	Arg	Leu	Thr	Ala		
			105					110					115				
gcg	cag	atg	cgc	agc	gtt	acc	cag	gtc	tagacttccg								488
Ala	Gln	Met	Arg	Ser	Val	Thr	Gln	Val									
		120					125										

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<210> 148
<211> 126
<212> PRT
<213> Corynebacterium glutamicum
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<400> 148
Met Lys Ile Ala Val Ile Gly Leu Gly Ser Thr Gly Ser Met Ala Leu
  1             5             10             15
Trp His Leu Ser Asn Ile Pro Gly Val Glu Ala Ile Gly Phe Glu Gln
          20             25             30
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Phe Gly Ile Ser His Gly Tyr Gly Ala Phe Thr Gly Glu Ser Arg Leu  
           35                          40                          45  
 Phe Arg Met Ala Tyr His Glu Gly Ser Thr Tyr Val Pro Leu Leu Lys  
           50                          55                          60  
 Arg Ala Arg Ala Leu Trp Ser Ser Leu Ser Glu Ile Ser Gly Arg Glu  
           65                          70                          75                          80  
 Leu Phe His Asn Phe Gly Val Leu Ser Thr Gly Lys Glu Asp Glu Ala  
                           85                          90                          95  
 Pro Phe Gln Arg Leu Val Glu Ser Val Glu Arg Tyr Glu Leu Pro His  
                           100                          105                          110  
 Glu Arg Leu Thr Ala Ala Gln Met Arg Ser Val Thr Gln Val  
           115                          120                          125

<210> 149  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(460)  
 <223> FRXA02263

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 tgtgggaatc acccgcactg gcttgagaga agaaacaaca atg aaa att gcg gta 115  
   Met Lys Ile Ala Val  
   1                          5  
 atc ggc ctt gga tca acc ggc tcc atg gca ctg tgg cac tta agt aac 163  
 Ile Gly Leu Gly Ser Thr Gly Ser Met Ala Leu Trp His Leu Ser Asn  
                           10                          15                          20  
 atc cca ggt gta gag gcc atc ggc ttt gaa caa ttc ggc atc tcc cat 211  
 Ile Pro Gly Val Glu Ala Ile Gly Phe Glu Gln Phe Gly Ile Ser His  
                           25                          30                          35  
 ggc tac ggc gca ttc aca ggg gag tcc cga ctg ttt cgc atg gcc tac 259  
 Gly Tyr Gly Ala Phe Thr Gly Glu Ser Arg Leu Phe Arg Met Ala Tyr  
                           40                          45                          50  
 cac gaa ggc agc acc tac gtt ccg ttg ctc aaa cgc gca cga gca cta 307  
 His Glu Gly Ser Thr Tyr Val Pro Leu Leu Lys Arg Ala Arg Ala Leu  
                           55                          60                          65  
 tgg tca tca ctg agc gag att tcc gga cgc gaa ctc ttc cac aac ttc 355  
 Trp Ser Ser Leu Ser Glu Ile Ser Gly Arg Glu Leu Phe His Asn Phe  
           70                          75                          80                          85  
 ggt gtc tta agc acc ggc aag gaa gac gaa gca ccc ttc caa cgc ctg 403  
 Gly Val Leu Ser Thr Gly Lys Glu Asp Glu Ala Pro Phe Gln Arg Leu  
                           90                          95                          100  
 gtg gaa tca gtg gaa cgt tat gag ctg cca cat gaa cga ctt acc gcc 451

Val Glu Ser Val Glu Arg Tyr Glu Leu Pro His Glu Arg Leu Thr Ala  
 105 110 115

gcg cag atg  
 Ala Gln Met  
 120

460

<210> 150  
 <211> 120  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 150  
 Met Lys Ile Ala Val Ile Gly Leu Gly Ser Thr Gly Ser Met Ala Leu  
 1 5 10 15  
 Trp His Leu Ser Asn Ile Pro Gly Val Glu Ala Ile Gly Phe Glu Gln  
 20 25 30  
 Phe Gly Ile Ser His Gly Tyr Gly Ala Phe Thr Gly Glu Ser Arg Leu  
 35 40 45  
 Phe Arg Met Ala Tyr His Glu Gly Ser Thr Tyr Val Pro Leu Leu Lys  
 50 55 60  
 Arg Ala Arg Ala Leu Trp Ser Ser Leu Ser Glu Ile Ser Gly Arg Glu  
 65 70 75 80  
 Leu Phe His Asn Phe Gly Val Leu Ser Thr Gly Lys Glu Asp Glu Ala  
 85 90 95  
 Pro Phe Gln Arg Leu Val Glu Ser Val Glu Arg Tyr Glu Leu Pro His  
 100 105 110  
 Glu Arg Leu Thr Ala Ala Gln Met  
 115 120

<210> 151  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1228)  
 <223> RXA02176

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 tggccctttt acttccaagc gcagaaagtt gcccggaagac atg acc gac ttc ccc 115  
 Met Thr Asp Phe Pro  
 1 5  
 acc ctg ccc tct gag ttc atc cct ggc gac ggc cgt ttc ggc tgc gga 163  
 Thr Leu Pro Ser Glu Phe Ile Pro Gly Asp Gly Arg Phe Gly Cys Gly  
 10 15 20  
 cct tcc aag gtt cga cca gaa cag att cag gct att gtc gac gga tcc 211

Pro	Ser	Lys	Val	Arg	Pro	Glu	Gln	Ile	Gln	Ala	Ile	Val	Asp	Gly	Ser	
			25					30					35			
gca	tcc	gtc	atc	ggc	acc	tca	cac	cgt	cag	ccg	gca	gta	aaa	aac	gtc	259
Ala	Ser	Val	Ile	Gly	Thr	Ser	His	Arg	Gln	Pro	Ala	Val	Lys	Asn	Val	
		40					45					50				
gtg	ggc	tca	atc	cgc	gag	gga	ctc	tcc	gac	ctc	ttc	tcc	ctt	cca	gaa	307
Val	Gly	Ser	Ile	Arg	Glu	Gly	Leu	Ser	Asp	Leu	Phe	Ser	Leu	Pro	Glu	
	55					60					65					
ggc	tac	gag	atc	atc	ctt	tcc	cta	ggc	ggc	gcg	acc	gca	ttc	tgg	gat	355
Gly	Tyr	Glu	Ile	Ile	Leu	Ser	Leu	Gly	Gly	Ala	Thr	Ala	Phe	Trp	Asp	
70					75					80					85	
gca	gca	acc	ttc	gga	ctc	att	gaa	aag	aag	tcc	ggc	cac	ctt	tct	ttc	403
Ala	Ala	Thr	Phe	Gly	Leu	Ile	Glu	Lys	Lys	Ser	Gly	His	Leu	Ser	Phe	
				90					95					100		
ggc	gag	ttc	tcc	tcc	aag	ttc	gca	aag	gct	tct	aag	ctt	gct	cct	tgg	451
Gly	Glu	Phe	Ser	Ser	Lys	Phe	Ala	Lys	Ala	Ser	Lys	Leu	Ala	Pro	Trp	
			105					110					115			
ctc	gac	gag	cca	gag	atc	gtc	acc	gca	gaa	acc	ggc	gac	tct	ccg	gcc	499
Leu	Asp	Glu	Pro	Glu	Ile	Val	Thr	Ala	Glu	Thr	Gly	Asp	Ser	Pro	Ala	
		120					125					130				
cca	cag	gca	ttc	gaa	ggc	gcc	gat	gtt	att	gca	tgg	gca	cac	aac	gaa	547
Pro	Gln	Ala	Phe	Glu	Gly	Ala	Asp	Val	Ile	Ala	Trp	Ala	His	Asn	Glu	
	135					140					145					
acc	tcc	act	ggc	gcc	atg	gtt	cca	gtt	ctt	cgc	ccc	gaa	ggc	tct	gaa	595
Thr	Ser	Thr	Gly	Ala	Met	Val	Pro	Val	Leu	Arg	Pro	Glu	Gly	Ser	Glu	
150					155					160					165	
ggc	tcc	ctg	gtt	gcc	att	gac	gca	acc	tcc	ggc	gct	ggc	gga	ctg	cca	643
Gly	Ser	Leu	Val	Ala	Ile	Asp	Ala	Thr	Ser	Gly	Ala	Gly	Gly	Leu	Pro	
				170					175					180		
gta	gac	atc	aag	aac	tcc	gat	gtt	tac	tac	ttc	tcc	cca	cag	aag	tgc	691
Val	Asp	Ile	Lys	Asn	Ser	Asp	Val	Tyr	Tyr	Phe	Ser	Pro	Gln	Lys	Cys	
			185					190					195			
ttc	gca	tcc	gac	ggc	ggc	ctg	tgg	ctt	gca	gcg	atg	agc	cca	gca	gct	739
Phe	Ala	Ser	Asp	Gly	Gly	Leu	Trp	Leu	Ala	Ala	Met	Ser	Pro	Ala	Ala	
		200					205					210				
ctc	gag	cgc	atc	gag	aag	atc	aac	gct	tcc	gat	cgc	ttc	atc	cct	gag	787
Leu	Glu	Arg	Ile	Glu	Lys	Ile	Asn	Ala	Ser	Asp	Arg	Phe	Ile	Pro	Glu	
	215					220					225					
ttc	ctc	aac	ctg	cag	acc	gca	gtg	gat	aac	tcc	ctg	aag	aac	cag	acc	835
Phe	Leu	Asn	Leu	Gln	Thr	Ala	Val	Asp	Asn	Ser	Leu	Lys	Asn	Gln	Thr	
230					235					240					245	
tac	aac	acc	cca	gct	gtt	gct	acc	ttg	ctg	atg	ctg	gac	aac	cag	gtc	883
Tyr	Asn	Thr	Pro	Ala	Val	Ala	Thr	Leu	Leu	Met	Leu	Asp	Asn	Gln	Val	
				250					255					260		
aag	tgg	atg	aac	tcc	aac	ggc	ggc	ctg	gat	gga	atg	gtt	gct	cgc	acc	931
Lys	Trp	Met	Asn	Ser	Asn	Gly	Gly	Leu	Asp	Gly	Met	Val	Ala	Arg	Thr	

[illegible]

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<210> 152
<211> 376
<212> PRT
<213> Corynebacterium glutamicum
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<400> 152
Met Thr Asp Phe Pro Thr Leu Pro Ser Glu Phe Ile Pro Gly Asp Gly
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Arg Phe Gly Cys Gly Pro Ser Lys Val Arg Pro Glu Gln Ile Gln Ala
          20                      25                      30
Ile Val Asp Gly Ser Ala Ser Val Ile Gly Thr Ser His Arg Gln Pro
          35                      40                      45
Ala Val Lys Asn Val Val Gly Ser Ile Arg Glu Gly Leu Ser Asp Leu
          50                      55                      60
Phe Ser Leu Pro Glu Gly Tyr Glu Ile Ile Leu Ser Leu Gly Gly Ala
  65                      70                      75                      80
Thr Ala Phe Trp Asp Ala Ala Thr Phe Gly Leu Ile Glu Lys Lys Ser
          85                      90                      95

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Gly His Leu Ser Phe Gly Glu Phe Ser Ser Lys Phe Ala Lys Ala Ser  
                     100                    105                    110  
 Lys Leu Ala Pro Trp Leu Asp Glu Pro Glu Ile Val Thr Ala Glu Thr  
                     115                    120                    125  
 Gly Asp Ser Pro Ala Pro Gln Ala Phe Glu Gly Ala Asp Val Ile Ala  
                     130                    135                    140  
 Trp Ala His Asn Glu Thr Ser Thr Gly Ala Met Val Pro Val Leu Arg  
 145                    150                    155                    160  
 Pro Glu Gly Ser Glu Gly Ser Leu Val Ala Ile Asp Ala Thr Ser Gly  
                     165                    170                    175  
 Ala Gly Gly Leu Pro Val Asp Ile Lys Asn Ser Asp Val Tyr Tyr Phe  
                     180                    185                    190  
 Ser Pro Gln Lys Cys Phe Ala Ser Asp Gly Gly Leu Trp Leu Ala Ala  
                     195                    200                    205  
 Met Ser Pro Ala Ala Leu Glu Arg Ile Glu Lys Ile Asn Ala Ser Asp  
                     210                    215                    220  
 Arg Phe Ile Pro Glu Phe Leu Asn Leu Gln Thr Ala Val Asp Asn Ser  
 225                    230                    235                    240  
 Leu Lys Asn Gln Thr Tyr Asn Thr Pro Ala Val Ala Thr Leu Leu Met  
                     245                    250                    255  
 Leu Asp Asn Gln Val Lys Trp Met Asn Ser Asn Gly Gly Leu Asp Gly  
                     260                    265                    270  
 Met Val Ala Arg Thr Thr Ala Ser Ser Ser Ala Leu Tyr Asn Trp Ala  
                     275                    280                    285  
 Glu Ala Arg Glu Glu Ala Ser Pro Tyr Val Ala Asp Ala Ala Lys Arg  
                     290                    295                    300  
 Ser Leu Val Val Gly Thr Ile Asp Phe Asp Asp Ser Ile Asp Ala Ala  
 305                    310                    315                    320  
 Val Ile Ala Lys Ile Leu Arg Ala Asn Gly Ile Leu Asp Thr Glu Pro  
                     325                    330                    335  
 Tyr Arg Lys Leu Gly Arg Asn Gln Leu Arg Ile Gly Met Phe Pro Ala  
                     340                    345                    350  
 Ile Asp Ser Thr Asp Val Glu Lys Leu Thr Gly Ala Ile Asp Phe Ile  
                     355                    360                    365  
 Leu Asp Gly Gly Phe Ala Arg Lys  
                     370                    375

&lt;210&gt; 153

&lt;211&gt; 1422

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;



&lt;221&gt; CDS

&lt;222&gt; (101)..(1399)

&lt;223&gt; RXN02758

&lt;400&gt; 153

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				Val	Thr	Glu	Leu	Ile		5
				1						

cag	aat	gaa	tcc	caa	gaa	atc	gct	gag	ctg	gaa	gcc	ggc	cag	cag	gtt	163
Gln	Asn	Glu	Ser	Gln	Glu	Ile	Ala	Glu	Leu	Glu	Ala	Gly	Gln	Gln	Val	
				10					15					20		

gca	ttg	cgt	gaa	ggg	tat	ctt	cct	gcg	gtg	atc	aca	gtg	agc	ggg	aaa	211
Ala	Leu	Arg	Glu	Gly	Tyr	Leu	Pro	Ala	Val	Ile	Thr	Val	Ser	Gly	Lys	
			25					30					35			

gac	cgc	cca	ggg	gtg	act	gcc	gcg	ttc	ttt	agg	gtc	ttg	tcc	gct	aat	259
Asp	Arg	Pro	Gly	Val	Thr	Ala	Ala	Phe	Phe	Arg	Val	Leu	Ser	Ala	Asn	
		40					45					50				

cag	gtt	cag	gtc	ttg	gac	gtt	gag	cag	tca	atg	ttc	cgt	ggc	ttt	ttg	307
Gln	Val	Gln	Val	Leu	Asp	Val	Glu	Gln	Ser	Met	Phe	Arg	Gly	Phe	Leu	
	55					60					65					

aac	ttg	gcg	gcg	ttt	gtg	ggg	atc	gca	cct	gag	cgt	gtc	gag	acc	gtc	355
Asn	Leu	Ala	Ala	Phe	Val	Gly	Ile	Ala	Pro	Glu	Arg	Val	Glu	Thr	Val	
70					75					80					85	

acc	aca	ggc	ctg	act	gac	acc	ctc	aag	gtg	cat	gga	cag	tcc	gtg	gtg	403
Thr	Thr	Gly	Leu	Thr	Asp	Thr	Leu	Lys	Val	His	Gly	Gln	Ser	Val	Val	
				90					95					100		

gtg	gag	ctg	cag	gaa	act	gtg	cag	tcg	tcc	cgt	cct	cgt	tct	tcc	cat	451
Val	Glu	Leu	Gln	Glu	Thr	Val	Gln	Ser	Ser	Arg	Pro	Arg	Ser	Ser	His	
			105					110					115			

gtt	gtt	gtg	gtg	ttg	ggg	gat	ccg	gtt	gat	gcg	ttg	gat	att	tcc	cgc	499
Val	Val	Val	Val	Leu	Gly	Asp	Pro	Val	Asp	Ala	Leu	Asp	Ile	Ser	Arg	
			120				125					130				

att	ggg	cag	acc	ctg	gcg	gat	tac	gat	gcc	aac	att	gac	acc	att	cgt	547
Ile	Gly	Gln	Thr	Leu	Ala	Asp	Tyr	Asp	Ala	Asn	Ile	Asp	Thr	Ile	Arg	
	135					140					145					

ggg	att	tcg	gat	tac	cct	gtg	acc	ggc	ctg	gag	ctg	aag	gtg	act	gtg	595
Gly	Ile	Ser	Asp	Tyr	Pro	Val	Thr	Gly	Leu	Glu	Leu	Lys	Val	Thr	Val	
150					155				160						165	

ccg	gat	gtc	agc	cct	ggg	ggg	ggg	gaa	gcg	atg	cgt	aag	gcg	ctt	gct	643
Pro	Asp	Val	Ser	Pro	Gly	Gly	Gly	Glu	Ala	Met	Arg	Lys	Ala	Leu	Ala	
				170				175						180		

gct	ctt	acc	tct	gag	ctg	aat	gtg	gat	att	gcg	att	gag	cgt	tct	ggg	691
Ala	Leu	Thr	Ser	Glu	Leu	Asn	Val	Asp	Ile	Ala	Ile	Glu	Arg	Ser	Gly	
			185				190						195			

ttg	ctg	cgt	cgt	tct	aag	cgt	ctg	gtg	tgc	ttc	gat	tgt	gat	tcc	acg	739
Leu	Leu	Arg	Arg	Ser	Lys	Arg	Leu	Val	Cys	Phe	Asp	Cys	Asp	Ser	Thr	

200						205						210						
ttg	atc	act	ggt	gag	gtc	att	gag	atg	ctg	gcg	gct	cac	gcg	ggc	aag	787		
Leu	Ile	Thr	Gly	Glu	Val	Ile	Glu	Met	Leu	Ala	Ala	His	Ala	Gly	Lys			
215			220			225												
gaa	gct	gaa	gtt	gcg	gca	gtt	act	gag	cgt	gcg	atg	cgc	ggt	gag	ctc	835		
Glu	Ala	Glu	Val	Ala	Ala	Val	Thr	Glu	Arg	Ala	Met	Arg	Gly	Glu	Leu			
230			235			240			245									
gat	ttc	gag	gag	tct	ctg	cgt	gag	cgt	gtg	aag	gcg	ttg	gct	ggt	ttg	883		
Asp	Phe	Glu	Glu	Ser	Leu	Arg	Glu	Arg	Val	Lys	Ala	Leu	Ala	Gly	Leu			
250				255				260										
gat	gcg	tcg	gtg	atc	gat	gag	gtc	gct	gcc	gct	att	gag	ctg	acc	cct	931		
Asp	Ala	Ser	Val	Ile	Asp	Glu	Val	Ala	Ala	Ala	Ile	Glu	Leu	Thr	Pro			
265			270			275												
ggt	gcg	cgc	acc	acg	atc	cgt	acg	ctg	aac	cgc	atg	ggt	tac	cag	acc	979		
Gly	Ala	Arg	Thr	Thr	Ile	Arg	Thr	Leu	Asn	Arg	Met	Gly	Tyr	Gln	Thr			
280			285			290												
gct	gtt	gtt	tcc	ggt	ggt	ttc	atc	cag	gtg	ttg	gaa	ggt	ttg	gct	gag			
1027	Ala	Val	Val	Ser	Gly	Gly	Phe	Ile	Gln	Val	Leu	Glu	Gly	Leu	Ala	Glu		
295			300			305												
gag	ttg	gag	ttg	gat	tat	gtc	cgc	gcc	aac	act	ttg	gaa	atc	gtt	gat			
1075	Glu	Leu	Glu	Leu	Asp	Tyr	Val	Arg	Ala	Asn	Thr	Leu	Glu	Ile	Val	Asp		
310			315			320			325									
ggc	aag	ctg	acc	ggc	aac	gtc	acc	gga	aag	atc	gtt	gac	cgc	gct	gcg			
1123	Gly	Lys	Leu	Thr	Gly	Asn	Val	Thr	Gly	Lys	Ile	Val	Asp	Arg	Ala	Ala		
330			335			340												
aag	gct	gag	ttc	ctc	cgt	gag	ttc	gct	gcg	gat	tct	ggc	ctg	aag	atg			
1171	Lys	Ala	Glu	Phe	Leu	Arg	Glu	Phe	Ala	Ala	Asp	Ser	Gly	Leu	Lys	Met		
345			350			355												
tac	cag	act	gtc	gct	gtc	ggt	gat	ggc	gct	aat	gac	atc	gat	atg	ctc			
1219	Tyr	Gln	Thr	Val	Ala	Val	Gly	Asp	Gly	Ala	Asn	Asp	Ile	Asp	Met	Leu		
360			365			370												
tcc	gct	gcg	ggt	ctg	ggt	gtt	gct	ttc	aac	gcg	aag	cct	gcg	ctg	aag			
1267	Ser	Ala	Ala	Gly	Leu	Gly	Val	Ala	Phe	Asn	Ala	Lys	Pro	Ala	Leu	Lys		
375			380			385												
gag	att	gcg	gat	act	tcc	gtg	aac	cac	cca	ttc	ctc	gac	gag	gtt	ttg			
1315	Glu	Ile	Ala	Asp	Thr	Ser	Val	Asn	His	Pro	Phe	Leu	Asp	Glu	Val	Leu		
390			395			400			405									
cac	atc	atg	ggc	att	tcc	cgc	gac	gag	atc	gat	ctg	gcg	gat	cag	gaa			
1363	His	Ile	Met	Gly	Ile	Ser	Arg	Asp	Glu	Ile	Asp	Leu	Ala	Asp	Gln	Glu		
410			415			420												

gac ggc act ttc cac cgc gtt cca ttg acc aat gcc taaagattcg

1409

Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn Ala

425

430

tttctcgacg ccc

1422

<210> 154

<211> 433

<212> PRT

<213> Corynebacterium glutamicum

<400> 154

Val Thr Glu Leu Ile Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu  
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Ala Gly Gln Gln Val Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile  
20 25 30

Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg  
35 40 45

Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met  
50 55 60

Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu  
65 70 75 80

Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His  
85 90 95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg  
100 105 110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala  
115 120 125

Leu Asp Ile Ser Arg Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn  
130 135 140

Ile Asp Thr Ile Arg Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu  
145 150 155 160

Leu Lys Val Thr Val Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met  
165 170 175

Arg Lys Ala Leu Ala Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala  
180 185 190

Ile Glu Arg Ser Gly Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe  
195 200 205

Asp Cys Asp Ser Thr Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala  
210 215 220

Ala His Ala Gly Lys Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala  
225 230 235 240

Met Arg Gly Glu Leu Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys  
 245 250 255

Ala Leu Ala Gly Leu Asp Ala Ser Val Ile Asp Glu Val Ala Ala Ala  
 260 265 270

Ile Glu Leu Thr Pro Gly Ala Arg Thr Thr Ile Arg Thr Leu Asn Arg  
 275 280 285

Met Gly Tyr Gln Thr Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu  
 290 295 300

Glu Gly Leu Ala Glu Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr  
 305 310 315 320

Leu Glu Ile Val Asp Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile  
 325 330 335

Val Asp Arg Ala Ala Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp  
 340 345 350

Ser Gly Leu Lys Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn  
 355 360 365

Asp Ile Asp Met Leu Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala  
 370 375 380

Lys Pro Ala Leu Lys Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe  
 385 390 395 400

Leu Asp Glu Val Leu His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp  
 405 410 415

Leu Ala Asp Gln Glu Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn  
 420 425 430

Ala

<210> 155  
 <211> 490  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101) .. (490)  
 <223> FRXA02479

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 Val Thr Glu Leu Ile  
 1 5

cag aat gaa tcc caa gaa atc gct gag ctg gaa gcc ggc cag cag gtt 163  
 Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu Ala Gly Gln Gln Val  
 10 15 20

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gca ttg cgt gaa ggt tat ctt cct gcg gtg atc aca gtg agc ggt aaa 211
Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile Thr Val Ser Gly Lys
      25              30              35

gac cgc cca ggt gtg act gcc gcg ttc ttt agg gtc ttg tcc gct aat 259
Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala Asn
      40              45              50

cag gtt cag gtc ttg gac gtt gag cag tca atg ttc cgt ggc ttt ttg 307
Gln Val Gln Val Leu Asp Val Glu Gln Ser Met Phe Arg Gly Phe Leu
      55              60              65

aac ttg gcg gcg ttt gtg ggt atc gca cct gag cgt gtc gag acc gtc 355
Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val
      70              75              80              85

acc aca ggc ctg act gac acc ctc aag gtg cat gga cag tcc gtg gtg 403
Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His Gly Gln Ser Val Val
      90              95              100

gtg gag ctg cag gaa act gtg cag tcg tcc cgt cct cgt tct tcc cat 451
Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His
      105              110              115

gtt gtt gtg gtg ttg ggt gat ccg gtt gat gcg ctg gat. 490
Val Val Val Val Leu Gly Asp Pro Val Asp Ala Leu Asp
      120              125              130

```

&lt;210&gt; 156

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 156

```

Val Thr Glu Leu Ile Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu
  1              5              10              15

Ala Gly Gln Gln Val Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile
      20              25              30

Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg
      35              40              45

Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met
      50              55              60

Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu
      65              70              75              80

Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His
      85              90              95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg
      100              105              110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala
      115              120              125

Leu Asp
      130

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<210> 157
<211> 558
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(535)
<223> FRXA02758
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<400> 157																				
aaggcg	ttgg	ctggt	ttt	gga	tgcgt	cgg	tg	atcg	atg	agg	tcgct	gcc	gc	tattg	agctg	60				
accct	tggtg	cg	cg	caccac	gatcc	gtacg	g	ttga	accgc	atg	ggt	tac	cag	acc		115				
										Met	Gly	Tyr	Gln	Thr						
										1				5						
gct	g	tt	g	tt	tcc	ggt	g	gt	t	tc	atc	cag	gtg	ttg	gaa	ggt	ttg	gct	gag	163
Ala	Val	Val	Ser	Gly	Gly	Phe	Ile	Gln	Val	Leu	Glu	Gly	Leu	Ala	Glu					
				10					15					20						
gag	ttg	gag	ttg	gat	tat	gtc	cgc	gcc	aac	act	ttg	gaa	atc	g	tt	gat				211
Glu	Leu	Glu	Leu	Asp	Tyr	Val	Arg	Ala	Asn	Thr	Leu	Glu	Ile	Val	Asp					
				25					30					35						
ggc	aag	ctg	acc	ggc	aac	gtc	acc	gga	aag	atc	g	tt	gac	cgc	gct	g	cg			259
Gly	Lys	Leu	Thr	Gly	Asn	Val	Thr	Gly	Lys	Ile	Val	Asp	Arg	Ala	Ala					
			40					45					50							
aag	gct	gag	ttc	ctc	cgt	gag	ttc	gct	gcg	gat	tct	ggc	ctg	aag	atg					307
Lys	Ala	Glu	Phe	Leu	Arg	Glu	Phe	Ala	Ala	Asp	Ser	Gly	Leu	Lys	Met					
			55					60					65							
tac	cag	act	gtc	gct	gtc	ggt	gat	ggc	gct	aat	gac	atc	gat	atg	ctc					355
Tyr	Gln	Thr	Val	Ala	Val	Gly	Asp	Gly	Ala	Asn	Asp	Ile	Asp	Met	Leu					
70					75					80					85					
tcc	gct	gcg	ggt	ctg	ggt	g	tt	gct	ttc	aac	gcg	aag	cct	gcg	ctg	aag				403
Ser	Ala	Ala	Gly	Leu	Gly	Val	Ala	Phe	Asn	Ala	Lys	Pro	Ala	Leu	Lys					
				90					95					100						
gag	att	gcg	gat	act	tcc	gtg	aac	cac	cca	ttc	ctc	gac	gag	g	tt	ttg				451
Glu	Ile	Ala	Asp	Thr	Ser	Val	Asn	His	Pro	Phe	Leu	Asp	Glu	Val	Leu					
				105					110					115						
cac	atc	atg	ggc	att	tcc	cgc	gac	gag	atc	gat	ctg	gcg	gat	cag	gaa					499
His	Ile	Met	Gly	Ile	Ser	Arg	Asp	Glu	Ile	Asp	Leu	Ala	Asp	Gln	Glu					
			120					125					130							
gac	ggc	act	ttc	cac	cgc	g	tt	cca	ttg	acc	aat	gcc	taa	agatt	cg					545
Asp	Gly	Thr	Phe	His	Arg	Val	Pro	Leu	Thr	Asn	Ala									
			135					140					145							
tttct	cgacg	ccc																558		

<210>	158
<211>	145
<212>	PRT

<213> Corynebacterium glutamicum

<400> 158

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Met Gly Tyr Gln Thr Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu
 1              5              10              15

Glu Gly Leu Ala Glu Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr
              20              25              30

Leu Glu Ile Val Asp Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile
              35              40              45

Val Asp Arg Ala Ala Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp
              50              55              60

Ser Gly Leu Lys Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn
65              70              75              80

Asp Ile Asp Met Leu Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala
              85              90              95

Lys Pro Ala Leu Lys Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe
              100             105             110

Leu Asp Glu Val Leu His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp
              115             120             125

Leu Ala Asp Gln Glu Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn
              130             135             140

Ala
145

```

<210> 159

<211> 205

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (72) .. (182)

<223> FRXA02759

<400> 159

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tcttacttct aagctgaatg tgatattgcg attaagcggt ctggtttgct gcgtcgttct 60

aagcgtctgg tgtg ctt cga ttg tat ccc acg ttg atc act ggt gag gtc 110
          Val Leu Arg Leu Tyr Pro Thr Leu Ile Thr Gly Glu Val
              1              5              10

att gag atg ctg gcg gct cac gcg ggc aag gaa gct aaa gtt gcg gca 158
Ile Glu Met Leu Ala Ala His Ala Gly Lys Glu Ala Lys Val Ala Ala
              15              20              25

gtt act gag cgt gcg atg cgc ggg tgagctcgat ttcgaggagt ctc 205
Val Thr Glu Arg Ala Met Arg Gly
              30              35

```

<210> 160

&lt;211&gt; 37

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 160

Val Leu Arg Leu Tyr Pro Thr Leu Ile Thr Gly Glu Val Ile Glu Met  
 1 5 10 15

Leu Ala Ala His Ala Gly Lys Glu Ala Lys Val Ala Ala Val Thr Glu  
 20 25 30

Arg Ala Met Arg Gly  
 35

&lt;210&gt; 161

&lt;211&gt; 1188

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1165)

&lt;223&gt; RXA02501

&lt;400&gt; 161

cgccccgaaa gctttaccat ggatacgata ctcaatggag atatccatta tcggtttggc 60

gtctgtgcgc tcatgaacca ggaagggtttt tgtttgtctc atg agc tct gaa gga 115  
 Met Ser Ser Glu Gly  
 1 5

aga aac cac aac tgg gac tac gcc gcc atc ggc acc cca gag gat ttc 163  
 Arg Asn His Asn Trp Asp Tyr Ala Ala Ile Gly Thr Pro Glu Asp Phe  
 10 15 20

ctc gcc agc tgg agc gca tcc cgc gga aat cta cga cgc ttt ttc gaa 211  
 Leu Ala Ser Trp Ser Ala Ser Arg Gly Asn Leu Arg Arg Phe Phe Glu  
 25 30 35

gac cac gca gcc gcc ccc ata aac gat gcc gcc cag cgc caa gca ggt 259  
 Asp His Ala Ala Ala Pro Ile Asn Asp Ala Ala Gln Arg Gln Ala Gly  
 40 45 50

gaa gcc gca gca acc caa gcc gtc gca gcg atc tac ggc atg gag ctc 307  
 Glu Ala Ala Ala Thr Gln Ala Val Ala Ala Ile Tyr Gly Met Glu Leu  
 55 60 65

aac gaa ttc aac gca ggt gtc gac gcc gtc gcc ggc gcc atc gaa tct 355  
 Asn Glu Phe Asn Ala Gly Val Asp Ala Val Ala Gly Ala Ile Glu Ser  
 70 75 80 85

gcc ggc gcc atc cac gtc agc atc ccc gat ccc gat gtc ccc caa gat 403  
 Ala Gly Ala Ile His Val Ser Ile Pro Asp Pro Asp Val Pro Gln Asp  
 90 95 100

gtc gga gcc gca gca ttt ttc gac gtc gac aac acc ctc atc caa ggc 451  
 Val Gly Ala Ala Ala Phe Phe Asp Val Asp Asn Thr Leu Ile Gln Gly  
 105 110 115

tcc tcc ctc atc gtt ttc gcc caa gga ctc ttc cgg aag aaa ttc ttc 499



Ser	Ser	Leu	Ile	Val	Phe	Ala	Gln	Gly	Leu	Phe	Arg	Lys	Lys	Phe	Phe		
		120					125					130					
acc	atc	aaa	gaa	atc	ctc	ccc	gtg	gtg	tgg	aaa	caa	gtg	aaa	ttc	aaa	547	
Thr	Ile	Lys	Glu	Ile	Leu	Pro	Val	Val	Trp	Lys	Gln	Val	Lys	Phe	Lys		
	135					140					145						
ctc	acc	ggc	tcc	gaa	aac	gcc	gac	gac	gtc	tcc	cgc	ggc	cgc	gaa	caa	595	
Leu	Thr	Gly	Ser	Glu	Asn	Ala	Asp	Asp	Val	Ser	Arg	Gly	Arg	Glu	Gln		
150					155					160					165		
gcc	ctc	gaa	ttc	atc	aaa	ggc	cgc	ccc	gtc	caa	gaa	cta	gtt	gac	ctc	643	
Ala	Leu	Glu	Phe	Ile	Lys	Gly	Arg	Pro	Val	Gln	Glu	Leu	Val	Asp	Leu		
				170					175					180			
tgc	gaa	gaa	atc	gtc	gac	caa	cgc	atg	gcc	gac	aaa	atg	tgg	ccc	ggc	691	
Cys	Glu	Glu	Ile	Val	Asp	Gln	Arg	Met	Ala	Asp	Lys	Met	Trp	Pro	Gly		
			185					190					195				
acc	aaa	caa	ctc	gcc	gac	atg	cac	atc	gcc	gcc	ggc	cac	caa	gtc	tgg	739	
Thr	Lys	Gln	Leu	Ala	Asp	Met	His	Ile	Ala	Ala	Gly	His	Gln	Val	Trp		
		200					205					210					
ctc	gtc	tcc	gca	acc	ccc	gtc	caa	ctc	gcc	caa	atc	ctg	gca	caa	cgc	787	
Leu	Val	Ser	Ala	Thr	Pro	Val	Gln	Leu	Ala	Gln	Ile	Leu	Ala	Gln	Arg		
	215					220					225						
ctc	ggc	ttc	acc	gga	gcg	atc	ggc	aca	gtc	gca	gaa	gca	aaa	gat	gga	835	
Leu	Gly	Phe	Thr	Gly	Ala	Ile	Gly	Thr	Val	Ala	Glu	Ala	Lys	Asp	Gly		
230					235				240					245			
gta	ttc	acc	ggc	cga	ctc	gtc	ggc	gac	atc	ctc	cac	gga	ccc	ggc	aaa	883	
Val	Phe	Thr	Gly	Arg	Leu	Val	Gly	Asp	Ile	Leu	His	Gly	Pro	Gly	Lys		
				250				255					260				
aga	cac	gca	gtc	gca	gca	ctc	gca	tcc	atc	gaa	caa	ctc	gac	ctc	acc	931	
Arg	His	Ala	Val	Ala	Ala	Leu	Ala	Ser	Ile	Glu	Gln	Leu	Asp	Leu	Thr		
			265					270					275				
cga	tgc	acc	gcc	tac	tcc	gac	tcc	atc	aac	gac	ctc	ccc	atg	ctc	tcc	979	
Arg	Cys	Thr	Ala	Tyr	Ser	Asp	Ser	Ile	Asn	Asp	Leu	Pro	Met	Leu	Ser		
		280				285						290					
atg	gtc	ggc	acc	gcc	gtc	gca	gta	aac	ccc	gac	tcc	aaa	ctc	cgc	aaa		
1027																	
Met	Val	Gly	Thr	Ala	Val	Ala	Val	Asn	Pro	Asp	Ser	Lys	Leu	Arg	Lys		
	295					300					305						
gaa	gcc	gaa	acc	cga	ggc	tgg	gac	gtc	cgc	gat	ttc	cga	agc	atc	cgc		
1075																	
Glu	Ala	Glu	Thr	Arg	Gly	Trp	Asp	Val	Arg	Asp	Phe	Arg	Ser	Ile	Arg		
310					315				320					325			
aaa	gcc	acc	cgc	gaa	tac	gga	atc	ccc	gcc	ctg	gtc	acc	gcc	gca	ttc		
1123																	
Lys	Ala	Thr	Arg	Glu	Tyr	Gly	Ile	Pro	Ala	Leu	Val	Thr	Ala	Ala	Phe		
				330				335						340			
agt	gtc	gcc	ggc	tgg	agt	cta	cgc	cgc	cga	tgg	aga	aaa	caa				
1165																	
Ser	Val	Ala	Gly	Trp	Ser	Leu	Arg	Arg	Arg	Trp	Arg	Lys	Gln				

345

350

355

taacgcacag gagccgtttt aag  
1188

&lt;210&gt; 162

&lt;211&gt; 355

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 162

Met Ser Ser Glu Gly Arg Asn His Asn Trp Asp Tyr Ala Ala Ile Gly  
1 5 10 15

Thr Pro Glu Asp Phe Leu Ala Ser Trp Ser Ala Ser Arg Gly Asn Leu  
20 25 30

Arg Arg Phe Phe Glu Asp His Ala Ala Ala Pro Ile Asn Asp Ala Ala  
35 40 45

Gln Arg Gln Ala Gly Glu Ala Ala Ala Thr Gln Ala Val Ala Ala Ile  
50 55 60

Tyr Gly Met Glu Leu Asn Glu Phe Asn Ala Gly Val Asp Ala Val Ala  
65 70 75 80

Gly Ala Ile Glu Ser Ala Gly Ala Ile His Val Ser Ile Pro Asp Pro  
85 90 95

Asp Val Pro Gln Asp Val Gly Ala Ala Ala Phe Phe Asp Val Asp Asn  
100 105 110

Thr Leu Ile Gln Gly Ser Ser Leu Ile Val Phe Ala Gln Gly Leu Phe  
115 120 125

Arg Lys Lys Phe Phe Thr Ile Lys Glu Ile Leu Pro Val Val Trp Lys  
130 135 140

Gln Val Lys Phe Lys Leu Thr Gly Ser Glu Asn Ala Asp Asp Val Ser  
145 150 155 160

Arg Gly Arg Glu Gln Ala Leu Glu Phe Ile Lys Gly Arg Pro Val Gln  
165 170 175

Glu Leu Val Asp Leu Cys Glu Glu Ile Val Asp Gln Arg Met Ala Asp  
180 185 190

Lys Met Trp Pro Gly Thr Lys Gln Leu Ala Asp Met His Ile Ala Ala  
195 200 205

Gly His Gln Val Trp Leu Val Ser Ala Thr Pro Val Gln Leu Ala Gln  
210 215 220

Ile Leu Ala Gln Arg Leu Gly Phe Thr Gly Ala Ile Gly Thr Val Ala  
225 230 235 240

Glu Ala Lys Asp Gly Val Phe Thr Gly Arg Leu Val Gly Asp Ile Leu  
245 250 255

His Gly Pro Gly Lys Arg His Ala Val Ala Ala Leu Ala Ser Ile Glu

	260		265		270										
Gln	Leu	Asp	Leu	Thr	Arg	Cys	Thr	Ala	Tyr	Ser	Asp	Ser	Ile	Asn	Asp
	275						280					285			
Leu	Pro	Met	Leu	Ser	Met	Val	Gly	Thr	Ala	Val	Ala	Val	Asn	Pro	Asp
	290					295					300				
Ser	Lys	Leu	Arg	Lys	Glu	Ala	Glu	Thr	Arg	Gly	Trp	Asp	Val	Arg	Asp
305					310					315					320
Phe	Arg	Ser	Ile	Arg	Lys	Ala	Thr	Arg	Glu	Tyr	Gly	Ile	Pro	Ala	Leu
				325					330					335	
Val	Thr	Ala	Ala	Phe	Ser	Val	Ala	Gly	Trp	Ser	Leu	Arg	Arg	Arg	Trp
			340					345					350		
Arg	Lys	Gln													
	355														

<210> 163  
 <211> 558  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(535)  
 <223> RXN03105

<400> 163  
 gggtgggggtc atcaaaggat gcggacatcg ctgtgggggtt gtgtaataat tgcacctgtg 60  
 aggtgccttt ctggcaggtg aatcaggact ctaagcaagc ttg att ctt cca gtt 115  
 Leu Ile Leu Pro Val  
 1 5  
 cag gag ggc att tcc tat ttt ccc acg ccg tta cac ctg aat cac atc 163  
 Gln Glu Gly Ile Ser Tyr Phe Pro Thr Pro Leu His Leu Asn His Ile  
 10 15 20  
 ggt gga tcc agg tta agc gca cat gta gaa gat gaa gat ctc cgc ctc 211  
 Gly Gly Ser Arg Leu Ser Ala His Val Glu Asp Glu Asp Leu Arg Leu  
 25 30 35  
 gac cgg gac gca gtc tct gaa ttt ggt cgg aaa acc cac gaa ctc ttc 259  
 Asp Arg Asp Ala Val Ser Glu Phe Gly Arg Lys Thr His Glu Leu Phe  
 40 45 50  
 ccc ggg gtc aac cca gag ccc aac cgt ttc agc gtc cac tat gac acc 307  
 Pro Gly Val Asn Pro Glu Pro Asn Arg Phe Ser Val His Tyr Asp Thr  
 55 60 65  
 tac act gca gac aaa tct cca att atc gac gcg gtt gac aat gtc att 355  
 Tyr Thr Ala Asp Lys Ser Pro Ile Ile Asp Ala Val Asp Asn Val Ile  
 70 75 80 85  
 gtg ctc acc gga gga tcc gga cac gcc ttc aag ctc tct cca gct tat 403  
 Val Leu Thr Gly Gly Ser Gly His Ala Phe Lys Leu Ser Pro Ala Tyr  
 90 95 100

ggc gaa ctc gca gca caa cga gcg gtc gga aac acc tcg ccg ctg tac 451  
 Gly Glu Leu Ala Ala Gln Arg Ala Val Gly Asn Thr Ser Pro Leu Tyr  
                   105                  110                  115

agc gaa gac ttt cgg atc gcc tcg cat gaa cca atc aaa gag cgg tgc 499  
 Ser Glu Asp Phe Arg Ile Ala Ser His Glu Pro Ile Lys Glu Arg Cys  
                   120                  125                  130

acg tat aga aag cta acc ttt tta agt gcg cgg ttt taggggtgaga 545  
 Thr Tyr Arg Lys Leu Thr Phe Leu Ser Ala Arg Phe  
                   135                  140                  145

atctaacgct gag 558

<210> 164  
 <211> 145  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 164  
 Leu Ile Leu Pro Val Gln Glu Gly Ile Ser Tyr Phe Pro Thr Pro Leu  
   1                  5                  10                  15  
 His Leu Asn His Ile Gly Gly Ser Arg Leu Ser Ala His Val Glu Asp  
                   20                  25                  30  
 Glu Asp Leu Arg Leu Asp Arg Asp Ala Val Ser Glu Phe Gly Arg Lys  
                   35                  40                  45  
 Thr His Glu Leu Phe Pro Gly Val Asn Pro Glu Pro Asn Arg Phe Ser  
                   50                  55                  60  
 Val His Tyr Asp Thr Tyr Thr Ala Asp Lys Ser Pro Ile Ile Asp Ala  
   65                  70                  75                  80  
 Val Asp Asn Val Ile Val Leu Thr Gly Gly Ser Gly His Ala Phe Lys  
                   85                  90                  95  
 Leu Ser Pro Ala Tyr Gly Glu Leu Ala Ala Gln Arg Ala Val Gly Asn  
                   100                  105                  110  
 Thr Ser Pro Leu Tyr Ser Glu Asp Phe Arg Ile Ala Ser His Glu Pro  
                   115                  120                  125  
 Ile Lys Glu Arg Cys Thr Tyr Arg Lys Leu Thr Phe Leu Ser Ala Arg  
                   130                  135                  140  
 Phe  
 145

<210> 165  
 <211> 687  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (62) .. (664)

&lt;223&gt; RXS01130

&lt;400&gt; 165

agttcgtggc ggatgctgtg aacgtttccg gtggtcgcgt gggcgaagag gttctgtgtg 60

gatg gat ctg gct cgc aag ctt ggt ctt ctt gct ggc aag ctt gtc gac 109  
 Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp  
           1                  5                  10                  15

gcc gcc cca gtc tcc att gag gtt gag gct cga ggc gag ctt tct tcc 157  
 Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser  
                   20                  25                  30

gag cag gtc aat gca ctt ggt ttg tcc gct gtt cgt ggt ttg ttc tcc 205  
 Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser  
                   35                  40                  45

gga att atc gaa gag tcc gtt act ttc gtc aac gct cct cgc att gct 253  
 Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala  
           50                  55                  60

gaa gag cgt ggc ctg gac atc tcc gtg aag acc aac tct gag tct gtt 301  
 Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val  
           65                  70                  75                  80

act cac cgt tcc gtc ctg cag gtc aag gtc att act ggc agc ggc gcg 349  
 Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala  
                   85                  90                  95

agc gca act gtt gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag 397  
 Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys  
                   100                  105                  110

atc acc cgc atc aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg 445  
 Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu  
                   115                  120                  125

aac ctc ttc ctg cag tac act gac gct cct ggt gca ctg ggt acc gtt 493  
 Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val  
           130                  135                  140

ggt acc aag ctg ggt gct gct ggc atc aac atc gag gct gct gcg ttg 541  
 Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu  
           145                  150                  155                  160

act cag gct gag aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag 589  
 Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu  
                   165                  170                  175

tcc gct gtc tct gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt 637  
 Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly  
                   180                  185                  190

gct act tcc ttc cag gtt gat ctt gac taattagaga tccatttgct 684  
 Ala Thr Ser Phe Gln Val Asp Leu Asp  
                   195                  200

tga 687

&lt;210&gt; 166

&lt;211&gt; 201

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 166

```

Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
 1           5           10           15
Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
          20           25           30
Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
          35           40           45
Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
          50           55           60
Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
        65           70           75           80
Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
          85           90           95
Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
          100          105          110
Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
          115          120          125
Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
          130          135          140
Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
        145          150          155          160
Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
          165          170          175
Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
          180          185          190
Ala Thr Ser Phe Gln Val Asp Leu Asp
          195          200

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&lt;210&gt; 167

&lt;211&gt; 604

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(604)

&lt;223&gt; RXS03112

&lt;400&gt; 167

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gctgcgtgag ggcgagtgga agcgggtcttc tttcaacggg gtg gaa att ttc gga 115
                               Val Glu Ile Phe Gly
                               1           5

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aaa act gtc ggt atc gtc ggt ttt ggc cac att ggt cag ttg ttt gct 163
Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala
      10      15      20

cag cgt ctt gct gcg ttt gag acc acc att gtt gct tac gat cct tac 211
Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr
      25      30      35

gct aac cct gct cgt gcg gct cag ctg aac gtt gag ttg gtt gag ttg 259
Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
      40      45      50

gat gag ctg atg agc cgt tct gac ttt gtc acc att cac ctt cct aag 307
Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
      55      60      65

acc aag gaa act gct ggc atg ttt gat gcg cac ctc ctt gct aag tcc 355
Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His Leu Leu Ala Lys Ser
      70      75      80      85

aag aag ggc cag atc atc atc aac gct gct cgt ggt ggc ctt gtt gat 403
Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
      90      95      100

gag cag gct ttg gct gat gcg att gag tcc ggt cac att cgt ggc gct 451
Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala
      105      110      115

ggt ttc gat gtg tac tcc acc gag cct tgc act gat tct cct ttg ttc 499
Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
      120      125      130

aag ttg cct cag gtt gtt gtg act cct cac ttg ggt gct tct act gaa 547
Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
      135      140      145

gag gct caa gat cgt gcg ggt act gac att gct gat tct gtg ctc aag 595
Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala Asp Ser Val Leu Lys
      150      155      160      165

gcg ctg gct
Ala Leu Ala 604

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&lt;210&gt; 168

&lt;211&gt; 168

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 168

```

Val Glu Ile Phe Gly Lys Thr Val Gly Ile Val Gly Phe Gly His Ile
  1      5      10      15

Gly Gln Leu Phe Ala Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val
  20      25      30

Ala Tyr Asp Pro Tyr Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val
  35      40      45

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Glu Leu Val Glu Leu Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr  
 50 55 60  
 Ile His Leu Pro Lys Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His  
 65 70 75 80  
 Leu Leu Ala Lys Ser Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg  
 85 90 95  
 Gly Gly Leu Val Asp Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly  
 100 105 110  
 His Ile Arg Gly Ala Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr  
 115 120 125  
 Asp Ser Pro Leu Phe Lys Leu Pro Gln Val Val Val Thr Pro His Leu  
 130 135 140  
 Gly Ala Ser Thr Glu Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala  
 145 150 155 160  
 Asp Ser Val Leu Lys Ala Leu Ala  
 165

<210> 169  
 <211> 1458  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101) .. (1435)  
 <223> RXN00969

<400> 169  
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 Met Thr Ser Ala Ser  
 1 5  
 gcc cca agc ttt aac ccc ggc aag ggt ccc ggc tca gca gtc gga att 163  
 Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly Ser Ala Val Gly Ile  
 10 15 20  
 gcc ctt tta gga ttc gga aca gtc ggc act gag gtg atg cgt ctg atg 211  
 Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu Val Met Arg Leu Met  
 25 30 35  
 acc gag tac ggt gat gaa ctt gcg cac cgc att ggt ggc cca ctg gag 259  
 Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile Gly Gly Pro Leu Glu  
 40 45 50  
 gtt cgt ggc att gct gtt tct gat atc tca aag cca cgt gaa ggc gtt 307  
 Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys Pro Arg Glu Gly Val  
 55 60 65  
 gca cct gag ctg ctc act gag gac gct ttt gca ctc atc gag cgc gag 355  
 Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala Leu Ile Glu Arg Glu  
 70 75 80 85



gat gtt gac atc gtc gtt gag gtt atc ggc ggc att gag tac cca cgt	403
Asp Val Asp Ile Val Val Glu Val Ile Gly Gly Ile Glu Tyr Pro Arg	
90 95 100	
gag gta gtt ctc gca gct ctg aag gcc ggc aag tct gtt gtt acc gcc	451
Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys Ser Val Val Thr Ala	
105 110 115	
aat aag gct ctt gtt gca gct cac tct gct gag ctt gct gat gca gcg	499
Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu Leu Ala Asp Ala Ala	
120 125 130	
gaa gcc gca aac gtt gac ctg tac ttc gag gct gct gtt gca tgc gca	547
Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala Ala Val Ala Cys Ala	
135 140 145	
att cca gtg gtt ggc cca ctg cgt cgc tcc ctg gct ggc gat cag atc	595
Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu Ala Gly Asp Gln Ile	
150 155 160 165	
cag tct gtg atg ggc atc gtt aac ggc acc acc aac ttc atc ttg gac	643
Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr Asn Phe Ile Leu Asp	
170 175 180	
gcc atg gat tcc acc ggc gct gac tat gca gat tct ttg gct gag gca	691
Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp Ser Leu Ala Glu Ala	
185 190 195	
act cgt ttg ggt tac gcc gaa gct gat cca act gca aac gtc gaa ggc	739
Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr Ala Asn Val Glu Gly	
200 205 210	
cat gac gcc gca tcc aag gct gca att ttg gca tgc atc gct ttc cac	787
His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala Cys Ile Ala Phe His	
215 220 225	
acc cgt gtt acc gcg gat gat gtg tac tgc gaa ggt att agg aac atc	835
Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu Gly Ile Arg Asn Ile	
230 235 240 245	
aac gct gcc gac att gag gca gca cag cag gca ggc cac acc atc aag	883
Asn Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala Gly His Thr Ile Lys	
250 255 260	
ttg ttg gcc atc tgt gag aag ttc acc aac aag gaa gga aag tcg gct	931
Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys Glu Gly Lys Ser Ala	
265 270 275	
att tct gct cgc gtg cac ccg act cta tta cct gtg tcc cac cca ctg	979
Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro Val Ser His Pro Leu	
280 285 290	
gcg tcg gta aac aag tcc ttt aat gca atc ttt gtt gaa gca gaa gca	
1027	
Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe Val Glu Ala Glu Ala	
295 300 305	
gct ggt cgc ctg atg ttc tac gga aac ggt gca ggt ggc gcg cca acc	
1075	
Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala Gly Gly Ala Pro Thr	

310                                      315                                      320                                      325  
 gcg tct gct gtg ctt ggc gac gtc gtt ggt gcc gca cga aac aag gtg  
 1123  
 Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala Ala Arg Asn Lys Val  
    330                                      335                                      340  
  
 cac ggt ggc cgt gct cca ggt gag tcc acc tac gct aac ctg ccg atc  
 1171  
 His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr Ala Asn Leu Pro Ile  
    345                                      350                                      355  
  
 gct gat ttc ggt gag acc acc act cgt tac cac ctc gac atg gat gtg  
 1219  
 Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His Leu Asp Met Asp Val  
    360                                      365                                      370  
  
 gaa gat cgc gtg ggg gtt ttg gct gaa ttg gct agc ctg ttc tct gag  
 1267  
 Glu Asp Arg Val Gly Val Leu Ala Glu Leu Ala Ser Leu Phe Ser Glu  
    375                                      380                                      385  
  
 caa gga atc tcc ctg cgt aca atc cga cag gaa gag cgc gat gat gat  
 1315  
 Gln Gly Ile Ser Leu Arg Thr Ile Arg Gln Glu Glu Arg Asp Asp Asp  
 390                                      395                                      400                                      405  
  
 gca cgt ctg atc gtg gtc acc cac tct gcg ctg gaa tct gat ctt tcc  
 1363  
 Ala Arg Leu Ile Val Val Thr His Ser Ala Leu Glu Ser Asp Leu Ser  
    410                                      415                                      420  
  
 cgc acc gtt gaa ctg ctg aag gct aag cct gtt gtt aag gca atc aac  
 1411  
 Arg Thr Val Glu Leu Leu Lys Ala Lys Pro Val Val Lys Ala Ile Asn  
    425                                      430                                      435  
  
 agt gtg atc cgc ctc gaa agg gac taattttact gacatggcaa ttg  
 1458  
 Ser Val Ile Arg Leu Glu Arg Asp  
    440                                      445

&lt;210&gt; 170

&lt;211&gt; 445

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 170

Met Thr Ser Ala Ser Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly  
   1  5  10  15  
  
 Ser Ala Val Gly Ile Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu  
   20  25  30  
  
 Val Met Arg Leu Met Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile  
   35  40  45  
  
 Gly Gly Pro Leu Glu Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys  
   50  55  60

Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala  
 65 70 75 80  
 Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly  
 85 90 95  
 Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys  
 100 105 110  
 Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu  
 115 120 125  
 Leu Ala Asp Ala Ala Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala  
 130 135 140  
 Ala Val Ala Cys Ala Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu  
 145 150 155 160  
 Ala Gly Asp Gln Ile Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr  
 165 170 175  
 Asn Phe Ile Leu Asp Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp  
 180 185 190  
 Ser Leu Ala Glu Ala Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr  
 195 200 205  
 Ala Asn Val Glu Gly His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala  
 210 215 220  
 Cys Ile Ala Phe His Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu  
 225 230 235 240  
 Gly Ile Arg Asn Ile Asn Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala  
 245 250 255  
 Gly His Thr Ile Lys Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys  
 260 265 270  
 Glu Gly Lys Ser Ala Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro  
 275 280 285  
 Val Ser His Pro Leu Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe  
 290 295 300  
 Val Glu Ala Glu Ala Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala  
 305 310 315 320  
 Gly Gly Ala Pro Thr Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala  
 325 330 335  
 Ala Arg Asn Lys Val His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr  
 340 345 350  
 Ala Asn Leu Pro Ile Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His  
 355 360 365  
 Leu Asp Met Asp Val Glu Asp Arg Val Gly Val Leu Ala Glu Leu Ala  
 370 375 380  
 Ser Leu Phe Ser Glu Gln Gly Ile Ser Leu Arg Thr Ile Arg Gln Glu

385		390		395		400
Glu Arg Asp Asp Asp Ala Arg Leu Ile Val Val Thr His Ser Ala Leu						
		405		410		415
Glu Ser Asp Leu Ser Arg Thr Val Glu Leu Leu Lys Ala Lys Pro Val						
		420		425		430
Val Lys Ala Ile Asn Ser Val Ile Arg Leu Glu Arg Asp						
		435		440		445

<210> 171  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> FRXA00974

<400> 171  
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 Met Thr Ser Ala Ser  
 1 5  
 gcc cca agc ttt aac ccc ggc aag ggt ccc ggc tca gca gtc gga att 163  
 Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly Ser Ala Val Gly Ile  
 10 15 20  
 gcc ctt tta gga ttc gga aca gtc ggc act gag gtg atg cgt ctg atg 211  
 Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu Val Met Arg Leu Met  
 25 30 35  
 acc gag tac ggt gat gaa ctt gcg cac cgc att ggt ggc cca ctg gag 259  
 Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile Gly Gly Pro Leu Glu  
 40 45 50  
 gtt cgt ggc att gct gtt tct gat atc tca aag cca cgt gaa ggc gtt 307  
 Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys Pro Arg Glu Gly Val  
 55 60 65  
 gca cct gag ctg ctc act gag gac gct ttt gca ctc atc gag cgc gag 355  
 Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala Leu Ile Glu Arg Glu  
 70 75 80 85  
 gat gtt gac atc gtc gtt gag gtt atc ggc ggc att gag tac cca cgt 403  
 Asp Val Asp Ile Val Val Glu Val Ile Gly Gly Ile Glu Tyr Pro Arg  
 90 95 100  
 gag gta gtt ctc gca gct ctg aag gcc ggc aag tct gtt gtt acc gcc 451  
 Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys Ser Val Val Thr Ala  
 105 110 115  
 aat aag gct ctt gtt gca gct cac tct gct gag ctt gct gat 493  
 Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu Leu Ala Asp  
 120 125 130

<210> 172  
 <211> 131  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 172  
 Met Thr Ser Ala Ser Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly  
   1                  5                  10                  15  
 Ser Ala Val Gly Ile Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu  
                   20                  25                  30  
 Val Met Arg Leu Met Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile  
                   35                  40                  45  
 Gly Gly Pro Leu Glu Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys  
           50                  55                  60  
 Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala  
   65                  70                  75                  80  
 Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly  
                   85                  90                  95  
 Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys  
                   100                  105                  110  
 Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu  
           115                  120                  125  
 Leu Ala Asp  
   130

<210> 173  
 <211> 1050  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1027)  
 <223> RXA00970

<400> 173  
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 aacagtgtga tccgcctcga aagggactaa ttttactgac atg gca att gaa ctg 115  
   Met Ala Ile Glu Leu  
   1                  5  
 aac gtc ggt cgt aag gtt acc gtc acg gta cct gga tct tct gca aac 163  
 Asn Val Gly Arg Lys Val Thr Val Thr Val Pro Gly Ser Ser Ala Asn  
                   10                  15                  20  
 ctc gga cct ggc ttt gac act tta ggt ttg gca ctg tcg gta tac gac 211  
 Leu Gly Pro Gly Phe Asp Thr Leu Gly Leu Ala Leu Ser Val Tyr Asp  
                   25                  30                  35  
 act gtc gaa gtg gaa att att cca tct ggc ttg gaa gtg gaa gtt ttt 259

Thr	Val	Glu	Val	Glu	Ile	Ile	Pro	Ser	Gly	Leu	Glu	Val	Glu	Val	Phe	
		40					45					50				
ggc	gaa	ggc	caa	ggc	gaa	gtc	cct	ctt	gat	ggc	tcc	cac	ctg	gtg	gtt	307
Gly	Glu	Gly	Gln	Gly	Glu	Val	Pro	Leu	Asp	Gly	Ser	His	Leu	Val	Val	
	55					60					65					
aaa	gct	att	cgt	gct	ggc	ctg	aag	gca	gct	gac	gct	gaa	gtt	cct	gga	355
Lys	Ala	Ile	Arg	Ala	Gly	Leu	Lys	Ala	Ala	Asp	Ala	Glu	Val	Pro	Gly	
70					75					80					85	
ttg	cga	gtg	gtg	tgc	cac	aac	aac	att	ccg	cag	tct	cgt	ggt	ctt	ggc	403
Leu	Arg	Val	Val	Cys	His	Asn	Asn	Ile	Pro	Gln	Ser	Arg	Gly	Leu	Gly	
				90					95					100		
tcc	tct	gct	gca	gcg	gcg	gtt	gct	ggg	gtt	gct	gca	gct	aat	ggt	ttg	451
Ser	Ser	Ala	Ala	Ala	Ala	Val	Ala	Gly	Val	Ala	Ala	Ala	Asn	Gly	Leu	
			105					110					115			
gcg	gat	ttc	ccg	ctg	act	caa	gag	cag	att	gtt	cag	ttg	tcc	tct	gcc	499
Ala	Asp	Phe	Pro	Leu	Thr	Gln	Glu	Gln	Ile	Val	Gln	Leu	Ser	Ser	Ala	
		120					125					130				
ttt	gaa	ggc	cac	cca	gat	aat	gct	gcg	gct	tct	gtg	ctg	ggt	gga	gca	547
Phe	Glu	Gly	His	Pro	Asp	Asn	Ala	Ala	Ala	Ser	Val	Leu	Gly	Gly	Ala	
	135					140					145					
gtg	gtg	tcg	tgg	aca	aat	ctg	tct	atc	gac	ggc	aag	agc	cag	cca	cag	595
Val	Val	Ser	Trp	Thr	Asn	Leu	Ser	Ile	Asp	Gly	Lys	Ser	Gln	Pro	Gln	
150					155					160					165	
tat	gct	gct	gta	cca	ctt	gag	gtg	cag	gac	aat	att	cgt	gcg	act	gcg	643
Tyr	Ala	Ala	Val	Pro	Leu	Glu	Val	Gln	Asp	Asn	Ile	Arg	Ala	Thr	Ala	
				170					175					180		
ctg	gtt	cct	aat	ttc	cac	gca	tcc	acc	gaa	gct	gtg	cgc	cga	gtc	ctt	691
Leu	Val	Pro	Asn	Phe	His	Ala	Ser	Thr	Glu	Ala	Val	Arg	Arg	Val	Leu	
			185					190					195			
ccc	act	gaa	gtc	act	cac	atc	gat	gcg	cga	ttt	aac	gtg	tcc	cgc	gtt	739
Pro	Thr	Glu	Val	Thr	His	Ile	Asp	Ala	Arg	Phe	Asn	Val	Ser	Arg	Val	
		200					205					210				
gca	gtg	atg	atc	gtt	gcg	ttg	cag	cag	cgt	cct	gat	ttg	ctg	tgg	gag	787
Ala	Val	Met	Ile	Val	Ala	Leu	Gln	Gln	Arg	Pro	Asp	Leu	Leu	Trp	Glu	
	215					220					225					
ggt	act	cgt	gac	cgt	ctg	cac	cag	cct	tat	cgt	gca	gaa	gtg	ttg	cct	835
Gly	Thr	Arg	Asp	Arg	Leu	His	Gln	Pro	Tyr	Arg	Ala	Glu	Val	Leu	Pro	
230					235					240					245	
att	acc	tct	gag	tgg	gta	aac	cgc	ctg	cgc	aac	cgt	ggc	tac	gcg	gca	883
Ile	Thr	Ser	Glu	Trp	Val	Asn	Arg	Leu	Arg	Asn	Arg	Gly	Tyr	Ala	Ala	
				250					255					260		
tac	ctt	tcc	ggt	gcc	ggc	cca	acc	gcc	atg	gtg	ctg	tcc	act	gag	cca	931
Tyr	Leu	Ser	Gly	Ala	Gly	Pro	Thr	Ala	Met	Val	Leu	Ser	Thr	Glu	Pro	
			265					270					275			
att	cca	gac	aag	gtt	ttg	gaa	gat	gct	cgt	gag	tct	ggc	att	aag	gtg	979
Ile	Pro	Asp	Lys	Val	Leu	Glu	Asp	Ala	Arg	Glu	Ser	Gly	Ile	Lys	Val	

280                                      285                                      290  
 ctt gag ctt gag gtt gcg gga cca gtc aag gtt gaa gtt aac caa cct  
 1027  
 Leu Glu Leu Glu Val Ala Gly Pro Val Lys Val Glu Val Asn Gln Pro  
 295                                      300                                      305  
  
 taggccaac aaggaaggcc ccc  
 1050  
  
 <210> 174  
 <211> 309  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 174  
 Met Ala Ile Glu Leu Asn Val Gly Arg Lys Val Thr Val Thr Val Pro  
 1                                      5                                      10                                      15  
 Gly Ser Ser Ala Asn Leu Gly Pro Gly Phe Asp Thr Leu Gly Leu Ala  
 20                                      25                                      30  
 Leu Ser Val Tyr Asp Thr Val Glu Val Glu Ile Ile Pro Ser Gly Leu  
 35                                      40                                      45  
 Glu Val Glu Val Phe Gly Glu Gly Gln Gly Glu Val Pro Leu Asp Gly  
 50                                      55                                      60  
 Ser His Leu Val Val Lys Ala Ile Arg Ala Gly Leu Lys Ala Ala Asp  
 65                                      70                                      75                                      80  
 Ala Glu Val Pro Gly Leu Arg Val Val Cys His Asn Asn Ile Pro Gln  
 85                                      90                                      95  
 Ser Arg Gly Leu Gly Ser Ser Ala Ala Ala Ala Val Ala Gly Val Ala  
 100                                      105                                      110  
 Ala Ala Asn Gly Leu Ala Asp Phe Pro Leu Thr Gln Glu Gln Ile Val  
 115                                      120                                      125  
 Gln Leu Ser Ser Ala Phe Glu Gly His Pro Asp Asn Ala Ala Ala Ser  
 130                                      135                                      140  
 Val Leu Gly Gly Ala Val Val Ser Trp Thr Asn Leu Ser Ile Asp Gly  
 145                                      150                                      155                                      160  
 Lys Ser Gln Pro Gln Tyr Ala Ala Val Pro Leu Glu Val Gln Asp Asn  
 165                                      170                                      175  
 Ile Arg Ala Thr Ala Leu Val Pro Asn Phe His Ala Ser Thr Glu Ala  
 180                                      185                                      190  
 Val Arg Arg Val Leu Pro Thr Glu Val Thr His Ile Asp Ala Arg Phe  
 195                                      200                                      205  
 Asn Val Ser Arg Val Ala Val Met Ile Val Ala Leu Gln Gln Arg Pro  
 210                                      215                                      220  
 Asp Leu Leu Trp Glu Gly Thr Arg Asp Arg Leu His Gln Pro Tyr Arg  
 225                                      230                                      235                                      240

Ala Glu Val Leu Pro Ile Thr Ser Glu Trp Val Asn Arg Leu Arg Asn  
245 250 255

Arg Gly Tyr Ala Ala Tyr Leu Ser Gly Ala Gly Pro Thr Ala Met Val  
260 265 270

Leu Ser Thr Glu Pro Ile Pro Asp Lys Val Leu Glu Asp Ala Arg Glu  
275 280 285

Ser Gly Ile Lys Val Leu Glu Leu Glu Val Ala Gly Pro Val Lys Val  
290 295 300

Glu Val Asn Gln Pro  
305

<210> 175

<211> 1566

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1543)

<223> RXA00330

<400> 175

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gggggagtat tgtgtcaccc cttgggatag ggttatatcc gtg gac tac att tcg 115  
Val Asp Tyr Ile Ser  
1 5

acg cgt gat gcc agc cgt acc cct gcc cgc ttc agt gat att ttg ctg 163  
Thr Arg Asp Ala Ser Arg Thr Pro Ala Arg Phe Ser Asp Ile Leu Leu  
10 15 20

ggc ggt cta gca cca gac ggc gga ctg tac ctg cct gca acc tac cct 211  
Gly Gly Leu Ala Pro Asp Gly Gly Leu Tyr Leu Pro Ala Thr Tyr Pro  
25 30 35

caa cta gat gat gcc cag ctg agt aaa tgg cgt gag gta tta gcc aac 259  
Gln Leu Asp Asp Ala Gln Leu Ser Lys Trp Arg Glu Val Leu Ala Asn  
40 45 50

gaa gga tac gca gct ttg gct gct gaa gtt atc tcc ctg ttt gtt gat 307  
Glu Gly Tyr Ala Ala Leu Ala Ala Glu Val Ile Ser Leu Phe Val Asp  
55 60 65

gac atc cca gta gaa gac atc aag gcg atc acc gca cgc gcc tac acc 355  
Asp Ile Pro Val Glu Asp Ile Lys Ala Ile Thr Ala Arg Ala Tyr Thr  
70 75 80 85

tac ccg aag ttc aac agc gaa gac atc gtt cct gtc acc gaa ctc gag 403  
Tyr Pro Lys Phe Asn Ser Glu Asp Ile Val Pro Val Thr Glu Leu Glu  
90 95 100

gac aac att tac ctg ggc cac ctt tcc gaa ggc cca acc gct gca ttc 451  
Asp Asn Ile Tyr Leu Gly His Leu Ser Glu Gly Pro Thr Ala Ala Phe  
105 110 115



aaa gac atg gcc atg cag ctg ctc ggc gaa ctt ttc gaa tac gag ctt	499
Lys Asp Met Ala Met Gln Leu Leu Gly Glu Leu Phe Glu Tyr Glu Leu	
120 125 130	
cgc cgc cgc aac gaa acc atc aac atc ctg ggc gct acc tct ggc gat	547
Arg Arg Arg Asn Glu Thr Ile Asn Ile Leu Gly Ala Thr Ser Gly Asp	
135 140 145	
acc ggc tcc tct gcg gaa tac gcc atg cgc ggc cgc gag gga atc cgc	595
Thr Gly Ser Ser Ala Glu Tyr Ala Met Arg Gly Arg Glu Gly Ile Arg	
150 155 160 165	
gta ttc atg ctg acc cca gct ggc cgc atg acc cca ttc cag caa gca	643
Val Phe Met Leu Thr Pro Ala Gly Arg Met Thr Pro Phe Gln Gln Ala	
170 175 180	
cag atg ttt ggc ctt gac gat cca aac atc ttc aac atc gcc ctc gac	691
Gln Met Phe Gly Leu Asp Asp Pro Asn Ile Phe Asn Ile Ala Leu Asp	
185 190 195	
ggc gtt ttc gac gat tgc caa gac gta gtc aag gct gtc tcc gcc gac	739
Gly Val Phe Asp Asp Cys Gln Asp Val Val Lys Ala Val Ser Ala Asp	
200 205 210	
gca gaa ttc aaa aaa gac aac cgc atc ggt gcc gtg aac tcc atc aac	787
Ala Glu Phe Lys Lys Asp Asn Arg Ile Gly Ala Val Asn Ser Ile Asn	
215 220 225	
tgg gca cgc ctt atg gca cag gtt gtg tac tac gtt tcc tca tgg atc	835
Trp Ala Arg Leu Met Ala Gln Val Val Tyr Tyr Val Ser Ser Trp Ile	
230 235 240 245	
cgc acc aca acc agc aat gac caa aag gtc agc ttc tcc gta cca acc	883
Arg Thr Thr Thr Ser Asn Asp Gln Lys Val Ser Phe Ser Val Pro Thr	
250 255 260	
ggc aac ttc ggt gac att tgc gca ggc cac atc gcc cgc caa atg gga	931
Gly Asn Phe Gly Asp Ile Cys Ala Gly His Ile Ala Arg Gln Met Gly	
265 270 275	
ctt ccc atc gat cgc ctc atc gtg gcc acc aac gaa aac gat gtg ctc	979
Leu Pro Ile Asp Arg Leu Ile Val Ala Thr Asn Glu Asn Asp Val Leu	
280 285 290	
gac gag ttc ttc cgt acc ggc gac tac cga gtc cgc agc tcc gca gac	
1027	
Asp Glu Phe Phe Arg Thr Gly Asp Tyr Arg Val Arg Ser Ser Ala Asp	
295 300 305	
acc cac gag acc tcc tca cct tcg atg gat atc tcc cgc gcc tcc aac	
1075	
Thr His Glu Thr Ser Ser Pro Ser Met Asp Ile Ser Arg Ala Ser Asn	
310 315 320 325	
ttc gag cgt ttc atc ttc gac ctg ctc ggc cgc gac gcc acc cgc gtc	
1123	
Phe Glu Arg Phe Ile Phe Asp Leu Leu Gly Arg Asp Ala Thr Arg Val	
330 335 340	

aac gat cta ttt ggt acc cag gtt cgc caa ggc gga ttc tca ctg gct  
1171

Asn Asp Leu Phe Gly Thr Gln Val Arg Gln Gly Gly Phe Ser Leu Ala  
345 350 355

gat gac gcc aac ttt gag aag gct gca gca gaa tac ggt ttc gcc tcc  
1219

Asp Asp Ala Asn Phe Glu Lys Ala Ala Ala Glu Tyr Gly Phe Ala Ser  
360 365 370

gga cga tcc acc cat gct gac cgt gtg gca acc atc gct gac gtg cat  
1267

Gly Arg Ser Thr His Ala Asp Arg Val Ala Thr Ile Ala Asp Val His  
375 380 385

tcc cgc ctc gac gta cta atc gat ccc cac acc gcc gac ggc gtt cac  
1315

Ser Arg Leu Asp Val Leu Ile Asp Pro His Thr Ala Asp Gly Val His  
390 395 400 405

gtg gca cgc cag tgg agg gac gag gtc aac acc cca atc atc gtc cta  
1363

Val Ala Arg Gln Trp Arg Asp Glu Val Asn Thr Pro Ile Ile Val Leu  
410 415 420

gaa act gca ctc cca gtg aaa ttt gcc gac acc atc gtc gaa gca att  
1411

Glu Thr Ala Leu Pro Val Lys Phe Ala Asp Thr Ile Val Glu Ala Ile  
425 430 435

ggt gaa gca cct caa act cca gag cgt ttc gcc gcg atc atg gat gct  
1459

Gly Glu Ala Pro Gln Thr Pro Glu Arg Phe Ala Ala Ile Met Asp Ala  
440 445 450

cca ttc aag gtt tcc gac cta cca aac gac acc gat gca gtt aag cag  
1507

Pro Phe Lys Val Ser Asp Leu Pro Asn Asp Thr Asp Ala Val Lys Gln  
455 460 465

tac ata gtc gat gcg att gca aac act tcc gtg aag taacttgctt  
1553

Tyr Ile Val Asp Ala Ile Ala Asn Thr Ser Val Lys  
470 475 480

tacgccaagg cct  
1566

<210> 176

<211> 481

<212> PRT

<213> Corynebacterium glutamicum

<400> 176

Val Asp Tyr Ile Ser Thr Arg Asp Ala Ser Arg Thr Pro Ala Arg Phe  
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Ser Asp Ile Leu Leu Gly Gly Leu Ala Pro Asp Gly Gly Leu Tyr Leu  
20 25 30

Pro Ala Thr Tyr Pro Gln Leu Asp Asp Ala Gln Leu Ser Lys Trp Arg  
 35 40 45  
 Glu Val Leu Ala Asn Glu Gly Tyr Ala Ala Leu Ala Ala Glu Val Ile  
 50 55 60  
 Ser Leu Phe Val Asp Asp Ile Pro Val Glu Asp Ile Lys Ala Ile Thr  
 65 70 75 80  
 Ala Arg Ala Tyr Thr Tyr Pro Lys Phe Asn Ser Glu Asp Ile Val Pro  
 85 90 95  
 Val Thr Glu Leu Glu Asp Asn Ile Tyr Leu Gly His Leu Ser Glu Gly  
 100 105 110  
 Pro Thr Ala Ala Phe Lys Asp Met Ala Met Gln Leu Leu Gly Glu Leu  
 115 120 125  
 Phe Glu Tyr Glu Leu Arg Arg Arg Asn Glu Thr Ile Asn Ile Leu Gly  
 130 135 140  
 Ala Thr Ser Gly Asp Thr Gly Ser Ser Ala Glu Tyr Ala Met Arg Gly  
 145 150 155 160  
 Arg Glu Gly Ile Arg Val Phe Met Leu Thr Pro Ala Gly Arg Met Thr  
 165 170 175  
 Pro Phe Gln Gln Ala Gln Met Phe Gly Leu Asp Asp Pro Asn Ile Phe  
 180 185 190  
 Asn Ile Ala Leu Asp Gly Val Phe Asp Asp Cys Gln Asp Val Val Lys  
 195 200 205  
 Ala Val Ser Ala Asp Ala Glu Phe Lys Lys Asp Asn Arg Ile Gly Ala  
 210 215 220  
 Val Asn Ser Ile Asn Trp Ala Arg Leu Met Ala Gln Val Val Tyr Tyr  
 225 230 235 240  
 Val Ser Ser Trp Ile Arg Thr Thr Thr Ser Asn Asp Gln Lys Val Ser  
 245 250 255  
 Phe Ser Val Pro Thr Gly Asn Phe Gly Asp Ile Cys Ala Gly His Ile  
 260 265 270  
 Ala Arg Gln Met Gly Leu Pro Ile Asp Arg Leu Ile Val Ala Thr Asn  
 275 280 285  
 Glu Asn Asp Val Leu Asp Glu Phe Phe Arg Thr Gly Asp Tyr Arg Val  
 290 295 300  
 Arg Ser Ser Ala Asp Thr His Glu Thr Ser Ser Pro Ser Met Asp Ile  
 305 310 315 320  
 Ser Arg Ala Ser Asn Phe Glu Arg Phe Ile Phe Asp Leu Leu Gly Arg  
 325 330 335  
 Asp Ala Thr Arg Val Asn Asp Leu Phe Gly Thr Gln Val Arg Gln Gly  
 340 345 350  
 Gly Phe Ser Leu Ala Asp Asp Ala Asn Phe Glu Lys Ala Ala Ala Glu

355	360	365
Tyr Gly Phe Ala Ser Gly Arg Ser Thr His Ala Asp Arg Val Ala Thr		
370	375	380
Ile Ala Asp Val His Ser Arg Leu Asp Val Leu Ile Asp Pro His Thr		
385	390	395
Ala Asp Gly Val His Val Ala Arg Gln Trp Arg Asp Glu Val Asn Thr		
	405	410
Pro Ile Ile Val Leu Glu Thr Ala Leu Pro Val Lys Phe Ala Asp Thr		
	420	425
Ile Val Glu Ala Ile Gly Glu Ala Pro Gln Thr Pro Glu Arg Phe Ala		
435	440	445
Ala Ile Met Asp Ala Pro Phe Lys Val Ser Asp Leu Pro Asn Asp Thr		
450	455	460
Asp Ala Val Lys Gln Tyr Ile Val Asp Ala Ile Ala Asn Thr Ser Val		
465	470	475
		480

Lys

<210> 177  
 <211> 1254  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1231)  
 <223> RXN00403

<400> 177  
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 aagtttttagt cttgtccacc cagaacaggc gggtatttttc atg ccc acc ctc gcg 115  
 Met Pro Thr Leu Ala  
 1 5  
 cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163  
 Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu  
 10 15 20  
 gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211  
 Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly  
 25 30 35  
 gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259  
 Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu  
 40 45 50  
 cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307  
 His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu  
 55 60 65  
 ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355

Leu	Gly	Pro	Gly	Lys	Ala	Ile	Asn	Thr	Asp	Ile	Tyr	Cys	Val	Ile	Cys	
70					75					80					85	
acc	aac	gtc	atc	ggg	ggg	tgc	aac	ggg	tcc	acc	gga	cct	ggc	tcc	atg	403
Thr	Asn	Val	Ile	Gly	Gly	Cys	Asn	Gly	Ser	Thr	Gly	Pro	Gly	Ser	Met	
				90					95					100		
cat	cca	gat	gga	aat	ttc	tgg	ggg	aat	cgc	ttc	ccc	gcc	acg	tcc	att	451
His	Pro	Asp	Gly	Asn	Phe	Trp	Gly	Asn	Arg	Phe	Pro	Ala	Thr	Ser	Ile	
			105					110					115			
cgt	gat	cag	gta	aac	gcc	gaa	aaa	caa	ttc	ctc	gac	gca	ctc	ggc	atc	499
Arg	Asp	Gln	Val	Asn	Ala	Glu	Lys	Gln	Phe	Leu	Asp	Ala	Leu	Gly	Ile	
		120					125					130				
acc	acg	gtc	gcc	gca	gta	ctt	ggg	ggg	tcc	atg	ggg	ggg	gcc	cgc	acc	547
Thr	Thr	Val	Ala	Ala	Val	Leu	Gly	Gly	Ser	Met	Gly	Gly	Ala	Arg	Thr	
	135					140					145					
cta	gag	tgg	gcc	gca	atg	tac	cca	gaa	act	gtt	ggc	gca	gct	gct	gtt	595
Leu	Glu	Trp	Ala	Ala	Met	Tyr	Pro	Glu	Thr	Val	Gly	Ala	Ala	Ala	Val	
150					155					160					165	
ctt	gca	gtt	tct	gca	cgc	gcc	agc	gcc	tgg	caa	atc	ggc	att	caa	tcc	643
Leu	Ala	Val	Ser	Ala	Arg	Ala	Ser	Ala	Trp	Gln	Ile	Gly	Ile	Gln	Ser	
				170					175					180		
gcc	caa	att	aag	gcg	att	gaa	aac	gac	cac	cac	tgg	cac	gaa	ggc	aac	691
Ala	Gln	Ile	Lys	Ala	Ile	Glu	Asn	Asp	His	His	Trp	His	Glu	Gly	Asn	
			185					190					195			
tac	tac	gaa	tcc	ggc	tgc	aac	cca	gcc	acc	gga	ctc	ggc	gcc	gcc	cga	739
Tyr	Tyr	Glu	Ser	Gly	Cys	Asn	Pro	Ala	Thr	Gly	Leu	Gly	Ala	Ala	Arg	
		200					205					210				
cgc	atc	gcc	cac	ctc	acc	tac	cgt	ggc	gaa	cta	gaa	atc	gac	gaa	cgc	787
Arg	Ile	Ala	His	Leu	Thr	Tyr	Arg	Gly	Glu	Leu	Glu	Ile	Asp	Glu	Arg	
	215					220					225					
ttc	ggc	acc	aaa	gcc	caa	aag	aac	gaa	aac	cca	ctc	ggg	ccc	tac	cgc	835
Phe	Gly	Thr	Lys	Ala	Gln	Lys	Asn	Glu	Asn	Pro	Leu	Gly	Pro	Tyr	Arg	
230					235					240					245	
aag	ccc	gac	cag	cgc	ttc	gcc	gtg	gaa	tcc	tac	ttg	gac	tac	caa	gca	883
Lys	Pro	Asp	Gln	Arg	Phe	Ala	Val	Glu	Ser	Tyr	Leu	Asp	Tyr	Gln	Ala	
			250						255					260		
gac	aag	cta	gta	cag	cgt	ttc	gac	gcc	ggc	tcc	tac	gtc	ttg	ctc	acc	931
Asp	Lys	Leu	Val	Gln	Arg	Phe	Asp	Ala	Gly	Ser	Tyr	Val	Leu	Leu	Thr	
			265					270					275			
gac	gcc	ctc	aac	cgc	cac	gac	att	ggg	cgc	gac	cgc	gga	ggc	ctc	aac	979
Asp	Ala	Leu	Asn	Arg	His	Asp	Ile	Gly	Arg	Asp	Arg	Gly	Gly	Leu	Asn	
		280					285					290				
aag	gca	ctc	gaa	tcc	atc	aaa	gtt	cca	gtc	ctt	gtc	gca	ggc	gta	gat	
1027																
Lys	Ala	Leu	Glu	Ser	Ile	Lys	Val	Pro	Val	Leu	Val	Ala	Gly	Val	Asp	
	295					300					305					

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac  
1075

Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn  
310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac  
1123

Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His  
330 335 340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac  
1171

Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn  
345 350 355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg acc tac atc  
1219

Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile  
360 365 370

gag ttc tac atc taataggtat ttacgacaaa tag  
1254

Glu Phe Tyr Ile  
375

<210> 178

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly  
1 5 10 15

Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala  
20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn  
35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp  
50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile  
65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr  
85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe  
100 105 110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu  
115 120 125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met  
130 135 140

Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val  
145 150 155 160

Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln  
 165 170 175  
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His  
 180 185 190  
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly  
 195 200 205  
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu  
 210 215 220  
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro  
 225 230 235 240  
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr  
 245 250 255  
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser  
 260 265 270  
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp  
 275 280 285  
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu  
 290 295 300  
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu  
 305 310 315 320  
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val  
 325 330 335  
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp  
 340 345 350  
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn  
 355 360 365  
 Pro Ser Thr Tyr Ile Glu Phe Tyr Ile  
 370 375

<210> 179  
 <211> 1210  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1210)  
 <223> FRXA00403

<400> 179  
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 aagtttttagt cttgtccacc cagaacaggc gggtattttc atg ccc acc ctc gcg 115  
 Met Pro Thr Leu Ala  
 1 5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163  
 Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu  
                   10                                  15                                  20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211  
 Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly  
                   25                                  30                                  35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259  
 Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu  
                   40                                  45                                  50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307  
 His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu  
                   55                                  60                                  65

ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355  
 Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys  
                   70                                  75                                  80                                  85

acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403  
 Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met  
                   90                                  95                                  100

cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att 451  
 His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile  
                   105                                  110                                  115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc 499  
 Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile  
                   120                                  125                                  130

acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547  
 Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr  
                   135                                  140                                  145

cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt 595  
 Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val  
                   150                                  155                                  160                                  165

ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc 643  
 Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser  
                   170                                  175                                  180

gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac 691  
 Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn  
                   185                                  190                                  195

tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga 739  
 Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg  
                   200                                  205                                  210

cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc 787  
 Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg  
                   215                                  220                                  225

ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc 835  
 Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg  
                   230                                  235                                  240                                  245

aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca 883



Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala  
 250 255 260

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931  
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr  
 265 270 275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979  
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn  
 280 285 290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat  
 1027  
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp  
 295 300 305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac  
 1075  
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn  
 310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac  
 1123  
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His  
 330 335 340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac  
 1171  
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn  
 345 350 355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg  
 1210  
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser  
 360 365 370

<210> 180  
 <211> 370  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 180  
 Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly  
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 Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala  
 20 25 30  
 Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn  
 35 40 45  
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp  
 50 55 60  
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile  
 65 70 75 80  
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr  
 85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe  
 100 105 110  
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu  
 115 120 125  
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met  
 130 135 140  
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val  
 145 150 155 160  
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln  
 165 170 175  
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His  
 180 185 190  
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly  
 195 200 205  
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu  
 210 215 220  
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro  
 225 230 235 240  
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr  
 245 250 255  
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser  
 260 265 270  
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp  
 275 280 285  
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu  
 290 295 300  
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu  
 305 310 315 320  
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val  
 325 330 335  
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp  
 340 345 350  
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn  
 355 360 365  
 Pro Ser  
 370

&lt;210&gt; 181

&lt;211&gt; 771

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (748)

&lt;223&gt; RXC01207

&lt;400&gt; 181

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atTTTTgaac aatccgtaca ccaacttcag gagaaaaaca gtg agc aga atc tat 115  
 Val Ser Arg Ile Tyr 5  
 1

gac tgt gcc gac caa gac tcc cgt gca gca ggc cta aag gcg gct gtc 163  
 Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val 20  
 10 15

gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt 211  
 Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu 35  
 25 30

tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259  
 Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu 50  
 40 45

ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc 307  
 Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val 65  
 55 60

ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag 355  
 Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln 85  
 70 75 80

gca aaa gcg ctt gtg gag gcg ttc tgg cct ggt gga ctg tcc atc atc 403  
 Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile 100  
 90 95

gtt ccg cag gca cca agc ctt ccg tgg aac ctt ggc gat acc cgt ggc 451  
 Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly 115  
 105 110

acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499  
 Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu 130  
 120 125

cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547  
 Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His 145  
 135 140

act cct cca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat 595  
 Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn 165  
 150 155 160

gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca 643  
 Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser 180  
 170 175

acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt 691  
 Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly 195  
 185 190

gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tcg gca gaa 739  
 Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu

200 205 210  
 agc ctg cgc taaatgggag tcggtttcgc ggg 771  
 Ser Leu Arg  
 215  
  
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 <211> 216  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 182  
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 Leu Lys Ala Ala Val Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu  
 20 25 30  
 Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu  
 35 40 45  
 Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro  
 50 55 60  
 Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His  
 65 70 75 80  
 Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly  
 85 90 95  
 Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu  
 100 105 110  
 Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val  
 115 120 125  
 Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala  
 130 135 140  
 Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln  
 145 150 155 160  
 Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala  
 165 170 175  
 Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys  
 180 185 190  
 Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu  
 195 200 205  
 Gly Val Ser Ala Glu Ser Leu Arg  
 210 215  
  
 <210> 183  
 <211> 1419  
 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1396)

&lt;223&gt; RXC00152

&lt;400&gt; 183

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caa	tag	tac	tgg	ccattcc	caactaaaac	tggagtaacg	atg	aca	gga	cta	atc						115
							Met	Thr	Gly	Leu	Ile						
							1				5						

ctc	gcc	ata	gtt	ttc	ctg	gtc	ttt	gtc	gcc	gtc	gtg	gtg	atc	aag	tcc		163
Leu	Ala	Ile	Val	Phe	Leu	Val	Phe	Val	Ala	Val	Val	Val	Ile	Lys	Ser		
				10					15					20			

ata	gcc	ctg	att	ccc	cag	ggt	gaa	gcc	gcc	gtc	att	gaa	cgc	ctt	ggt		211
Ile	Ala	Leu	Ile	Pro	Gln	Gly	Glu	Ala	Ala	Val	Ile	Glu	Arg	Leu	Gly		
			25				30						35				

agc	tac	acc	cgc	acc	gtt	tca	ggt	ggc	ctg	acc	ctg	ctg	gtt	cca	ttc		259
Ser	Tyr	Thr	Arg	Thr	Val	Ser	Gly	Gly	Leu	Thr	Leu	Leu	Val	Pro	Phe		
		40					45					50					

gtg	gac	cga	gta	cgc	gca	agg	atc	gac	acc	cgt	gag	cgc	gtg	gtc	tca		307
Val	Asp	Arg	Val	Arg	Ala	Arg	Ile	Asp	Thr	Arg	Glu	Arg	Val	Val	Ser		
	55					60					65						

ttc	cca	ccg	cag	gct	gtt	att	acc	caa	gac	aac	ctg	acc	gtg	gcc	atc		355
Phe	Pro	Pro	Gln	Ala	Val	Ile	Thr	Gln	Asp	Asn	Leu	Thr	Val	Ala	Ile		
70				75						80					85		

gat	atc	gtg	gtg	acc	ttc	caa	atc	aac	gaa	cca	gag	cgc	gcc	atc	tac		403
Asp	Ile	Val	Val	Thr	Phe	Gln	Ile	Asn	Glu	Pro	Glu	Arg	Ala	Ile	Tyr		
				90				95						100			

ggc	gtg	gac	aac	tac	atc	gtc	ggt	gtg	gag	cag	att	tct	gta	gca	aca		451
Gly	Val	Asp	Asn	Tyr	Ile	Val	Gly	Val	Glu	Gln	Ile	Ser	Val	Ala	Thr		
			105				110						115				

ctt	cga	gac	gtt	gtc	ggt	ggc	atg	acc	ctg	gaa	gaa	acc	ctc	act	tca		499
Leu	Arg	Asp	Val	Val	Gly	Gly	Met	Thr	Leu	Glu	Glu	Thr	Leu	Thr	Ser		
		120					125					130					

cgt	gac	gtg	atc	aac	cgc	cgc	ctc	cgt	ggc	gag	ctc	gat	gca	gca	acc		547
Arg	Asp	Val	Ile	Asn	Arg	Arg	Leu	Arg	Gly	Glu	Leu	Asp	Ala	Ala	Thr		
	135					140					145						

acc	aaa	tgg	ggc	ctg	cgc	atc	agc	cgt	gtg	gaa	cta	aag	gca	att	gat		595
Thr	Lys	Trp	Gly	Leu	Arg	Ile	Ser	Arg	Val	Glu	Leu	Lys	Ala	Ile	Asp		
150					155					160					165		

ccg	cca	cca	tcc	atc	cag	caa	tcg	atg	gaa	aag	cag	atg	aag	gca	gac		643
Pro	Pro	Pro	Ser	Ile	Gln	Gln	Ser	Met	Glu	Lys	Gln	Met	Lys	Ala	Asp		
				170					175					180			

cgt	gaa	aag	cgc	gcc	acc	att	ttg	acc	gca	gaa	ggt	cag	cgc	gaa	gcc		691
Arg	Glu	Lys	Arg	Ala	Thr	Ile	Leu	Thr	Ala	Glu	Gly	Gln	Arg	Glu	Ala		
			185				190						195				

gac	atc	aaa	act	gcc	gaa	ggt	gaa	aag	caa	gcc	aag	atc	ctc	caa	gct		739
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Asp	Ile	Lys	Thr	Ala	Glu	Gly	Glu	Lys	Gln	Ala	Lys	Ile	Leu	Gln	Ala	
		200					205					210				
gag	ggt	gaa	aag	cac	gca	tcc	atc	ctg	aac	gca	gaa	gca	gaa	cgc	caa	787
Glu	Gly	Glu	Lys	His	Ala	Ser	Ile	Leu	Asn	Ala	Glu	Ala	Glu	Arg	Gln	
		215					220				225					
gcg	atg	atc	ctg	cgc	gcc	gaa	ggt	gaa	cgc	gca	gca	cgc	tac	ctc	cag	835
Ala	Met	Ile	Leu	Arg	Ala	Glu	Gly	Glu	Arg	Ala	Ala	Arg	Tyr	Leu	Gln	
230					235					240					245	
gcg	cag	ggt	gaa	gcc	cga	gca	atc	caa	aag	gtc	aac	gca	gca	atc	aag	883
Ala	Gln	Gly	Glu	Ala	Arg	Ala	Ile	Gln	Lys	Val	Asn	Ala	Ala	Ile	Lys	
				250					255					260		
tct	gcc	aag	ttg	acc	cca	gag	gtt	ctt	gct	tat	caa	tac	ctc	gaa	aag	931
Ser	Ala	Lys	Leu	Thr	Pro	Glu	Val	Leu	Ala	Tyr	Gln	Tyr	Leu	Glu	Lys	
			265					270					275			
ctt	cct	aag	atc	gca	gag	ggc	aac	gcc	tcc	aag	atg	tgg	gtc	atc	cca	979
Leu	Pro	Lys	Ile	Ala	Glu	Gly	Asn	Ala	Ser	Lys	Met	Trp	Val	Ile	Pro	
		280					285					290				
agc	cag	ttc	tcc	gat	tct	ctg	gaa	ggt	ttt	gcg	aag	cag	ttc	ggc	gca	
1027																
Ser	Gln	Phe	Ser	Asp	Ser	Leu	Glu	Gly	Phe	Ala	Lys	Gln	Phe	Gly	Ala	
	295					300					305					
aag	gat	gca	gaa	ggt	gtc	ttc	cgc	tac	gaa	cca	aac	acc	gtg	gat	gaa	
1075																
Lys	Asp	Ala	Glu	Gly	Val	Phe	Arg	Tyr	Glu	Pro	Asn	Thr	Val	Asp	Glu	
310					315					320					325	
gaa	acc	cgc	gac	atc	gca	aac	gcc	gac	aac	gtg	gaa	gac	tgg	ttc	tcc	
1123																
Glu	Thr	Arg	Asp	Ile	Ala	Asn	Ala	Asp	Asn	Val	Glu	Asp	Trp	Phe	Ser	
				330					335					340		
acc	gaa	tca	gac	cct	gaa	atc	gca	gca	gca	gtc	gcc	gca	gca	aac	gcc	
1171																
Thr	Glu	Ser	Asp	Pro	Glu	Ile	Ala	Ala	Ala	Val	Ala	Ala	Ala	Asn	Ala	
			345					350					355			
gtg	gcc	aac	aag	cca	gtc	gat	cca	gaa	ccc	ggt	gag	atc	ctt	tcc	aag	
1219																
Val	Ala	Asn	Lys	Pro	Val	Asp	Pro	Glu	Pro	Gly	Glu	Ile	Leu	Ser	Lys	
		360					365					370				
aag	acc	gca	cga	cgc	gtt	gaa	cct	gaa	gca	gta	ttg	gag	gct	ttg	caa	
1267																
Lys	Thr	Ala	Arg	Arg	Val	Glu	Pro	Glu	Ala	Val	Leu	Glu	Ala	Leu	Gln	
	375					380					385					
aac	gga	acc	act	aca	caa	cct	gag	gtt	gag	gca	gca	cct	cct	acc	gca	
1315																
Asn	Gly	Thr	Thr	Thr	Gln	Pro	Glu	Val	Glu	Ala	Ala	Pro	Pro	Thr	Ala	
390					395					400					405	
aac	ttc	gcc	caa	gaa	ttc	cct	gca	cca	cag	gca	aac	cct	gaa	gat	tac	
1363																
Asn	Phe	Ala	Gln	Glu	Phe	Pro	Ala	Pro	Gln	Ala	Asn	Pro	Glu	Asp	Tyr	

410 415 420  
 tcc gac caa cac cga gag aat cct tac gga aac taatcaggca taagaaaagg  
 1416  
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 425 430  
  
 cgg  
 1419  
  
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 <211> 432  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 184  
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 Val Val Ile Lys Ser Ile Ala Leu Ile Pro Gln Gly Glu Ala Ala Val  
 20 25 30  
 Ile Glu Arg Leu Gly Ser Tyr Thr Arg Thr Val Ser Gly Gly Leu Thr  
 35 40 45  
 Leu Leu Val Pro Phe Val Asp Arg Val Arg Ala Arg Ile Asp Thr Arg  
 50 55 60  
 Glu Arg Val Val Ser Phe Pro Pro Gln Ala Val Ile Thr Gln Asp Asn  
 65 70 75 80  
 Leu Thr Val Ala Ile Asp Ile Val Val Thr Phe Gln Ile Asn Glu Pro  
 85 90 95  
 Glu Arg Ala Ile Tyr Gly Val Asp Asn Tyr Ile Val Gly Val Glu Gln  
 100 105 110  
 Ile Ser Val Ala Thr Leu Arg Asp Val Val Gly Gly Met Thr Leu Glu  
 115 120 125  
 Glu Thr Leu Thr Ser Arg Asp Val Ile Asn Arg Arg Leu Arg Gly Glu  
 130 135 140  
 Leu Asp Ala Ala Thr Thr Lys Trp Gly Leu Arg Ile Ser Arg Val Glu  
 145 150 155 160  
 Leu Lys Ala Ile Asp Pro Pro Pro Ser Ile Gln Gln Ser Met Glu Lys  
 165 170 175  
 Gln Met Lys Ala Asp Arg Glu Lys Arg Ala Thr Ile Leu Thr Ala Glu  
 180 185 190  
 Gly Gln Arg Glu Ala Asp Ile Lys Thr Ala Glu Gly Glu Lys Gln Ala  
 195 200 205  
 Lys Ile Leu Gln Ala Glu Gly Glu Lys His Ala Ser Ile Leu Asn Ala  
 210 215 220  
 Glu Ala Glu Arg Gln Ala Met Ile Leu Arg Ala Glu Gly Glu Arg Ala  
 225 230 235 240

Ala Arg Tyr Leu Gln Ala Gln Gly Glu Ala Arg Ala Ile Gln Lys Val  
 245 250 255

Asn Ala Ala Ile Lys Ser Ala Lys Leu Thr Pro Glu Val Leu Ala Tyr  
 260 265 270

Gln Tyr Leu Glu Lys Leu Pro Lys Ile Ala Glu Gly Asn Ala Ser Lys  
 275 280 285

Met Trp Val Ile Pro Ser Gln Phe Ser Asp Ser Leu Glu Gly Phe Ala  
 290 295 300

Lys Gln Phe Gly Ala Lys Asp Ala Glu Gly Val Phe Arg Tyr Glu Pro  
 305 310 315 320

Asn Thr Val Asp Glu Glu Thr Arg Asp Ile Ala Asn Ala Asp Asn Val  
 325 330 335

Glu Asp Trp Phe Ser Thr Glu Ser Asp Pro Glu Ile Ala Ala Ala Val  
 340 345 350

Ala Ala Ala Asn Ala Val Ala Asn Lys Pro Val Asp Pro Glu Pro Gly  
 355 360 365

Glu Ile Leu Ser Lys Lys Thr Ala Arg Arg Val Glu Pro Glu Ala Val  
 370 375 380

Leu Glu Ala Leu Gln Asn Gly Thr Thr Thr Gln Pro Glu Val Glu Ala  
 385 390 395 400

Ala Pro Pro Thr Ala Asn Phe Ala Gln Glu Phe Pro Ala Pro Gln Ala  
 405 410 415

Asn Pro Glu Asp Tyr Ser Asp Gln His Arg Glu Asn Pro Tyr Gly Asn  
 420 425 430

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 <211> 1170  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1147)  
 <223> RXA00115

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 Met Leu Asp Asn Ser  
 1 5  
 ttt tac acc gca gag gtt cag ggc cca tac gaa acc gct tcc att ggc 163  
 Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu Thr Ala Ser Ile Gly  
 10 15 20



cg	g	ctc	gaa	ctc	gaa	gaa	ggg	ggt	gtg	att	gag	gat	tgc	tgg	ttg	gct	211
Arg	Leu	Glu	Leu	Glu	Glu	Gly	Gly	Val	Ile	Glu	Asp	Cys	Trp	Leu	Ala		
			25					30						35			
tac	gct	aca	gct	gga	acg	ctc	aac	gag	gac	aag	tcc	aac	gcc	atc	ctc	259	
Tyr	Ala	Thr	Ala	Gly	Thr	Leu	Asn	Glu	Asp	Lys	Ser	Asn	Ala	Ile	Leu		
		40					45					50					
att	ccg	acg	tgg	tac	tcc	gga	acc	cat	cag	acc	tgg	ttc	cag	cag	tac	307	
Ile	Pro	Thr	Trp	Tyr	Ser	Gly	Thr	His	Gln	Thr	Trp	Phe	Gln	Gln	Tyr		
	55					60					65						
atc	ggc	act	gat	cat	gcg	ctg	gat	cca	tca	aag	tat	ttc	atc	atc	tcc	355	
Ile	Gly	Thr	Asp	His	Ala	Leu	Asp	Pro	Ser	Lys	Tyr	Phe	Ile	Ile	Ser		
	70				75					80					85		
atc	aac	caa	atc	ggt	aat	ggt	ttg	tcg	gtc	tcc	cct	gcc	aac	acg	gct	403	
Ile	Asn	Gln	Ile	Gly	Asn	Gly	Leu	Ser	Val	Ser	Pro	Ala	Asn	Thr	Ala		
				90					95					100			
gat	gac	agc	atc	tcg	atg	tcc	aag	ttc	ccg	aat	gtt	cgc	att	ggt	gat	451	
Asp	Asp	Ser	Ile	Ser	Met	Ser	Lys	Phe	Pro	Asn	Val	Arg	Ile	Gly	Asp		
			105					110					115				
gat	gtc	gtt	gcc	cag	gac	cgg	ctc	ttg	cgc	caa	gag	ttt	ggt	att	acc	499	
Asp	Val	Val	Ala	Gln	Asp	Arg	Leu	Leu	Arg	Gln	Glu	Phe	Gly	Ile	Thr		
		120					125					130					
gag	ctc	ttt	gcc	gtc	gtt	ggt	ggt	tcg	atg	ggt	gcg	cag	caa	acc	tat	547	
Glu	Leu	Phe	Ala	Val	Val	Gly	Gly	Ser	Met	Gly	Ala	Gln	Gln	Thr	Tyr		
	135					140					145						
gag	tgg	att	gtt	cgc	ttc	cct	gac	caa	gtt	cat	cga	gca	gct	ccg	atc	595	
Glu	Trp	Ile	Val	Arg	Phe	Pro	Asp	Gln	Val	His	Arg	Ala	Ala	Pro	Ile		
	150				155					160					165		
gcg	ggc	act	gcg	aag	aac	act	cct	cat	gat	ttc	atc	ttc	acc	cag	act	643	
Ala	Gly	Thr	Ala	Lys	Asn	Thr	Pro	His	Asp	Phe	Ile	Phe	Thr	Gln	Thr		
				170					175					180			
ctt	aat	gag	acc	gtt	gag	gcc	gat	cca	ggg	ttc	aat	ggc	ggc	gaa	tac	691	
Leu	Asn	Glu	Thr	Val	Glu	Ala	Asp	Pro	Gly	Phe	Asn	Gly	Gly	Glu	Tyr		
			185					190					195				
tcc	tcc	cat	gaa	gag	gta	gct	gat	gga	ctt	cgc	cgt	caa	tcg	cat	ctt	739	
Ser	Ser	His	Glu	Glu	Val	Ala	Asp	Gly	Leu	Arg	Arg	Gln	Ser	His	Leu		
		200					205					210					
tgg	gct	gcc	atg	gga	ttt	tcc	aca	gag	ttc	tgg	aag	cag	gag	gca	tgg	787	
Trp	Ala	Ala	Met	Gly	Phe	Ser	Thr	Glu	Phe	Trp	Lys	Gln	Glu	Ala	Trp		
	215					220					225						
cgt	cgc	ctg	gga	ctt	gaa	agt	aag	gag	tca	gtg	ctc	gcg	gac	ttc	ctg	835	
Arg	Arg	Leu	Gly	Leu	Glu	Ser	Lys	Glu	Ser	Val	Leu	Ala	Asp	Phe	Leu		
	230				235					240					245		
gat	ccg	ctg	ttc	atg	tcc	atg	gat	cct	aat	acc	ttg	ctc	aac	aac	gct	883	
Asp	Pro	Leu	Phe	Met	Ser	Met	Asp	Pro	Asn	Thr	Leu	Leu	Asn	Asn	Ala		
				250					255					260			

tgg aag tgg cag cat ggc gat gtc tct cgc cac acc ggc ggc gac ttg 931  
 Trp Lys Trp Gln His Gly Asp Val Ser Arg His Thr Gly Gly Asp Leu  
                   265                                  270                                  275

gca gcg gct ctt ggc cga gtg aag gct aag acc ttc gtt atg ccc atc 979  
 Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr Phe Val Met Pro Ile  
                   280                                  285                                  290

agc gag gac atg ttc ttt cct gtt cgt gac tgt gcc gca gaa caa gca  
 1027  
 Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys Ala Ala Glu Gln Ala  
           295                                  300                                  305

ctc atc cca ggc agc gag ctt cga gtg atc gaa gac atc gcc ggt cac  
 1075  
 Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu Asp Ile Ala Gly His  
           310                                  315                                  320                                  325

ctt ggg ctt ttt aac gtc tct gag aat tac atc cca cag atc gac aaa  
 1123  
 Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile Pro Gln Ile Asp Lys  
                                   330                                  335                                  340

aat ctg aaa gag ctg ttc gag agc taaacactga tgtcaaagag cct  
 1170  
 Asn Leu Lys Glu Leu Phe Glu Ser  
                                   345

<210> 186

<211> 349

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

Met Leu Asp Asn Ser Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu  
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Thr Ala Ser Ile Gly Arg Leu Glu Leu Glu Gly Gly Val Ile Glu  
                   20                                  25                                  30

Asp Cys Trp Leu Ala Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys  
           35                                  40                                  45

Ser Asn Ala Ile Leu Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr  
           50                                  55                                  60

Trp Phe Gln Gln Tyr Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys  
   65                                  70                                  75                                  80

Tyr Phe Ile Ile Ser Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser  
                                   85                                  90                                  95

Pro Ala Asn Thr Ala Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn  
                   100                                  105                                  110

Val Arg Ile Gly Asp Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln  
           115                                  120                                  125

Glu Phe Gly Ile Thr Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly  
   130                                  135                                  140

Ala Gln Gln Thr Tyr Glu Trp Ile Val Arg Phe Pro Asp Gln Val His  
 145 150 155 160

Arg Ala Ala Pro Ile Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe  
 165 170 175

Ile Phe Thr Gln Thr Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe  
 180 185 190

Asn Gly Gly Glu Tyr Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg  
 195 200 205

Arg Gln Ser His Leu Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp  
 210 215 220

Lys Gln Glu Ala Trp Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val  
 225 230 235 240

Leu Ala Asp Phe Leu Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr  
 245 250 255

Leu Leu Asn Asn Ala Trp Lys Trp Gln His Gly Asp Val Ser Arg His  
 260 265 270

Thr Gly Gly Asp Leu Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr  
 275 280 285

Phe Val Met Pro Ile Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys  
 290 295 300

Ala Ala Glu Gln Ala Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu  
 305 310 315 320

Asp Ile Ala Gly His Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile  
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Pro Gln Ile Asp Lys Asn Leu Lys Glu Leu Phe Glu Ser  
 340 345

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aagtttttagt cttgtccacc cagaacaggc ggattattttc atg ccc acc ctc gcg 115  
 Met Pro Thr Leu Ala  
 1 5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163  
 Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu  
 10 15 20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt	211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly	
25 30 35	
gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa	259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu	
40 45 50	
cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg	307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu	
55 60 65	
ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt	355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys	
70 75 80 85	
acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg	403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met	
90 95 100	
cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att	451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile	
105 110 115	
cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc	499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile	
120 125 130	
acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc	547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr	
135 140 145	
cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt	595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val	
150 155 160 165	
ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc	643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser	
170 175 180	
gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac	691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn	
185 190 195	
tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga	739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg	
200 205 210	
cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc	787
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg	
215 220 225	
ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc	835
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg	
230 235 240 245	
aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca	883
Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala	
250 255 260	

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931  
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr  
                   265                                  270                                  275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979  
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn  
                   280                                  285                                  290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat  
 1027  
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp  
                   295                                  300                                  305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac  
 1075  
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn  
 310                                  315                                  320                                  325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac  
 1123  
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His  
                                   330                                  335                                  340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac  
 1171  
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn  
                                   345                                  350                                  355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg acc tac atc  
 1219  
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile  
                   360                                  365                                  370

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<213> Corynebacterium glutamicum

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                   20                                  25                                  30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn  
                   35                                  40                                  45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp  
           50                                  55                                  60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile  
           65                                  70                                  75                                  80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr

85								90				95			
Gly	Pro	Gly	Ser	Met	His	Pro	Asp	Gly	Asn	Phe	Trp	Gly	Asn	Arg	Phe
			100					105				110			
Pro	Ala	Thr	Ser	Ile	Arg	Asp	Gln	Val	Asn	Ala	Glu	Lys	Gln	Phe	Leu
		115					120					125			
Asp	Ala	Leu	Gly	Ile	Thr	Thr	Val	Ala	Ala	Val	Leu	Gly	Gly	Ser	Met
	130					135					140				
Gly	Gly	Ala	Arg	Thr	Leu	Glu	Trp	Ala	Ala	Met	Tyr	Pro	Glu	Thr	Val
145					150					155					160
Gly	Ala	Ala	Ala	Val	Leu	Ala	Val	Ser	Ala	Arg	Ala	Ser	Ala	Trp	Gln
				165					170					175	
Ile	Gly	Ile	Gln	Ser	Ala	Gln	Ile	Lys	Ala	Ile	Glu	Asn	Asp	His	His
			180					185					190		
Trp	His	Glu	Gly	Asn	Tyr	Tyr	Glu	Ser	Gly	Cys	Asn	Pro	Ala	Thr	Gly
		195					200					205			
Leu	Gly	Ala	Ala	Arg	Arg	Ile	Ala	His	Leu	Thr	Tyr	Arg	Gly	Glu	Leu
	210					215					220				
Glu	Ile	Asp	Glu	Arg	Phe	Gly	Thr	Lys	Ala	Gln	Lys	Asn	Glu	Asn	Pro
225					230					235					240
Leu	Gly	Pro	Tyr	Arg	Lys	Pro	Asp	Gln	Arg	Phe	Ala	Val	Glu	Ser	Tyr
				245					250					255	
Leu	Asp	Tyr	Gln	Ala	Asp	Lys	Leu	Val	Gln	Arg	Phe	Asp	Ala	Gly	Ser
			260				265						270		
Tyr	Val	Leu	Leu	Thr	Asp	Ala	Leu	Asn	Arg	His	Asp	Ile	Gly	Arg	Asp
		275					280					285			
Arg	Gly	Gly	Leu	Asn	Lys	Ala	Leu	Glu	Ser	Ile	Lys	Val	Pro	Val	Leu
	290					295					300				
Val	Ala	Gly	Val	Asp	Thr	Asp	Ile	Leu	Tyr	Pro	Tyr	His	Gln	Gln	Glu
305					310					315					320
His	Leu	Ser	Arg	Asn	Leu	Gly	Asn	Leu	Leu	Ala	Met	Ala	Lys	Ile	Val
				325					330					335	
Ser	Pro	Val	Gly	His	Asp	Ala	Phe	Leu	Thr	Glu	Ser	Arg	Gln	Met	Asp
			340					345					350		
Arg	Ile	Val	Arg	Asn	Phe	Phe	Ser	Leu	Ile	Ser	Pro	Asp	Glu	Asp	Asn
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Pro	Ser	Thr	Tyr	Ile	Glu	Phe	Tyr	Ile							
		370				375									

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&lt;211&gt; 1210

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

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aagtttttagt cttgtccacc cagaacaggc ggttatttttc atg ccc acc ctc gcg 115
                                         Met Pro Thr Leu Ala
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cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
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gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
                        25                               30                               35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
                        40                               45                               50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
                        55                               60                               65

ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys
70                               75                               80                               85

acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met
                        90                               95                               100

cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att 451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile
                        105                               110                               115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc 499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile
                        120                               125                               130

acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr
                        135                               140                               145

cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt 595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val
150                               155                               160                               165

ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc 643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser
                        170                               175                               180

gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac 691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn
                        185                               190                               195

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tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga 739  
 Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg  
 200 205 210

cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc 787  
 Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg  
 215 220 225

ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc 835  
 Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg  
 230 235 240 245

aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca 883  
 Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala  
 250 255 260

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931  
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr  
 265 270 275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979  
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn  
 280 285 290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat  
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 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp  
 295 300 305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac  
 1075  
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn  
 310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac  
 1123  
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His  
 330 335 340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac  
 1171  
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn  
 345 350 355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg  
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 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser  
 360 365 370

&lt;210&gt; 190

&lt;211&gt; 370

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 190

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Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala  
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Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn  
                   35                                  40                                  45  
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp  
                   50                                  55                                  60  
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile  
                   65                                  70                                  75                                  80  
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr  
                                   85                                  90                                  95  
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe  
                                   100                                  105                                  110  
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu  
                                   115                                  120                                  125  
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met  
                   130                                  135                                  140  
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val  
                   145                                  150                                  155                                  160  
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln  
                                   165                                  170                                  175  
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His  
                                   180                                  185                                  190  
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly  
                   195                                  200                                  205  
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu  
                   210                                  215                                  220  
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro  
                   225                                  230                                  235                                  240  
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr  
                                   245                                  250                                  255  
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser  
                                   260                                  265                                  270  
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp  
                   275                                  280                                  285  
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu  
                   290                                  295                                  300  
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu  
                   305                                  310                                  315                                  320  
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val  
                                   325                                  330                                  335  
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp  
                                   340                                  345                                  350

Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn  
 355 360 365

Pro Ser  
 370

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 <223> RXS03158

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 Leu His Ser Thr Thr  
 1 5  
 aag tac atc gaa gga cac tcc gac gtt gtt ggc ggc ctt gtg ggt acc 163  
 Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly Gly Leu Val Gly Thr  
 10 15 20  
 aac gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc 211  
 Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile  
 25 30 35  
 gga ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc 259  
 Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu  
 40 45 50  
 aag acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag 307  
 Lys Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys  
 55 60 65  
 atc gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac 355  
 Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr  
 70 75 80 85  
 cca ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg 403  
 Pro Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met  
 90 95 100  
 aag cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa 451  
 Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu  
 105 110 115  
 gca gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag 499  
 Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu  
 120 125 130  
 tcc ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc 547  
 Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr  
 135 140 145  
 cac cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg 595

His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val  
 150 155 160 165

cgc atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc 643  
 Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val  
 170 175 180

gag cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 687  
 Glu Gln Ala Leu Asn Asn Leu  
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<211> 188

<212> PRT

<213> Corynebacterium glutamicum

<400> 192

Leu His Ser Thr Thr Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly  
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 20 25 30

Met Gln Gly Gly Ile Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu  
 35 40 45

Thr Ala Arg Gly Leu Lys Thr Leu Ala Val Arg Met Asp Arg His Cys  
 50 55 60

Asp Asn Ala Glu Lys Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val  
 65 70 75 80

Ser Thr Val Leu Tyr Pro Gly Leu Lys Asn His Pro Gly His Glu Val  
 85 90 95

Ala Ala Lys Gln Met Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe  
 100 105 110

Ala Gly Gly Glu Glu Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu  
 115 120 125

Ile Cys Leu Ala Glu Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His  
 130 135 140

Pro Ala Thr Met Thr His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val  
 145 150 155 160

Pro Arg Asp Leu Val Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp  
 165 170 175

Leu Leu Ala Asp Val Glu Gln Ala Leu Asn Asn Leu  
 180 185

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<211> 617

<212> DNA

<213> Corynebacterium glutamicum

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1 5 10 15	
tac atc gga gga cac tcc gac gtt gtt ggc ggc ctt gtg gtt acc aac	96
Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn	
20 25 30	
gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc gga	144
Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly	
35 40 45	
ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc aag	192
Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys	
50 55 60	
acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag atc	240
Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile	
65 70 75 80	
gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac cca	288
Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro	
85 90 95	
ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg aag	336
Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys	
100 105 110	
cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa gca	384
Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala	
115 120 125	
gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag tcc	432
Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser	
130 135 140	
ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc cac	480
Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His	
145 150 155 160	
cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg cgc	528
Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg	
165 170 175	
atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc gag	576
Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu	
180 185 190	
cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca	617
Gln Ala Leu Asn Asn Leu	
195	

<210> 194  
 <211> 198  
 <212> PRT

<213> Corynebacterium glutamicum

<400> 194

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Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys
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Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn
              20              25              30

Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly
              35              40              45

Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys
              50              55              60

Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile
 65              70              75              80

Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro
              85              90              95

Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys
              100              105              110

Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala
 115              120              125

Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser
 130              135              140

Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His
 145              150              155              160

Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg
              165              170              175

Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu
 180              185              190

Gln Ala Leu Asn Asn Leu
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<211> 1170

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1147)

<223> RXA02532

<400> 195

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tgtgcaagcg ggacggccag ccagaactcc tgggtgcgccg atg aac cca cct atc      115
                               Met Asn Pro Pro Ile
                               1              5

acg ttg tcc agc act tat gtt cat gat tca gaa aaa gct tat ggg cgc      163

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Thr	Leu	Ser	Ser	Thr	Tyr	Val	His	Asp	Ser	Glu	Lys	Ala	Tyr	Gly	Arg	
				10					15					20		
gat	ggc	aat	gat	gga	tgg	ggt	gca	ttt	gag	gct	gcc	atg	gga	act	cta	211
Asp	Gly	Asn	Asp	Gly	Trp	Gly	Ala	Phe	Glu	Ala	Ala	Met	Gly	Thr	Leu	
			25					30					35			
gat	ggt	ggg	ttc	gcg	gta	tct	tat	tct	tca	ggt	ttg	gca	gcg	gca	acg	259
Asp	Gly	Gly	Phe	Ala	Val	Ser	Tyr	Ser	Ser	Gly	Leu	Ala	Ala	Ala	Thr	
		40					45					50				
tcg	att	gct	gat	ttg	gtt	cct	act	ggt	ggc	aca	gtt	gtt	tta	cct	aaa	307
Ser	Ile	Ala	Asp	Leu	Val	Pro	Thr	Gly	Gly	Thr	Val	Val	Leu	Pro	Lys	
	55					60					65					
gct	gcc	tat	tat	ggc	gtg	acc	aat	att	ttc	gcc	agg	atg	gaa	gcc	cgc	355
Ala	Ala	Tyr	Tyr	Gly	Val	Thr	Asn	Ile	Phe	Ala	Arg	Met	Glu	Ala	Arg	
70					75					80					85	
gga	agg	ctg	aag	gtt	cga	act	gtt	gat	gca	gac	aat	acc	gaa	gaa	gtg	403
Gly	Arg	Leu	Lys	Val	Arg	Thr	Val	Asp	Ala	Asp	Asn	Thr	Glu	Glu	Val	
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att	gct	gct	gct	caa	ggt	gca	gat	gtg	gtg	tgg	gtg	gaa	tcg	atc	gct	451
Ile	Ala	Ala	Ala	Gln	Gly	Ala	Asp	Val	Val	Trp	Val	Glu	Ser	Ile	Ala	
				105				110					115			
aat	ccg	acg	atg	gtg	gta	gct	gat	atc	cct	gca	ata	gtc	gac	ggt	gtg	499
Asn	Pro	Thr	Met	Val	Val	Ala	Asp	Ile	Pro	Ala	Ile	Val	Asp	Gly	Val	
		120					125					130				
cgt	ggg	ctt	gga	gtt	ttg	act	gtc	gtt	gac	gcg	act	ttc	gca	acg	cca	547
Arg	Gly	Leu	Gly	Val	Leu	Thr	Val	Val	Asp	Ala	Thr	Phe	Ala	Thr	Pro	
	135					140					145					
ctt	cgt	caa	cgt	cca	ttg	gaa	ctt	ggt	gct	gat	att	gtg	ctt	tac	tcg	595
Leu	Arg	Gln	Arg	Pro	Leu	Glu	Leu	Gly	Ala	Asp	Ile	Val	Leu	Tyr	Ser	
150					155					160					165	
gca	acc	aaa	ctt	atc	ggt	gga	cac	tct	gat	ctt	ctt	ctt	gga	gtc	gca	643
Ala	Thr	Lys	Leu	Ile	Gly	Gly	His	Ser	Asp	Leu	Leu	Leu	Gly	Val	Ala	
				170					175					180		
gtg	tgc	aag	tct	gag	cac	cat	gcg	cag	ttt	ctt	gcc	act	cac	cgt	cat	691
Val	Cys	Lys	Ser	Glu	His	His	Ala	Gln	Phe	Leu	Ala	Thr	His	Arg	His	
			185					190					195			
gat	cat	ggt	tca	gtg	ccg	gga	ggt	ctt	gaa	gcg	ttt	ctt	gct	ctc	cgt	739
Asp	His	Gly	Ser	Val	Pro	Gly	Gly	Leu	Glu	Ala	Phe	Leu	Ala	Leu	Arg	
		200					205					210				
gga	ttg	tat	tcc	ttg	gcg	gtg	cgt	ctt	gat	cga	gca	gaa	tcc	aac	gca	787
Gly	Leu	Tyr	Ser	Leu	Ala	Val	Arg	Leu	Asp	Arg	Ala	Glu	Ser	Asn	Ala	
	215					220					225					
gca	gaa	ctt	tcg	cgg	cga	ctt	aac	gcg	cat	cct	tcg	gtt	acc	cgc	gtc	835
Ala	Glu	Leu	Ser	Arg	Arg	Leu	Asn	Ala	His	Pro	Ser	Val	Thr	Arg	Val	
230					235					240					245	
aat	tat	cca	gga	ctt	cct	gat	gat	ccc	caa	cat	gaa	aaa	gcc	gtg	cga	883
Asn	Tyr	Pro	Gly	Leu	Pro	Asp	Asp	Pro	Gln	His	Glu	Lys	Ala	Val	Arg	

	250	255	260	
gtc cta ccc tct gga tgt gga aac atg ttg tca ttt gag ctt gat gca				931
Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser Phe Glu Leu Asp Ala				
	265	270	275	
aca cct gaa cga act gat gag att ctc gaa agc ctg tca ctt tta acc				979
Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser Leu Ser Leu Leu Thr				
	280	285	290	
cac gcg acc agt tgg gga ggt gtg gaa aca gcc att gaa cgt cgc acc				
1027				
His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala Ile Glu Arg Arg Thr				
	295	300	305	
agg cgg gat gct gaa gtg gtg gca gaa gta ccg atg act ctt tgc cgc				
1075				
Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro Met Thr Leu Cys Arg				
	310	315	320	325
gtt tcc gta gga att gaa gac gtt gaa gat cta tgg gaa gac ctc aac				
1123				
Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu Trp Glu Asp Leu Asn				
	330	335	340	
gcc tca atc gac aaa gtt ctg ggt tagaactcgt agccagtaac cag				
1170				
Ala Ser Ile Asp Lys Val Leu Gly				
	345			

&lt;210&gt; 196

&lt;211&gt; 349

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 196

Met Asn Pro Pro Ile Thr Leu Ser Ser Thr Tyr Val His Asp Ser Glu																
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Lys Ala Tyr Gly Arg Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala																
			20					25						30		
Ala Met Gly Thr Leu Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly																
		35				40							45			
Leu Ala Ala Ala Thr Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr																
	50					55					60					
Val Val Leu Pro Lys Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala																
	65				70				75						80	
Arg Met Glu Ala Arg Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp																
				85				90						95		
Asn Thr Glu Glu Val Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp																
		100					105						110			
Val Glu Ser Ile Ala Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala																
	115					120						125				

Ile Val Asp Gly Val Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala  
 130 135 140  
 Thr Phe Ala Thr Pro Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp  
 145 150 155 160  
 Ile Val Leu Tyr Ser Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu  
 165 170 175  
 Leu Leu Gly Val Ala Val Cys Lys Ser Glu His His Ala Gln Phe Leu  
 180 185 190  
 Ala Thr His Arg His Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala  
 195 200 205  
 Phe Leu Ala Leu Arg Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg  
 210 215 220  
 Ala Glu Ser Asn Ala Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro  
 225 230 235 240  
 Ser Val Thr Arg Val Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His  
 245 250 255  
 Glu Lys Ala Val Arg Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser  
 260 265 270  
 Phe Glu Leu Asp Ala Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser  
 275 280 285  
 Leu Ser Leu Leu Thr His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala  
 290 295 300  
 Ile Glu Arg Arg Thr Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro  
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 Met Thr Leu Cys Arg Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu  
 325 330 335  
 Trp Glu Asp Leu Asn Ala Ser Ile Asp Lys Val Leu Gly  
 340 345

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<220>  
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 <223> RXS03159

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 Leu Ser Phe Asp Pro  
 1 5  
 aac acc cag ggt ttc tcc act gca tcg att cac gct ggg tat gag cca 163



Asn	Thr	Gln	Gly	Phe	Ser	Thr	Ala	Ser	Ile	His	Ala	Gly	Tyr	Glu	Pro	
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gac	gac	tac	tac	ggt	tcg	att	aac	acc	cca	atc	tat	gcc	tcc	acc	acc	211
Asp	Asp	Tyr	Tyr	Gly	Ser	Ile	Asn	Thr	Pro	Ile	Tyr	Ala	Ser	Thr	Thr	
			25					30					35			
ttc	gcg	cag	aac	gct	cca	aac	gaa	ctg	cgc	aaa	ggc	tac	gag	tac	acc	259
Phe	Ala	Gln	Asn	Ala	Pro	Asn	Glu	Leu	Arg	Lys	Gly	Tyr	Glu	Tyr	Thr	
		40					45					50				
cgt	gtg	ggc	aac	ccc	acc	atc	gtg	gca	tta	gag	cag	acc	gtc	gca	gca	307
Arg	Val	Gly	Asn	Pro	Thr	Ile	Val	Ala	Leu	Glu	Gln	Thr	Val	Ala	Ala	
	55					60					65					
ctc	gaa	ggc	gca	aag	tat	ggc	cgc	gca	ttc	tcc	tcc	ggc	atg	gct	gca	355
Leu	Glu	Gly	Ala	Lys	Tyr	Gly	Arg	Ala	Phe	Ser	Ser	Gly	Met	Ala	Ala	
70					75					80					85	
acc	gac	atc	ctg	ttc	cgc	atc	atc	ctc	aag	ccg	ggc	gat	cac	atc	gtc	403
Thr	Asp	Ile	Leu	Phe	Arg	Ile	Ile	Leu	Lys	Pro	Gly	Asp	His	Ile	Val	
				90					95					100		
ctc	ggc	aac	gat	gct	tac	ggc	gga	acc	tac	cgc	ctg	atc	gac	acc	gta	451
Leu	Gly	Asn	Asp	Ala	Tyr	Gly	Gly	Thr	Tyr	Arg	Leu	Ile	Asp	Thr	Val	
			105					110					115			
ttc	acc	gca	tgg	ggc	gtc	gaa	tac	acc	gtt	gtt	gat	acc	tcc	gtc	gtg	499
Phe	Thr	Ala	Trp	Gly	Val	Glu	Tyr	Thr	Val	Val	Asp	Thr	Ser	Val	Val	
		120					125					130				
gaa	gag	gtc	aag	gca	gcg	atc	aag	gac	aac	acc	aag	ctg	atc	tgg	gtg	547
Glu	Glu	Val	Lys	Ala	Ala	Ile	Lys	Asp	Asn	Thr	Lys	Leu	Ile	Trp	Val	
	135					140					145					
gaa	acc	cca	acc	aac	cca	gca	ctt	ggc	atc	acc	gac	atc	gaa	gca	gta	595
Glu	Thr	Pro	Thr	Asn	Pro	Ala	Leu	Gly	Ile	Thr	Asp	Ile	Glu	Ala	Val	
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gca	aag	ctc	acc	gaa	ggc	acc	aac	gcc	aag	ttg	gtt	gtt	gac	aac	acc	643
Ala	Lys	Leu	Thr	Glu	Gly	Thr	Asn	Ala	Lys	Leu	Val	Val	Asp	Asn	Thr	
				170				175						180		
ttg	gca	tcc	cca	tac	ctg	cag	cag	cca	cta	aaa	ctc	ggc	gca	cac	gca	691
Leu	Ala	Ser	Pro	Tyr	Leu	Gln	Gln	Pro	Leu	Lys	Leu	Gly	Ala	His	Ala	
			185					190					195			
agt	cct	tgc	act	cca	cca	cca	agt	aca	tcg	aag	gac	act	ccg	acg	ttg	739
Ser	Pro	Cys	Thr	Pro	Pro	Pro	Ser	Thr	Ser	Lys	Asp	Thr	Pro	Thr	Leu	
		200					205					210				
ttg	gcg	gcc	ttg	tgg	gta	cca	acg	acc	agg	aaa	tgg	acg	aag	aac	tgc	787
Leu	Ala	Ala	Leu	Trp	Val	Pro	Thr	Thr	Arg	Lys	Trp	Thr	Lys	Asn	Cys	
	215					220					225					
tgt	tca	tgc	agg	gcg	gca	tcg	gac	cga	tcc	cat	cag	ttt	tcg	atg	cat	835
Cys	Ser	Cys	Arg	Ala	Ala	Ser	Asp	Arg	Ser	His	Gln	Phe	Ser	Met	His	
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Thr																

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 198

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			20					25					30		
Tyr	Ala	Ser	Thr	Thr	Phe	Ala	Gln	Asn	Ala	Pro	Asn	Glu	Leu	Arg	Lys
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Gly	Tyr	Glu	Tyr	Thr	Arg	Val	Gly	Asn	Pro	Thr	Ile	Val	Ala	Leu	Glu
	50					55					60				
Gln	Thr	Val	Ala	Ala	Leu	Glu	Gly	Ala	Lys	Tyr	Gly	Arg	Ala	Phe	Ser
65					70					75					80
Ser	Gly	Met	Ala	Ala	Thr	Asp	Ile	Leu	Phe	Arg	Ile	Ile	Leu	Lys	Pro
				85					90					95	
Gly	Asp	His	Ile	Val	Leu	Gly	Asn	Asp	Ala	Tyr	Gly	Gly	Thr	Tyr	Arg
			100					105					110		
Leu	Ile	Asp	Thr	Val	Phe	Thr	Ala	Trp	Gly	Val	Glu	Tyr	Thr	Val	Val
		115					120					125			
Asp	Thr	Ser	Val	Val	Glu	Glu	Val	Lys	Ala	Ala	Ile	Lys	Asp	Asn	Thr
	130					135					140				
Lys	Leu	Ile	Trp	Val	Glu	Thr	Pro	Thr	Asn	Pro	Ala	Leu	Gly	Ile	Thr
145					150					155					160
Asp	Ile	Glu	Ala	Val	Ala	Lys	Leu	Thr	Glu	Gly	Thr	Asn	Ala	Lys	Leu
				165					170					175	
Val	Val	Asp	Asn	Thr	Leu	Ala	Ser	Pro	Tyr	Leu	Gln	Gln	Pro	Leu	Lys
			180					185					190		
Leu	Gly	Ala	His	Ala	Ser	Pro	Cys	Thr	Pro	Pro	Pro	Ser	Thr	Ser	Lys
		195					200					205			
Asp	Thr	Pro	Thr	Leu	Leu	Ala	Ala	Leu	Trp	Val	Pro	Thr	Thr	Arg	Lys
	210					215					220				
Trp	Thr	Lys	Asn	Cys	Cys	Ser	Cys	Arg	Ala	Ala	Ser	Asp	Arg	Ser	His
225					230					235					240
Gln	Phe	Ser	Met	His	Thr										
				245											

<210> 199  
 <211> 703  
 <212> DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(703)

&lt;223&gt; FRXA02768

&lt;400&gt; 199

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tttagggcca tagaattctg attacaggag ttgatctacc ttg tct ttt gac cca 115
                                   Leu Ser Phe Asp Pro
                                   1       5

aac acc cag ggt ttc tcc act gca tcg att cac gct ggg tat gag cca 163
Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
                        10                        15                        20

gac gac tac tac ggt tcg att aac acc cca atc tat gcc tcc acc acc 211
Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
                        25                        30                        35

ttc gcg cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc 259
Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
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cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca 307
Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala
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ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca 355
Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
70                        75                        80                        85

acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc 403
Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
                        90                        95                        100

ctc ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta 451
Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
                        105                        110                        115

ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg 499
Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
                        120                        125                        130

gaa gag gtc aag gca gcg atc aag gac aac acc aag gct gat ctt ggt 547
Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Ala Asp Leu Gly
135                        140                        145

gga aac ccc aac caa ccc agc act ttg gca tta ccc gac atc gaa gca 595
Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu Pro Asp Ile Glu Ala
150                        155                        160                        165

gtn tgc aaa act tca ccc gaa agg cac caa ccc caa gct tgt tgt ttg 643
Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro Gln Ala Cys Cys Leu
                        170                        175                        180

aca aca cct tcg cat tcc cca tac ctg cag can cca ctt aaa ant tnn 691
Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa Pro Leu Lys Xaa Xaa
                        185                        190                        195

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gng cac acg cag  
Xaa His Thr Gln  
200

703

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<212> PRT  
<213> Corynebacterium glutamicum

<400> 200

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Ala	Gly	Tyr	Glu	Pro	Asp	Asp	Tyr	Tyr	Gly	Ser	Ile	Asn	Thr	Pro	Ile
			20					25					30		
Tyr	Ala	Ser	Thr	Thr	Phe	Ala	Gln	Asn	Ala	Pro	Asn	Glu	Leu	Arg	Lys
		35					40					45			
Gly	Tyr	Glu	Tyr	Thr	Arg	Val	Gly	Asn	Pro	Thr	Ile	Val	Ala	Leu	Glu
	50					55					60				
Gln	Thr	Val	Ala	Ala	Leu	Glu	Gly	Ala	Lys	Tyr	Gly	Arg	Ala	Phe	Ser
65					70				75						80
Ser	Gly	Met	Ala	Ala	Thr	Asp	Ile	Leu	Phe	Arg	Ile	Ile	Leu	Lys	Pro
				85					90					95	
Gly	Asp	His	Ile	Val	Leu	Gly	Asn	Asp	Ala	Tyr	Gly	Gly	Thr	Tyr	Arg
			100				105						110		
Leu	Ile	Asp	Thr	Val	Phe	Thr	Ala	Trp	Gly	Val	Glu	Tyr	Thr	Val	Val
		115					120					125			
Asp	Thr	Ser	Val	Val	Glu	Glu	Val	Lys	Ala	Ala	Ile	Lys	Asp	Asn	Thr
	130					135					140				
Lys	Ala	Asp	Leu	Gly	Gly	Asn	Pro	Asn	Gln	Pro	Ser	Thr	Leu	Ala	Leu
145					150				155						160
Pro	Asp	Ile	Glu	Ala	Val	Cys	Lys	Thr	Ser	Pro	Glu	Arg	His	Gln	Pro
				165					170					175	
Gln	Ala	Cys	Cys	Leu	Thr	Thr	Pro	Ser	His	Ser	Pro	Tyr	Leu	Gln	Xaa
			180					185					190		
Pro	Leu	Lys	Xaa	Xaa	Xaa	His	Thr	Gln							
		195					200								

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<212> DNA  
<213> Corynebacterium glutamicum

<220>  
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<222> (101)..(1090)  
<223> RXA00216

&lt;400&gt; 201

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                                   Leu Gly Ala Tyr Gly
                                   1       5

tta ggt gag ctt cct gga aaa tcc gcc gcg gaa gcc gcc gac att att 163
Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu Ala Ala Asp Ile Ile
                                   10       15       20

cag ggt gaa acg ggc gat ctt ctc cat att cct cag ctt ccg gcg cga 211
Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg
                                   25       30       35

ggg ttg ggt gct gat ctg atc ggt cga acc gtc ggt ctg ctg gac atg 259
Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val Gly Leu Leu Asp Met
                                   40       45       50

atc aac gtt gat cgc ggg gcc cga tct tgg gtg atg agc aca cgc ccc 307
Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val Met Ser Thr Arg Pro
                                   55       60       65

agc aga ttg acg cac ctg acc ggc gat ttc ctt gac atg gat ttg gat 355
Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu Asp Met Asp Leu Asp
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gcg tgc gag gaa acc tgg gga acg ggc gtc gac aag cta aaa atc caa 403
Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp Lys Leu Lys Ile Gln
                                   90       95       100

gtt gct ggt ccc tgg act tta ggt gcg cgc att gag ttg gcc aat ggc 451
Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile Glu Leu Ala Asn Gly
                                   105       110       115

cat cgc gtt ttg tct gat cgc ggt gcg atg cgt gat ctc acg cag gcg 499
His Arg Val Leu Ser Asp Arg Gly Ala Met Arg Asp Leu Thr Gln Ala
                                   120       125       130

ctg atc gcc ggc atc gat gcg cat gca cgc aag gtt gct ggg cga ttt 547
Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys Val Ala Gly Arg Phe
                                   135       140       145

cgc gcc gaa gtg cag gtg caa att gat gag ccg gag ctg aaa tcg ctt 595
Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro Glu Leu Lys Ser Leu
                                   150       155       160       165

atc gac ggc tcc ctc cct ggc act tcc acc ttt gac att att cct gcg 643
Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe Asp Ile Ile Pro Ala
                                   170       175       180

gtg aat gtc gct gat gcc agt gaa cgt ttg cag cag gtc ttt agc tcg 691
Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln Gln Val Phe Ser Ser
                                   185       190       195

att gag ggg ccg aca tat ctc aac ctc acc ggc cag att cct act tgg 739
Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly Gln Ile Pro Thr Trp
                                   200       205       210

gat gtg gct cgg ggt gcg ggc gcc gat act gtg cag att tcc atg gat 787

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Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val Gln Ile Ser Met Asp  
 215 220 225  
 caa gtc cgt gga aat gaa cat ttg gat ggt ttt ggt gaa acc atc acc 835  
 Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe Gly Glu Thr Ile Thr  
 230 235 240 245  
 agt gga att cgt ctt ggt ttg ggc att acg aca gga aaa gat gtc gta 883  
 Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr Gly Lys Asp Val Val  
 250 255 260  
 gat gaa ctg ctc gag cga ccg cgg caa aag gcc gtt gag gta gca cgc 931  
 Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala Val Glu Val Ala Arg  
 265 270 275  
 ttt ttt gat cgt tta ggt gtg ggc cga aac tat ctc gtg gat gct gtt 979  
 Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val  
 280 285 290  
 gat att cat ccg ggt gag gat ttg gtg cag ggg acc atc acc gag gcc  
 1027  
 Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly Thr Ile Thr Glu Ala  
 295 300 305  
 gcg cag gct tat cgc atg gcc cgg gtg atg tcg gag atg ttg tcg aag  
 1075  
 Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys  
 310 315 320 325  
 gat tca tgc gac ctt taaggcttta ccggcgctgg gtg  
 1113  
 Asp Ser Cys Asp Leu  
 330

<210> 202  
 <211> 330  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 202  
 Leu Gly Ala Tyr Gly Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu  
 1 5 10 15  
 Ala Ala Asp Ile Ile Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro  
 20 25 30  
 Gln Leu Pro Ala Arg Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val  
 35 40 45  
 Gly Leu Leu Asp Met Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val  
 50 55 60  
 Met Ser Thr Arg Pro Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu  
 65 70 75 80  
 Asp Met Asp Leu Asp Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp  
 85 90 95  
 Lys Leu Lys Ile Gln Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile  
 100 105 110

Glu Leu Ala Asn Gly His Arg Val Leu Ser Asp Arg Gly Ala Met Arg  
 115 120 125  
 Asp Leu Thr Gln Ala Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys  
 130 135 140  
 Val Ala Gly Arg Phe Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro  
 145 150 155 160  
 Glu Leu Lys Ser Leu Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe  
 165 170 175  
 Asp Ile Ile Pro Ala Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln  
 180 185 190  
 Gln Val Phe Ser Ser Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly  
 195 200 205  
 Gln Ile Pro Thr Trp Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val  
 210 215 220  
 Gln Ile Ser Met Asp Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe  
 225 230 235 240  
 Gly Glu Thr Ile Thr Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr  
 245 250 255  
 Gly Lys Asp Val Val Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala  
 260 265 270  
 Val Glu Val Ala Arg Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr  
 275 280 285  
 Leu Val Asp Ala Val Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly  
 290 295 300  
 Thr Ile Thr Glu Ala Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser  
 305 310 315 320  
 Glu Met Leu Ser Lys Asp Ser Cys Asp Leu  
 325 330

<210> 203  
 <211> 623  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(600)  
 <223> RXN00402

<400> 203  
 act gac gaa aag gat gga aag cca gta ttg ccc tac ttc gtc act cca 48  
 Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro  
 1 5 10 15  
 gat gct gct tac cac gga ttg aag tac gca gac ctt ggt gca cca gcc 96  
 Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala

20										25					30					
ttc	ggc	ctc	aag	gtt	cgc	gtt	ggc	ctt	cta	cgc	gac	acc	ggc	tcc	acc	144				
Phe	Gly	Leu	Lys	Val	Arg	Val	Gly	Leu	Leu	Arg	Asp	Thr	Gly	Ser	Thr					
35			40			45														
ctc	tcc	gca	ttc	aac	gca	tgg	gct	gca	gtc	cag	ggc	atc	gac	acc	ctt	192				
Leu	Ser	Ala	Phe	Asn	Ala	Trp	Ala	Ala	Val	Gln	Gly	Ile	Asp	Thr	Leu					
50			55			60														
tcc	ctg	cgc	ctg	gag	cgc	cac	aac	gaa	aac	gcc	atc	aag	gtt	gca	gaa	240				
Ser	Leu	Arg	Leu	Glu	Arg	His	Asn	Glu	Asn	Ala	Ile	Lys	Val	Ala	Glu					
65			70			75			80											
ttc	ctc	aac	aac	cac	gag	aag	gtg	gaa	aag	gtt	aac	ttc	gca	ggc	ctg	288				
Phe	Leu	Asn	Asn	His	Glu	Lys	Val	Glu	Lys	Val	Asn	Phe	Ala	Gly	Leu					
85			90			95														
aag	gat	tcc	cct	tgg	tac	gca	acc	aag	gaa	aag	ctt	ggc	ctg	aag	tac	336				
Lys	Asp	Ser	Pro	Trp	Tyr	Ala	Thr	Lys	Glu	Lys	Leu	Gly	Leu	Lys	Tyr					
100			105			110														
acc	ggc	tcc	gtt	ctc	acc	ttc	gag	atc	aag	ggc	ggc	aag	gat	gag	gct	384				
Thr	Gly	Ser	Val	Leu	Thr	Phe	Glu	Ile	Lys	Gly	Gly	Lys	Asp	Glu	Ala					
115			120			125														
tgg	gca	ttt	atc	gac	gcc	ctg	aag	cta	cac	tcc	aac	ctt	gca	aac	atc	432				
Trp	Ala	Phe	Ile	Asp	Ala	Leu	Lys	Leu	His	Ser	Asn	Leu	Ala	Asn	Ile					
130			135			140														
ggc	gat	gtt	cgc	tcc	ctc	gtt	gtt	cac	cca	gca	acc	acc	acc	cat	tca	480				
Gly	Asp	Val	Arg	Ser	Leu	Val	Val	His	Pro	Ala	Thr	Thr	Thr	His	Ser					
145			150			155			160											
cag	tcc	gac	gaa	gct	ggc	ctg	gca	cgc	gcg	ggc	gtt	acc	cag	tcc	acc	528				
Gln	Ser	Asp	Glu	Ala	Gly	Leu	Ala	Arg	Ala	Gly	Val	Thr	Gln	Ser	Thr					
165			170			175														
gtc	cgc	ctg	tcc	gtt	ggc	atc	gag	acc	att	gat	gat	atc	atc	gct	gac	576				
Val	Arg	Leu	Ser	Val	Gly	Ile	Glu	Thr	Ile	Asp	Asp	Ile	Ile	Ala	Asp					
180			185			190														
ctc	gaa	ggc	ggc	ttt	gct	gca	atc	tagcttttaa	tagactcacc	cca						623				
Leu	Glu	Gly	Gly	Phe	Ala	Ala	Ile													
195			200																	

&lt;210&gt; 204

&lt;211&gt; 200

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 204

Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro  
 1 5 10 15

Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala  
 20 25 30

Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr  
 35 40 45



Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu  
 50 55 60  
 Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu  
 65 70 75 80  
 Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu  
 85 90 95  
 Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr  
 100 105 110  
 Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala  
 115 120 125  
 Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile  
 130 135 140  
 Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser  
 145 150 155 160  
 Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr  
 165 170 175  
 Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp  
 180 185 190  
 Leu Glu Gly Gly Phe Ala Ala Ile  
 195 200

&lt;210&gt; 205

&lt;211&gt; 599

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(576)

&lt;223&gt; FRXA00402

&lt;400&gt; 205

gta ttg ccc tac ttc gtc act cca gat gct gct tac cac gga ttg aag 48  
 Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys  
 1 5 10 15  
 tac gca gac ctt ggt gca cca gcc ttc ggc ctc aag gtt cgc gtt ggc 96  
 Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly  
 20 25 30  
 ctt cta cgc gac acc ggc tcc acc ctc tcc gca ttc aac gca tgg gct 144  
 Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala  
 35 40 45  
 gca gtc cag ggc atc gac acc ctt tcc ctg cgc ctg gag cgc cac aac 192  
 Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn  
 50 55 60  
 gaa aac gcc atc aag gtt gca gaa ttc ctc aac aac cac gag aag gtg 240  
 Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val

65	70	75	80	
gaa aag gtt aac ttc gca ggc ctg aag gat tcc cct tgg tac gca acc				288
Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr	85	90	95	
aag gaa aag ctt ggc ctg aag tac acc ggc tcc gtt ctc acc ttc gag				336
Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu	100	105	110	
atc aag ggc ggc aag gat gag gct tgg gca ttt atc gac gcc ctg aag				384
Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys	115	120	125	
cta cac tcc aac ctt gca aac atc ggc gat gtt cgc tcc ctc gtt gtt				432
Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val	130	135	140	
cac cca gca acc acc acc cat tca cag tcc gac gaa gct ggc ctg gca				480
His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala	145	150	155	160
cgc gcg ggc gtt acc cag tcc acc gtc cgc ctg tcc gtt ggc atc gag				528
Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu	165	170	175	
acc att gat gat atc atc gct gac ctc gaa ggc ggc ttt gct gca atc				576
Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile	180	185	190	
tagctttaaa tagactcacc cca				599

&lt;210&gt; 206

&lt;211&gt; 192

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 206

Val	Leu	Pro	Tyr	Phe	Val	Thr	Pro	Asp	Ala	Ala	Tyr	His	Gly	Leu	Lys
1				5					10					15	

Tyr	Ala	Asp	Leu	Gly	Ala	Pro	Ala	Phe	Gly	Leu	Lys	Val	Arg	Val	Gly
			20					25					30		

Leu	Leu	Arg	Asp	Thr	Gly	Ser	Thr	Leu	Ser	Ala	Phe	Asn	Ala	Trp	Ala
		35					40					45			

Ala	Val	Gln	Gly	Ile	Asp	Thr	Leu	Ser	Leu	Arg	Leu	Glu	Arg	His	Asn
	50					55					60				

Glu	Asn	Ala	Ile	Lys	Val	Ala	Glu	Phe	Leu	Asn	Asn	His	Glu	Lys	Val
65					70					75				80	

Glu	Lys	Val	Asn	Phe	Ala	Gly	Leu	Lys	Asp	Ser	Pro	Trp	Tyr	Ala	Thr
				85					90					95	

Lys	Glu	Lys	Leu	Gly	Leu	Lys	Tyr	Thr	Gly	Ser	Val	Leu	Thr	Phe	Glu
			100				105						110		

Ile	Lys	Gly	Gly	Lys	Asp	Glu	Ala	Trp	Ala	Phe	Ile	Asp	Ala	Leu	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115	120	125
Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val		
130	135	140
His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala		
145	150	155
Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu		
	165	170
Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile		
	180	185
		190

<210> 207  
 <211> 613  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(613)  
 <223> RXA00405

<400> 207  
 agaataaatt tataccacac agtctattgc aatagaccaa gctgttcagt aggggtgcatg 60

ggagaagaat ttcctaataa aaactcttaa ggacctccaa atg cca aag tac gac 115  
 Met Pro Lys Tyr Asp  
 1 5

aat tcc aat gct gac cag tgg ggc ttt gaa acc cgc tcc att cac gca 163  
 Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr Arg Ser Ile His Ala  
 10 15 20

ggc cag tca gta gac gca cag acc agc gca cga aac ctt ccg atc tac 211  
 Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr  
 25 30 35

caa tcc acc gct ttc gtg ttc gac tcc gct gag cac gcc aag cag cgt 259  
 Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu His Ala Lys Gln Arg  
 40 45 50

ttc gca ctt gag gat cta ggc cct gtt tac tcc cgc ctc acc aac cca 307  
 Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro  
 55 60 65

acc gtt gag gct ttg gaa aac cgc atc gct tcc ctc gaa ggt ggc gtc 355  
 Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser Leu Glu Gly Gly Val  
 70 75 80 85

cac gct gta gcg ttc tcc tcc gga cag gcc gca acc acc aac gcc att 403  
 His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile  
 90 95 100

ttg aac ctg gca gga gcg ggc gac cac atc gtc acc tcc cca cgc ctc 451  
 Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val Thr Ser Pro Arg Leu

	105	110	115	
tac ggt ggc acc gag act cta ttc ctt atc act ctt aac cgc ctg ggt				499
Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly				
	120	125	130	
atc gat gtt tcc ttc gtg gaa aac ccc gac gac cct gag tcc tgg cag				547
Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln				
	135	140	145	
gca gcc gtt cag cca aac acc aaa gca ttc ttc ggc gag act ttc gcc				595
Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala				
	150	155	160	165
aac cca cag gca gac gtc				613
Asn Pro Gln Ala Asp Val				
	170			

<210> 208  
 <211> 171  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 208  
 Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr  
 1 5 10 15  
 Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg  
 20 25 30  
 Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu  
 35 40 45  
 His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser  
 50 55 60  
 Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser  
 65 70 75 80  
 Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala  
 85 90 95  
 Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val  
 100 105 110  
 Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr  
 115 120 125  
 Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp  
 130 135 140  
 Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe  
 145 150 155 160  
 Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val  
 165 170

<210> 209  
 <211> 551

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(528)

&lt;223&gt; RXA02197

&lt;400&gt; 209

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gcc gaa cgc atg cgc ttt agc ttc cca cgc cag cag cgc ggc agg ttc      48
Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe
  1                      5                      10                      15

ttg tgc atc gcg gat ttc att cgc cca cgc gag caa gct gtc aag gac      96
Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
                20                      25                      30

ggc caa gtg gac gtc atg cca ttc cag ctg gtc acc atg ggt aat cct      144
Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
                35                      40                      45

att gct gat ttc gcc aac gag ttg ttc gca gcc aat gaa tac cgc gag      192
Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
                50                      55                      60

tac ttg gaa gtt cac ggc atc ggc gtg cag ctc acc gaa gca ttg gcc      240
Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
        65                      70                      75                      80

gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt      288
Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
                85                      90                      95

gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac      336
Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
                100                      105                      110

ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct      384
Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
                115                      120                      125

gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt      432
Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
        130                      135                      140

atc ggc gtg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc      480
Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
        145                      150                      155                      160

aca gac gcg ttt gtg ctc tac cac cca gag gca aag tac ttt aac gtc      528
Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
                165                      170                      175

taacaccttt gagagggaaa act                                          551

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&lt;210&gt; 210

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 210

Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe  
 1 5 10 15

Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp  
 20 25 30

Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro  
 35 40 45

Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu  
 50 55 60

Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala  
 65 70 75 80

Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly  
 85 90 95

Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp  
 100 105 110

Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro  
 115 120 125

Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg  
 130 135 140

Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser  
 145 150 155 160

Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val  
 165 170 175

&lt;210&gt; 211

&lt;211&gt; 2599

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2599)

&lt;223&gt; RXN02198

&lt;400&gt; 211

agactagtgg cgctttgcct gtgttgctta ggcggcggttg aaaatgaact acgaatgaaa 60

agttcgggaa ttgtctaatac cgtactaagc tgtctacaca atg tct act tca .gtt 115  
 Met Ser Thr Ser Val  
 1 5

act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163  
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala  
 10 15 20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211  
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu

25	30	35	
caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly 40 45 50			259
tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile 55 60 65			307
cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr 70 75 80 85			355
ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg 90 95 100			403
tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala 105 110 115			451
gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly 120 125 130			499
tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr 135 140 145			547
gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp 150 155 160 165			595
ggg ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln 170 175 180			643
gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp 185 190 195			691
aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr 200 205 210			739
atg ctc atg ggt tct gag atc ggt gcc gcg ttg aca gcg ctg cag cca Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro 215 220 225			787
ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu 230 235 240 245			835
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val 250 255 260			883
tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala 265 270 275			931

gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc 979  
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 295 300 305

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 Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu  
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1603  
Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln  
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1651  
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600 605 610

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2131

Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile  
665 670 675

gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag  
2179

Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys  
680 685 690

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2227

Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met  
695 700 705

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2275

Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe  
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2323

Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu  
730 735 740

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2371

Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu  
745 750 755

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2419

Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp  
760 765 770

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2467

Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp  
775 780 785

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2515

Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala  
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2563

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Leu	Asp	Leu	Glu	Gly	Cys	Asn	Glu	Ile	Leu	Asn	Asp	Thr	Arg	Pro	Asp
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Val	Leu	Arg	Gln	Ile	His	Arg	Ala	Tyr	Phe	Glu	Ala	Gly	Ala	Asp	Leu
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Val	Glu	Thr	Asn	Thr	Phe	Gly	Cys	Asn	Leu	Pro	Asn	Leu	Ala	Asp	Tyr
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Asp	Ile	Ala	Asp	Arg	Cys	Arg	Glu	Leu	Ala	Tyr	Lys	Gly	Thr	Ala	Val
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Ala	Arg	Glu	Val	Ala	Asp	Glu	Met	Gly	Pro	Gly	Arg	Asn	Gly	Met	Arg
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Arg	Phe	Val	Val	Gly	Ser	Leu	Gly	Pro	Gly	Thr	Lys	Leu	Pro	Ser	Leu
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Gly	His	Ala	Pro	Tyr	Ala	Asp	Leu	Arg	Gly	His	Tyr	Lys	Glu	Ala	Ala
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Leu	Gly	Ile	Ile	Asp	Gly	Gly	Gly	Asp	Ala	Phe	Leu	Ile	Glu	Thr	Ala
				165					170					175	
Gln	Asp	Leu	Leu	Gln	Val	Lys	Ala	Ala	Val	His	Gly	Val	Gln	Asp	Ala
			180					185					190		
Met	Ala	Glu	Leu	Asp	Thr	Phe	Leu	Pro	Ile	Ile	Cys	His	Val	Thr	Val
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Glu	Thr	Thr	Gly	Thr	Met	Leu	Met	Gly	Ser	Glu	Ile	Gly	Ala	Ala	Leu
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Thr	Ala	Leu	Gln	Pro	Leu	Gly	Ile	Asp	Met	Ile	Gly	Leu	Asn	Cys	Ala
225					230					235					240
Thr	Gly	Pro	Asp	Glu	Met	Ser	Glu	His	Leu	Arg	Tyr	Leu	Ser	Lys	His
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Ala	Asp	Ile	Pro	Val	Ser	Val	Met	Pro	Asn	Ala	Gly	Leu	Pro	Val	Leu
			260					265					270		
Gly	Lys	Asn	Gly	Ala	Glu	Tyr	Pro	Leu	Glu	Ala	Glu	Asp	Leu	Ala	Gln
		275					280					285			
Ala	Leu	Ala	Gly	Phe	Val	Ser	Glu	Tyr	Gly	Leu	Ser	Met	Val	Gly	Gly
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Cys	Cys	Gly	Thr	Thr	Pro	Glu	His	Ile	Arg	Ala	Val	Arg	Asp	Ala	Val
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Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala  
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 Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val  
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 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile  
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 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile  
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 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala  
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 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys  
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 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu  
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 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu  
 545 550 555 560  
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile  
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 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe  
 580 585 590  
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser  
 595 600 605  
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val  
 610 615 620  
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu  
 625 630 635 640  
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys

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		675					680					685			
Glu	Ala	Gly	Met	Lys	Glu	Lys	Ser	Pro	Ile	Ala	Ile	Ile	Asn	Glu	Asp
	690					695					700				
Leu	Leu	Asn	Gly	Met	Lys	Thr	Val	Gly	Glu	Leu	Phe	Gly	Ser	Gly	Gln
705				710					715						720
Met	Gln	Leu	Pro	Phe	Val	Leu	Gln	Ser	Ala	Glu	Thr	Met	Lys	Thr	Ala
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Val	Ala	Tyr	Leu	Glu	Pro	Phe	Met	Glu	Glu	Glu	Ala	Glu	Ala	Thr	Gly
			740					745					750		
Ser	Ala	Gln	Ala	Glu	Gly	Lys	Gly	Lys	Ile	Val	Val	Ala	Thr	Val	Lys
	755					760						765			
Gly	Asp	Val	His	Asp	Ile	Gly	Lys	Asn	Leu	Val	Asp	Ile	Ile	Leu	Ser
	770					775					780				
Asn	Asn	Gly	Tyr	Asp	Val	Val	Asn	Leu	Gly	Ile	Lys	Gln	Pro	Leu	Ser
785				790					795						800
Ala	Met	Leu	Glu	Ala	Ala	Glu	Glu	His	Lys	Ala	Asp	Val	Ile	Gly	Met
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Asp

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 Met Ser Thr Ser Val  
 1 5  
 act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163  
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala  
 10 15 20  
 ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211

Leu	Ala	Asn	His	Val	Leu	Ile	Gly	Asp	Gly	Ala	Met	Gly	Thr	Gln	Leu		
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caa	ggc	ttt	gac	ctg	gac	gtg	gaa	aag	gat	ttc	ctt	gat	ctg	gag	ggg	259	
Gln	Gly	Phe	Asp	Leu	Asp	Val	Glu	Lys	Asp	Phe	Leu	Asp	Leu	Glu	Gly		
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tgt	aat	gag	att	ctc	aac	gac	acc	cgc	cct	gat	gtg	ttg	agg	cag	att	307	
Cys	Asn	Glu	Ile	Leu	Asn	Asp	Thr	Arg	Pro	Asp	Val	Leu	Arg	Gln	Ile		
	55				60						65						
cac	cgc	gcc	tac	ttt	gag	gcg	gga	gct	gac	ttg	gtt	gag	acc	aat	act	355	
His	Arg	Ala	Tyr	Phe	Glu	Ala	Gly	Ala	Asp	Leu	Val	Glu	Thr	Asn	Thr		
	70				75					80					85		
ttt	ggc	tgc	aac	ctg	ccg	aac	ttg	gcg	gat	tat	gac	atc	gct	gat	cgt	403	
Phe	Gly	Cys	Asn	Leu	Pro	Asn	Leu	Ala	Asp	Tyr	Asp	Ile	Ala	Asp	Arg		
				90					95					100			
tgc	cgt	gag	ctt	gcc	tac	aag	ggc	act	gca	gtg	gct	agg	gaa	gtg	gct	451	
Cys	Arg	Glu	Leu	Ala	Tyr	Lys	Gly	Thr	Ala	Val	Ala	Arg	Glu	Val	Ala		
			105					110					115				
gat	gag	atg	ggg	ccg	ggc	cga	aac	ggc	atg	cgg	cgt	ttc	gtg	gtt	ggc	499	
Asp	Glu	Met	Gly	Pro	Gly	Arg	Asn	Gly	Met	Arg	Arg	Phe	Val	Val	Gly		
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tcc	ctg	gga	cct	gga	acg	aag	ctt	cca	tcg	ctg	ggc	cat	gca	ccg	tat	547	
Ser	Leu	Gly	Pro	Gly	Thr	Lys	Leu	Pro	Ser	Leu	Gly	His	Ala	Pro	Tyr		
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Ala	Asp	Leu	Arg	Gly	His	Tyr	Lys	Glu	Ala	Ala	Leu	Gly	Ile	Ile	Asp		
	150				155				160						165		
ggc	ggc	gat	gcc	ttt	ttg	att	gag	act	gct	cag	gac	ttg	ctt	cag		643	
Gly	Gly	Gly	Asp	Ala	Phe	Leu	Ile	Glu	Thr	Ala	Gln	Asp	Leu	Leu	Gln		
			170					175					180				
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Val	Lys	Ala	Ala	Val	His	Gly	Val	Gln	Asp	Ala	Met	Ala	Glu	Leu	Asp		
			185				190						195				
aca	ttc	ttg	ccc	att	att	tgc	cac	gtc	acc	gta	gag	acc	acc	ggc	acc	739	
Thr	Phe	Leu	Pro	Ile	Ile	Cys	His	Val	Thr	Val	Glu	Thr	Thr	Gly	Thr		
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Met	Ser	Glu	His	Leu	Arg	Tyr	Leu	Ser	Lys	His	Ala	Asp	Ile	Pro	Val		
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Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe			
280	285	290	
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1027			
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr			
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1075			
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu			
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cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag			
1123			
Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln			
	330	335	340
gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc			
1171			
Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr			
	345	350	355
tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc			
1219			
Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg			
	360	365	370
acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc			
1267			
Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly			
	375	380	385
gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt			
1315			
Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly			
390	395	400	405
gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc			
1363			
Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr			
	410	415	420
gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg			
1411			
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	425	430	435
cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt			
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Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu			
	440	445	450
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1507			
Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp			
	455	460	465

ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag  
1555

Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys  
470 475 480 485

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1603

Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln  
490 495 500

gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac  
1651

Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp  
505 510 515

gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac  
1699

Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp  
520 525 530

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1747

Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp  
535 540 545

ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca  
1795

Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro  
550 555 560 565

gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac  
1843

Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn  
570 575 580

cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att  
1891

Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile  
585 590 595

gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg  
1939

Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro  
600 605 610

atg aac cgc att gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc  
1987

Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val  
615 620 625

tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag  
2035

Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln  
630 635 640 645

ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa  
2083

Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu  
650 655 660



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 Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile  
                   665                                  670                                  675

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 Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys  
                   680                                  685                                  690

gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg  
 2227  
 Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met  
                   695                                  700                                  705

aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc  
 2275  
 Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe  
                   710                                  715                                  720                                  725

gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa  
 2323  
 Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu  
                   730                                  735                                  740

ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag  
 2371  
 Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu  
                   745                                  750                                  755

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat  
 2419  
 Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp  
                   760                                  765                                  770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac  
 2467  
 Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp  
                   775                                  780                                  785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca  
 2515  
 Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala  
                   790                                  795                                  800                                  805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg  
 2563  
 Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val  
                   810                                  815                                  820

aag tcc acc gtg gtg  
 2578  
 Lys Ser Thr Val Val  
                   825

<210> 214

<211> 826

<212> PRT

<213> Corynebacterium glutamicum

<400> 214  
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 Glu Phe Leu Asp Ala Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala  
 20 25 30  
 Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe  
 35 40 45  
 Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp  
 50 55 60  
 Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu  
 65 70 75 80  
 Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr  
 85 90 95  
 Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val  
 100 105 110  
 Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg  
 115 120 125  
 Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu  
 130 135 140  
 Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala  
 145 150 155 160  
 Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala  
 165 170 175  
 Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala  
 180 185 190  
 Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val  
 195 200 205  
 Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu  
 210 215 220  
 Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala  
 225 230 235 240  
 Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His  
 245 250 255  
 Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu  
 260 265 270  
 Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln  
 275 280 285  
 Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly  
 290 295 300  
 Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val  
 305 310 315 320

Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala  
 325 330 335  
 Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val  
 340 345 350  
 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser  
 355 360 365  
 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu  
 370 375 380  
 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln  
 385 390 395 400  
 Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val  
 405 410 415  
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala  
 420 425 430  
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val  
 435 440 445  
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser  
 450 455 460  
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile  
 465 470 475 480  
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile  
 485 490 495  
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala  
 500 505 510  
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys  
 515 520 525  
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu  
 530 535 540  
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu  
 545 550 555 560  
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile  
 565 570 575  
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe  
 580 585 590  
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser  
 595 600 605  
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val  
 610 615 620  
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu  
 625 630 635 640  
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys

	645	650	655
Asp	Ala Arg	Ala Glu Gln Leu	Ala Ala Met Pro Leu Phe Glu Arg Leu
	660	665	670
Ala	Gln Arg	Ile Ile Asp Gly	Asp Lys Asn Gly Leu Glu Asp Asp Leu
	675	680	685
Glu	Ala Gly Met	Lys Glu Lys Ser Pro	Ile Ala Ile Ile Asn Glu Asp
	690	695	700
Leu	Leu Asn Gly	Met Lys Thr Val	Gly Glu Leu Phe Gly Ser Gly Gln
	705	710	715
Met	Gln Leu Pro	Phe Val Leu Gln	Ser Ala Glu Thr Met Lys Thr Ala
	725	730	735
Val	Ala Tyr Leu	Glu Pro Phe Met	Glu Glu Glu Ala Glu Ala Thr Gly
	740	745	750
Ser	Ala Gln Ala	Glu Gly Lys Gly	Lys Ile Val Val Ala Thr Val Lys
	755	760	765
Gly	Asp Val His	Asp Ile Gly Lys	Asn Leu Val Asp Ile Ile Leu Ser
	770	775	780
Asn	Asn Gly Tyr	Asp Val Val Asn	Leu Gly Ile Lys Gln Pro Leu Ser
	785	790	795
Ala	Met Leu Glu	Ala Ala Glu Glu	His Lys Ala Asp Val Ile Gly Met
	805	810	815
Ser	Gly Leu Leu	Val Lys Ser Thr	Val Val
	820	825	

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(598)  
 <223> RXN03074

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 tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115  
 Met Thr Gln Ser Ala  
 1 5  
 cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163  
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
 10 15 20  
 gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211  
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259  
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
           40                          45                          50  
  
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307  
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
           55                          60                          65  
  
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355  
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala  
           70                          75                          80                          85  
  
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403  
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
                           90                          95                          100  
  
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
                           105                          110                          115  
  
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499  
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
           120                          125                          130  
  
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547  
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
           135                          140                          145  
  
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
           150                          155                          160                          165  
  
 cag taatttggtt tgacgacgca gta 621  
 Gln

&lt;210&gt; 216

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 216

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp  
   1                          5                          10                          15  
  
 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu  
           20                          25                          30  
  
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
           35                          40                          45  
  
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
           50                          55                          60  
  
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
           65                          70                          75                          80  
  
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
           85                          90                          95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr  
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr  
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe  
 130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr  
 145 150 155 160

Glu Ala Pro Ile Lys Gln  
 165

<210> 217  
 <211> 621  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(598)  
 <223> FRXA02906

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 Met Thr Gln Ser Ala  
 1 5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163  
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
 10 15 20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211  
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259  
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
 40 45 50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307  
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
 55 60 65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355  
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala  
 70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403  
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
 90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
 105 110 115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499  
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
           120                          125                          130  
  
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547  
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
           135                          140                          145  
  
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
           150                          155                          160                          165  
  
 cag taatttggtt tgacgacgca gta 621  
 Gln

<210> 218  
 <211> 166  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 218  
 Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp  
       1                          5                          10                          15  
  
 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu  
           20                          25                          30  
  
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
           35                          40                          45  
  
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
       50                          55                          60  
  
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
       65                          70                          75                          80  
  
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
           85                          90                          95  
  
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr  
           100                          105                          110  
  
 Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr  
           115                          120                          125  
  
 Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe  
       130                          135                          140  
  
 Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr  
       145                          150                          155                          160  
  
 Glu Ala Pro Ile Lys Gln  
                           165

<210> 219  
 <211> 1557  
 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1534)

&lt;223&gt; RXN00132

&lt;400&gt; 219

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tttcctaatt ttcattttct taaaaggagc tgcgccaggac atg gca cag gtt atg 115
                                         Met Ala Gln Val Met
                                         1                               5

gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag 163
Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln
                        10                               15                               20

att cgt ctt gca gag tat gag atg cca ggt ctc atg cag ttg cgc aag 211
Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu Met Gln Leu Arg Lys
                        25                               30                               35

gaa ttc gca gac gag cag cct ttg aag ggc gcc cga att gct ggt tct 259
Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala Arg Ile Ala Gly Ser
                        40                               45                               50

atc cac atg acg gtc cag acc gcc gtg ctt att gag acc ctc act gct 307
Ile His Met Thr Val Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala
                        55                               60                               65

ttg ggc gct gag gtt cgt tgg gct tcc tgc aac att ttc tcc acc cag 355
Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn Ile Phe Ser Thr Gln
70                               75                               80                               85

gat gag gct gca gcg gct atc gtt gtc ggc tcc ggc acc gtc gaa gag 403
Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser Gly Thr Val Glu Glu
                        90                               95                               100

cca gct ggt gtt cca gta ttc gcg tgg aag ggt gag tca ctg gag gag 451
Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly Glu Ser Leu Glu Glu
                        105                               110                               115

tac tgg tgg tgc atc aac cag atc ttc agc tgg ggc gat gag ctg cca 499
Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp Gly Asp Glu Leu Pro
120                               125                               130

aac atg atc ctc gac gac ggc ggt gac gcc acc atg gct gtt att cgc 547
Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg
135                               140                               145

ggt cgc gaa tac gag cag gct ggt ctg gtt cca cca gca gag gcc aac 595
Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro Pro Ala Glu Ala Asn
150                               155                               160                               165

gat tcc gat gag tac atc gca ttc ttg ggc atg ctg cgt gag gtt ctt 643
Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met Leu Arg Glu Val Leu
170                               175                               180

gct gca gag cct ggc aag tgg ggc aag atc gct gag gcc gtt aag ggt 691
Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala Glu Ala Val Lys Gly
185                               190                               195

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gtc acc gag gaa acc acc acc ggt gtg cac cgc ctg tac cac ttc gct 739  
 Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala  
 200 205 210

gaa gaa ggc gtg ctg cct ttc cca gcg atg aac gtc aac gac gct gtc 787  
 Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val  
 215 220 225

acc aag tcc aag ttt gat aac aag tac ggc acc cgc cac tcc ctg atc 835  
 Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile  
 230 235 240 245

gac ggc atc aac cgc gcc act gac atg ctc atg ggc ggc aag aac gtg 883  
 Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val  
 250 255 260

ctt gtc tgc ggt tac ggc gat gtc ggc aag ggc tgc gct gag gct ttc 931  
 Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe  
 265 270 275

gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac 979  
 Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn  
 280 285 290

gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag  
 1027  
 Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu  
 295 300 305

gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac  
 1075  
 Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp  
 310 315 320 325

atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg  
 1123  
 Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu  
 330 335 340

ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg  
 1171  
 Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu  
 345 350 355

cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag  
 1219  
 His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu  
 360 365 370

ttc acc ttc tcc acc ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc  
 1267  
 Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg  
 375 380 385

ctg ttg aac ctt ggc aac gcc acc gga cac cca tca ttt gtc atg tcc  
 1315  
 Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser  
 390 395 400 405

aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac  
 1363

Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn  
 410 415 420

gaa gga cag tac gag aac gag gtc tac cgt ctg cct aag gtt ctc gac  
 1411

Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu Pro Lys Val Leu Asp  
 425 430 435

gaa aag gtg gca cgc atc cac gtt gag gct ctc ggc ggt cag ctc acc  
 1459

Glu Lys Val Ala Arg Ile His Val Glu Ala Leu Gly Gly Gln Leu Thr  
 440 445 450

gaa ctg acc aag gag cag gct gag tac atc ggc gtt gac gtt gca ggc  
 1507

Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly Val Asp Val Ala Gly  
 455 460 465

cca ttc aag ccg gag cac tac cgc tac taatgattgt cagcattgag  
 1554

Pro Phe Lys Pro Glu His Tyr Arg Tyr  
 470 475

gga  
 1557

<210> 220

<211> 478

<212> PRT

<213> Corynebacterium glutamicum

<400> 220

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 20 25 30

Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala  
 35 40 45

Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile  
 50 55 60

Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn  
 65 70 75 80

Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser  
 85 90 95

Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly  
 100 105 110

Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp  
 115 120 125

Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr  
 130 135 140

Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro

145	150	155	160
Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met	165	170	175
Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala	180	185	190
Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg	195	200	205
Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn	210	215	220
Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr	225	230	235
Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met	245	250	255
Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly	260	265	270
Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu	275	280	285
Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val	290	295	300
Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala	305	310	315
Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys	325	330	335
Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp	340	345	350
Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys	355	360	365
Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val	370	375	380
Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro	385	390	395
Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile	405	410	415
Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu	420	425	430
Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His Val Glu Ala Leu	435	440	445
Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly	450	455	460
Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr Arg Tyr	465	470	475

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(105)  
 <223> FRXA00132

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 His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln  
 1 5 10 15  
 gct gag tac atc ggc gtt gac gtt gca ggc cca ttc aag ccg gag cac 96  
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His  
 20 25 30  
 tac cgc tac taatgattgt cagcattgag gga 128  
 Tyr Arg Tyr  
 35

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 1 5 10 15  
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His  
 20 25 30  
 Tyr Arg Tyr  
 35

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 <222> (101)..(1396)  
 <223> FRXA01371

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 tttcctaatt ttcattttct taaaaggagc tcgccaggac atg gca cag gtt atg 115  
 Met Ala Gln Val Met  
 1 5  
 gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag 163  
 Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln

10	15	20	
att cgt ctt gca gag tat gag atg cca ggt ctc atg cag ttg cgc aag Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu Met Gln Leu Arg Lys 25 30 35			211
gaa ttc gca gac gag cag cct ttg aag ggc gcc cga att gct ggt tct Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala Arg Ile Ala Gly Ser 40 45 50			259
atc cac atg acg gtc cag acc gcc gtg ctt att gag acc ctc act gct Ile His Met Thr Val Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala 55 60 65			307
ttg ggc gct gag gtt cgt tgg gct tcc tgc aac att ttc tcc acc cag Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn Ile Phe Ser Thr Gln 70 75 80 85			355
gat gag gct gca gcg gct atc gtt gtc ggc tcc ggc acc gtc gaa gag Asp Glu Ala Ala Ala Ile Val Val Gly Ser Gly Thr Val Glu Glu 90 95 100			403
cca gct ggt gtt cca gta ttc gcg tgg aag ggt gag tca ctg gag gag Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly Glu Ser Leu Glu Glu 105 110 115			451
tac tgg tgg tgc atc aac cag atc ttc agc tgg ggc gat gag ctg cca Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp Gly Asp Glu Leu Pro 120 125 130			499
aac atg atc ctc gac gac ggc ggt gac gcc acc atg gct gtt att cgc Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg 135 140 145			547
ggt cgc gaa tac gag cag gct ggt ctg gtt cca cca gca gag gcc aac Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro Pro Ala Glu Ala Asn 150 155 160 165			595
gat tcc gat gag tac atc gca ttc ttg ggc atg ctg cgt gag gtt ctt Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met Leu Arg Glu Val Leu 170 175 180			643
gct gca gag cct ggc aag tgg ggc aag atc gct gag gcc gtt aag ggt Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala Glu Ala Val Lys Gly 185 190 195			691
gtc acc gag gaa acc acc acc ggt gtg cac cgc ctg tac cac ttc gct Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala 200 205 210			739
gaa gaa ggc gtg ctg cct ttc cca gcg atg aac gtc aac gac gct gtc Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val 215 220 225			787
acc aag tcc aag ttt gat aac aag tac ggc acc cgc cac tcc ctg atc Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile 230 235 240 245			835
gac ggc atc aac cgc gcc act gac atg ctc atg ggc ggc aag aac gtg Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val 250 255 260			883

ctt gtc tgc ggt tac ggc gat gtc ggc aag ggc tgc gct gag gct ttc 931  
 Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe  
                   265                                  270                                  275

gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac 979  
 Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn  
                   280                                  285                                  290

gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag  
 1027  
 Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu  
                   295                                  300                                  305

gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac  
 1075  
 Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp  
 310                                  315                                  320                                  325

atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg  
 1123  
 Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu  
                   330                                  335                                  340

ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg  
 1171  
 Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu  
                   345                                  350                                  355

cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag  
 1219  
 His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu  
                   360                                  365                                  370

ttc acc ttc tcc acc ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc  
 1267  
 Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg  
                   375                                  380                                  385

ctg ttg aac ctt ggc aac gcc acc gga cac cca tca ttt gtc atg tcc  
 1315  
 Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser  
 390                                  395                                  400                                  405

aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac  
 1363  
 Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn  
                   410                                  415                                  420

gaa gga cag tac gag aac gag gtc tac cgt ctg  
 1396  
 Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu  
                   425                                  430

&lt;210&gt; 224

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 224

Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu  
 1 5 10 15  
 Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu  
 20 25 30  
 Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala  
 35 40 45  
 Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile  
 50 55 60  
 Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn  
 65 70 75 80  
 Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser  
 85 90 95  
 Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly  
 100 105 110  
 Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp  
 115 120 125  
 Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr  
 130 135 140  
 Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro  
 145 150 155 160  
 Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met  
 165 170 175  
 Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala  
 180 185 190  
 Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg  
 195 200 205  
 Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn  
 210 215 220  
 Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr  
 225 230 235 240  
 Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met  
 245 250 255  
 Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly  
 260 265 270  
 Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu  
 275 280 285  
 Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val  
 290 295 300  
 Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala  
 305 310 315 320  
 Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys



				325					330					335		
Asp	His	Ala	Leu	Leu	Gly	Asn	Ile	Gly	His	Phe	Asp	Asn	Glu	Ile	Asp	
			340					345					350			
Met	His	Ser	Leu	Leu	His	Arg	Asp	Asp	Val	Thr	Arg	Thr	Thr	Ile	Lys	
		355					360					365				
Pro	Gln	Val	Asp	Glu	Phe	Thr	Phe	Ser	Thr	Gly	Arg	Ser	Ile	Ile	Val	
	370					375					380					
Leu	Ser	Glu	Gly	Arg	Leu	Leu	Asn	Leu	Gly	Asn	Ala	Thr	Gly	His	Pro	
385					390					395					400	
Ser	Phe	Val	Met	Ser	Asn	Ser	Phe	Ala	Asp	Gln	Thr	Ile	Ala	Gln	Ile	
				405					410					415		
Glu	Leu	Phe	Gln	Asn	Glu	Gly	Gln	Tyr	Glu	Asn	Glu	Val	Tyr	Arg	Leu	
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<211> 2358
<212> DNA
<213> Corynebacterium glutamicum
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<223> RXN02085
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gatccgcacg ttcgggtcaa gcagaaagtc tttaactcac																115
										atg	act	tcc	aac	ttt		
										Met	Thr	Ser	Asn	Phe		
										1				5		
tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg																163
Ser	Ser	Thr	Val	Ala	Gly	Leu	Pro	Arg	Ile	Gly	Ala	Lys	Arg	Glu	Leu	
				10					15					20		
aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa																211
Lys	Phe	Ala	Leu	Glu	Gly	Tyr	Trp	Asn	Gly	Ser	Ile	Glu	Gly	Arg	Glu	
			25					30					35			
ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg																259
Leu	Ala	Gln	Thr	Ala	Arg	Gln	Leu	Val	Asn	Thr	Ala	Ser	Asp	Ser	Leu	
		40					45					50				
tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca																307
Ser	Gly	Leu	Asp	Ser	Val	Pro	Phe	Ala	Gly	Arg	Ser	Tyr	Tyr	Asp	Ala	
	55					60					65					
atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat																355
Met	Leu	Asp	Thr	Ala	Ala	Ile	Leu	Gly	Val	Leu	Pro	Glu	Arg	Phe	Asp	
70					75					80				85		



gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc 403  
 Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg  
                     90                    95                    100

tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg 451  
 Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met  
                     105                    110                    115

acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct 499  
 Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser  
                     120                    125                    130

gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc 547  
 Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu  
                     135                    140                    145

cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt 595  
 Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly  
                     150                    155                    160                    165

cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct 643  
 Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro  
                     170                    175                    180

ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag 691  
 Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys  
                     185                    190                    195

tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc 739  
 Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr  
                     200                    205                    210

gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act 787  
 Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr  
                     215                    220                    225

ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc 835  
 Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly  
                     230                    235                    240                    245

gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc 883  
 Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly  
                     250                    255                    260

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931  
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly  
                     265                    270                    275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979  
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg  
                     280                    285                    290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc  
 1027  
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg  
                     295                    300                    305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac  
 1075  
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr  
                     310                    315                    320                    325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc  
 1123  
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala  
 330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta  
 1171  
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu  
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att  
 1219  
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile  
 360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc  
 1267  
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu  
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag  
 1315  
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu  
 390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc  
 1363  
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe  
 410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa  
 1411  
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu  
 425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat  
 1459  
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp  
 440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac  
 1507  
 Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His  
 455 460 465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc  
 1555  
 Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu  
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gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc  
 1603  
 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser  
 490 495 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg  
 1651  
 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala  
 505 510 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag  
1699

Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys  
520 525 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc  
1747

His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser  
535 540 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca  
1795

Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala  
550 555 560 565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag  
1843

Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys  
570 575 580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccg cta cga  
1891

Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg  
585 590 595

gac gtc gat aag cct gcc tac ctg cag tgg tcc gtg gac tcc ttc cgc  
1939

Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg  
600 605 610

ctg gcg act gcc ggc gca ccc gac gac gtc caa atc cac acc cac atg  
1987

Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met  
615 620 625

tgc tac tcc gag ttc aac gaa gtg atc tcc tcg gtc atc gcg ttg gat  
2035

Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp  
630 635 640 645

gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc  
2083

Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu  
650 655 660

gct gct ctg aaa tct tcc ggc ttc gag ctc ggc gtc gga cct ggt gtg  
2131

Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val  
665 670 675

tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt  
2179

Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly  
680 685 690

ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc  
2227

Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val  
695 700 705

aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gct  
2275

Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala  
710 715 720 725

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc  
2323

Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile  
730 735 740

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2358

Gly Ala Thr Ile  
745

<210> 226

<211> 745

<212> PRT

<213> Corynebacterium glutamicum

<400> 226

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20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr  
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu  
100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu  
115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala  
130 135 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg  
145 150 155 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr  
165 170 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr  
180 185 190

Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
195 200 205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg  
 210 215 220  
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr  
 225 230 235 240  
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly  
 245 250 255  
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu  
 260 265 270  
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly  
 275 280 285  
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys  
 290 295 300  
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu  
 305 310 315 320  
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val  
 325 330 335  
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu  
 340 345 350  
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala  
 355 360 365  
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro  
 370 375 380  
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg  
 385 390 395 400  
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr  
 405 410 415  
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala  
 420 425 430  
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met  
 435 440 445  
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu  
 450 455 460  
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr  
 465 470 475 480  
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val  
 485 490 495  
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn  
 500 505 510  
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln  
 515 520 525  
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr

332

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aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa				211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu				
	25	30	35	
ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg				259
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu				
	40	45	50	
tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca				307
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala				
	55	60	65	
atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat				355
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp				
	70	75	80	85
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc				403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg				
	90	95	100	
tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg				451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met				
	105	110	115	
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct				499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser				
	120	125	130	
gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc				547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu				
	135	140	145	
cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt				595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly				
	150	155	160	165
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct				643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro				
	170	175	180	
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag				691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys				
	185	190	195	
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc				739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr				
	200	205	210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act				787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr				
	215	220	225	
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc				835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly				
	230	235	240	245
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc				883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly				
	250	255	260	

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931  
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly  
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979  
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg  
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc  
 1027  
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg  
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac  
 1075  
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr  
 310 315 320 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc  
 1123  
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala  
 330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta  
 1171  
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu  
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att  
 1219  
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile  
 360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc  
 1267  
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu  
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag  
 1315  
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu  
 390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc  
 1363  
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe  
 410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa  
 1411  
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu  
 425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat  
 1459  
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp  
 440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac  
 1507



Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His  
 455 460 465  
 ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc  
 1555  
 Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu  
 470 475 480 485  
 gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc  
 1603  
 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser  
 490 495 500  
 cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg  
 1651  
 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala  
 505 510 515  
 cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag  
 1699  
 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys  
 520 525 530  
 cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc  
 1747  
 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser  
 535 540 545  
 ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca  
 1795  
 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala  
 550 555 560 565  
 ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag  
 1843  
 Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys  
 570 575 580  
 atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg  
 1891  
 Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr  
 585 590 595  
 aga cgt cga taagcctgcc tacctgcagt ggt  
 1923  
 Arg Arg Arg  
 600

&lt;210&gt; 228

&lt;211&gt; 600

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 228

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly  
 1 5 10 15

Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser  
 20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr  
 35 40 45  
 Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
 50 55 60  
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
 65 70 75 80  
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
 85 90 95  
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu  
 100 105 110  
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu  
 115 120 125  
 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala  
 130 135 140  
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg  
 145 150 155 160  
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr  
 165 170 175  
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr  
 180 185 190  
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
 195 200 205  
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg  
 210 215 220  
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr  
 225 230 235 240  
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly  
 245 250 255  
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu  
 260 265 270  
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly  
 275 280 285  
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys  
 290 295 300  
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu  
 305 310 315 320  
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val  
 325 330 335  
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu  
 340 345 350  
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala

355					360					365					
Ala	Ser	Ala	Ala	Ile	Ala	Ser	Arg	Arg	Thr	Ser	Pro	Arg	Thr	Ala	Pro
370					375					380					
Ile	Thr	Gln	Glu	Leu	Pro	Gly	Arg	Ser	Arg	Gly	Ser	Phe	Asp	Thr	Arg
385					390					395					400
Val	Thr	Leu	Gln	Glu	Lys	Ser	Leu	Glu	Leu	Pro	Ala	Leu	Pro	Thr	Thr
				405					410					415	
Thr	Ile	Gly	Ser	Phe	Pro	Gln	Thr	Pro	Ser	Ile	Arg	Ser	Ala	Arg	Ala
			420					425					430		
Arg	Leu	Arg	Lys	Glu	Ser	Ile	Thr	Leu	Glu	Gln	Tyr	Glu	Glu	Ala	Met
			435				440					445			
Arg	Glu	Glu	Ile	Asp	Leu	Val	Ile	Ala	Lys	Gln	Glu	Glu	Leu	Gly	Leu
						455					460				
Asp	Val	Leu	Val	His	Gly	Glu	Pro	Glu	Arg	Asn	Asp	Met	Val	Gln	Tyr
465					470					475					480
Phe	Ser	Glu	Leu	Leu	Asp	Gly	Phe	Leu	Ser	Thr	Ala	Asn	Gly	Trp	Val
				485					490					495	
Gln	Ser	Tyr	Gly	Ser	Arg	Cys	Val	Arg	Pro	Pro	Val	Leu	Phe	Gly	Asn
			500					505					510		
Val	Ser	Arg	Pro	Ala	Pro	Met	Thr	Val	Lys	Trp	Phe	Gln	Tyr	Ala	Gln
			515				520					525			
Ser	Leu	Thr	Gln	Lys	His	Val	Lys	Gly	Met	Leu	Thr	Gly	Pro	Val	Thr
						535					540				
Ile	Leu	Ala	Trp	Ser	Phe	Val	Arg	Asp	Asp	Gln	Pro	Leu	Ala	Thr	Thr
545					550					555					560
Ala	Asp	Gln	Val	Ala	Leu	Ala	Leu	Arg	Asp	Glu	Ile	Asn	Asp	Leu	Ile
				565					570					575	
Glu	Ala	Gly	Ala	Lys	Ile	Ile	Gln	Val	Asp	Glu	Pro	Ala	Ile	Arg	Glu
			580				585						590		
Leu	Leu	Pro	Ala	Thr	Arg	Arg	Arg								
		595				600									

<210> 229  
 <211> 603  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(580)  
 <223> FRXA02086

<400> 229  
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[illegible]

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<210> 230
<211> 160
<212> PRT
<213> Corynebacterium glutamicum
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<400> 230
Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys
   1                               5                                10                    15

Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
          20                      25                          30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
      35                        40                            45
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Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr  
 50 55 60  
 Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys  
 65 70 75 80  
 Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His  
 85 90 95  
 Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala  
 100 105 110  
 Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys  
 115 120 125  
 Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val  
 130 135 140  
 Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile  
 145 150 155 160

<210> 231  
 <211> 1326  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1303)  
 <223> RXN02648

<400> 231  
 atgaataaaa ttccgggtgc agtgaccgta ggtgaggtaa acgcgggttag agtcgaatga 60  
 gagtttgata ctttcttttcg acttttagat tggattttca atg agc cag aac cgc 115  
 Met Ser Gln Asn Arg  
 1 5  
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163  
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu  
 10 15 20  
 gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211  
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe  
 25 30 35  
 ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259  
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val  
 40 45 50  
 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307  
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr  
 55 60 65  
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355  
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg

70	75	80	85	
ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa	403			
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu				
90 95 100				
gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat	451			
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp				
105 110 115				
cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct	499			
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser				
120 125 130				
ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga	547			
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly				
135 140 145				
cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg	595			
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu				
150 155 160 165				
ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca	643			
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala				
170 175 180				
gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac	691			
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp				
185 190 195				
act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa	739			
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu				
200 205 210				
tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca ccg	787			
Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala Pro				
215 220 225				
gac ttg gca gaa gca tgg gat cag atc aac cca gag cca agc gtg aag	835			
Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys				
230 235 240 245				
gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca	883			
Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala				
250 255 260				
gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc	931			
Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly				
265 270 275				
tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att	979			
Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile				
280 285 290				
ggg gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca	1027			
Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala				
295 300 305				
tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt	1075			

Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu  
 310 315 320 325

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac  
 1123

Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn  
 330 335 340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc  
 1171

Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala  
 345 350 355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg  
 1219

Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu  
 360 365 370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta  
 1267

Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu  
 375 380 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac  
 1313

Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
 390 395 400

aacgagggtt gct  
 1326

<210> 232

<211> 401

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 232

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg  
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Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu  
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn  
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg  
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu  
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr  
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn  
 130 135 140  
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln  
 145 150 155 160  
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr  
 165 170 175  
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr  
 180 185 190  
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp  
 195 200 205  
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val  
 210 215 220  
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro  
 225 230 235 240  
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp  
 245 250 255  
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu  
 260 265 270  
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro  
 275 280 285  
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe  
 290 295 300  
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp  
 305 310 315 320  
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val  
 325 330 335  
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg  
 340 345 350  
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser  
 355 360 365  
 Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala  
 370 375 380  
 Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu  
 385 390 395 400

Phe

&lt;210&gt; 233

&lt;211&gt; 548

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(525)

&lt;223&gt; FRXA02648

&lt;400&gt; 233

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gac gca ccg gac ttg gca gaa gca tgg gat cag atc aac cca gag cca 48
Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1           5           10           15

agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96
Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
          20           25           30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144
Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
          35           40           45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
          50           55           60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240
Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
        65           70           75           80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
          85           90           95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
          100          105          110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384
Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
          115          120          125

cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
          130          135          140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
          145          150          155          160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
          165          170          175

taagctagac aacgagggtt gct 548

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&lt;210&gt; 234

&lt;211&gt; 175

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 234

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Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1           5           10           15

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344

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307  
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr  
 55 60 65  
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355  
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg  
 70 75 80 85  
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403  
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu  
 90 95 100  
 gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451  
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp  
 105 110 115  
 cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499  
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser  
 120 125 130  
 ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547  
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly  
 135 140 145  
 cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595  
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu  
 150 155 160 165  
 ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643  
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala  
 170 175 180  
 gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691  
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp  
 185 190 195  
 act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739  
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu  
 200 205 210  
 tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784  
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala  
 215 220 225

&lt;210&gt; 236

&lt;211&gt; 228

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 236

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg  
 1 5 10 15  
 Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
 20 25 30  
 Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
 35 40 45  
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu



50	55	60	
Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn			
65	70	75	80
Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg			
	85	90	95
Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu			
	100	105	110
Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr			
	115	120	125
Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn			
	130	135	140
Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln			
145	150	155	160
Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr			
	165	170	175
Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr			
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Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp			
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Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val			
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Gln Leu Asp Ala			
225			
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Val Thr Asn Val Ser 1 5			
aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163			
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile 10 15 20			
acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211			
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr 25 30 35			



gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259  
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe  
40 45 50

tac	cat	cag	gca	gat	gag	gga	gta	ttc	gag	ttc	atc	gga	cca	ttg	gtt	307
Tyr	His	Gln	Ala	Asp	Glu	Gly	Val	Phe	Glu	Phe	Ile	Gly	Pro	Leu	Val	
	55					60					65					

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355  
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile  
70 75 80 85

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aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca      405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly
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**cac** 408

<210> 238

**<211> 95**

<212> PRT

<213> Corynebacterium glutamicum

<400> 238

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp  
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Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys  
20 25 30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg  
35 40 45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe  
50 55 60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile  
65 70 75 80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly  
85 90 95

**<210> 239**

<211> 1827

**<212> DNA**

<213> Corynebacterium glutamicum

**<220>**

<221> CDS

**<222> (101) . . (1804)**

<223> RXC00128

**<400> 239**

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Val Ser Lys Ile Ser  
1 5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg	163
Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val	
10 15 20	
gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc	211
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg	
25 30 35	
tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg	259
Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro	
40 45 50	
aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg	307
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala	
55 60 65	
tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg	355
Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly	
70 75 80 85	
acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc	403
Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg	
90 95 100	
att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att	451
Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile	
105 110 115	
gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat	499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr	
120 125 130	
cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa	547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu	
135 140 145	
gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag	595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu	
150 155 160 165	
aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt	643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe	
170 175 180	
gat cct tct ggc cag gtg ttg gtg ggg gat cgg cgt tgg ttg ttc aat	691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn	
185 190 195	
gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt	739
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly	
200 205 210	
cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat	787
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp	
215 220 225	
gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg	835
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu	
230 235 240 245	
gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg	883

Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val  
 250 255 260

tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct 931  
 Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala  
 265 270 275

gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac 979  
 Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp  
 280 285 290

ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg  
 1027  
 Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu  
 295 300 305

ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg  
 1075  
 Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val  
 310 315 320 325

agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg  
 1123  
 Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala  
 330 335 340

att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac  
 1171  
 Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn  
 345 350 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg  
 1219  
 Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala  
 360 365 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt  
 1267  
 Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser  
 375 380 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga  
 1315  
 Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg  
 390 395 400 405

tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg  
 1363  
 Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu  
 410 415 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act  
 1411  
 Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr  
 425 430 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc  
 1459  
 Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val  
 440 445 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag  
1507

Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu  
455 460 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca  
1555

Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro  
470 475 480 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg  
1603

Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp  
490 495 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat  
1651

Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn  
505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac  
1699

Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr  
520 525 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat  
1747

Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp  
535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg  
1795

Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val  
550 555 560 565

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1827

Val Ala Tyr

<210> 240

<211> 568

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser  
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Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp  
20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile  
35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe  
50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala  
65 70 75 80



Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr  
 85 90 95  
 Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn  
 100 105 110  
 Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu  
 115 120 125  
 Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile  
 130 135 140  
 Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp  
 145 150 155 160  
 Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His  
 165 170 175  
 Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg  
 180 185 190  
 Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala  
 195 200 205  
 Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn  
 210 215 220  
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr  
 225 230 235 240  
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe  
 245 250 255  
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro  
 260 265 270  
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr  
 275 280 285  
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn  
 290 295 300  
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val  
 305 310 315 320  
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp  
 325 330 335  
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val  
 340 345 350  
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly  
 355 360 365  
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe  
 370 375 380  
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro  
 385 390 395 400

Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu  
 405 410 415  
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe  
 420 425 430  
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys  
 435 440 445  
 Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val  
 450 455 460  
 Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser  
 465 470 475 480  
 Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro  
 485 490 495  
 Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser  
 500 505 510  
 Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser  
 515 520 525  
 Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro  
 530 535 540  
 Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr  
 545 550 555 560  
 Arg Ala Ala Pro Val Val Ala Tyr  
 565

<210> 241  
 <211> 1344  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1321)  
 <223> RXA02240

<400> 241  
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 aagactattt attctcaact tcttcgaaag aagggtattt gtg gct cag cca acc 115  
 Val Ala Gln Pro Thr  
 1 5  
 gcc gtc cgt ttg ttc acc agt gaa tct gta act gag gga cat cca gac 163  
 Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His Pro Asp  
 10 15 20  
 aaa ata tgt gat gct att tcc gat acc att ttg gac gcg ctg ctc gaa 211  
 Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu Asp Ala Leu Leu Glu  
 25 30 35  
 aaa gat ccg cag tcg cgc gtc gca gtg gaa act gtg gtc acc acc gga 259  
 Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr Val Val Thr Thr Gly

40	45	50	
atc gtc cat gtt gtt ggc gag gtc cgt acc agc gct tac gta gag atc Ile Val His Val Val Gly Glu Val Arg Thr Ser Ala Tyr Val Glu Ile 55 60 65			307
cct caa tta gtc cgc aac aag ctc atc gaa atc gga ttc aac tcc tct Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile Gly Phe Asn Ser Ser 70 75 80 85			355
gag gtt gga ttc gac gga cgc acc tgt ggc gtc tca gta tcc atc ggt Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val Ser Val Ser Ile Gly 90 95 100			403
gag cag tcc cag gaa atc gct gac ggc gtg gat aac tcc gac gaa gcc Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp Asn Ser Asp Glu Ala 105 110 115			451
cgc acc aac ggc gac gtt gaa gaa gac gac cgc gca ggt gct ggc gac Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg Ala Gly Ala Gly Asp 120 125 130			499
cag ggc ctg atg ttc ggc tac gcc acc aac gaa acc gaa gag tac atg Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu Thr Glu Glu Tyr Met 135 140 145			547
cct ctt cct atc gcg ttg gcg cac cga ctg tca cgt cgt ctg acc cag Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser Arg Arg Leu Thr Gln 150 155 160 165			595
gtt cgt aaa gag ggc atc gtt cct cac ctg cgt cca gac gga aaa acc Val Arg Lys Glu Gly Ile Val Pro His Leu Arg Pro Asp Gly Lys Thr 170 175 180			643
cag gtc acc ttc gca tac gat gcg caa gac cgc cct agc cac ctg gat Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg Pro Ser His Leu Asp 185 190 195			691
acc gtt gtc atc tcc acc cag cac gac cca gaa gtt gac cgt gca tgg Thr Val Val Ile Ser Thr Gln His Asp Pro Glu Val Asp Arg Ala Trp 200 205 210			739
ttg gaa acc caa ctg cgc gaa cac gtc att gat tgg gta atc aaa gac Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp Trp Val Ile Lys Asp 215 220 225			787
gca ggc att gag gat ctg gca acc ggt gag atc acc gtg ttg atc aac Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile Thr Val Leu Ile Asn 230 235 240 245			835
cct tca ggt tcc ttc att ctg ggt ggc ccc atg ggt gat gcg ggt ctg Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met Gly Asp Ala Gly Leu 250 255 260			883
acc ggc cgc aag atc atc gtg gat acc tac ggt ggc atg gct cgc cat Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His 265 270 275			931
ggt ggt gga gca ttc tcc ggt aag gat cca agc aag gtg gac cgc tct Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp Arg Ser 280 285 290			979

gct gca tac gcc atg cgt tgg gta gca aag aac atc gtg gca gca ggc  
1027

Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn Ile Val Ala Ala Gly  
295 300 305

ctt gct gat cgc gct gaa gtt cag gtt gca tac gcc att gga cgc gca  
1075

Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala  
310 315 320 325

aag cca gtc gga ctt tac gtt gaa acc ttt gac acc aac aag gaa ggc  
1123

Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp Thr Asn Lys Glu Gly  
330 335 340

ctg agc gac gag cag att cag gct gcc gtg ttg gag gtc ttt gac ctg  
1171

Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu Glu Val Phe Asp Leu  
345 350 355

cgt cca gca gca att atc cgt gag ctt gat ctg ctt cgt ccg atc tac  
1219

Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr  
360 365 370

gct gac act gct gcc tac ggc cac ttt ggt cgc act gat ttg gac ctt  
1267

Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg Thr Asp Leu Asp Leu  
375 380 385

cct tgg gag gct atc gac cgc gtt gat gaa ctt cgc gca gcc ctc aag  
1315

Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu Arg Ala Ala Leu Lys  
390 395 400 405

ttg gcc taaaaatctg atgtagtatac ttc  
1344

Leu Ala

<210> 242

<211> 407

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

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Glu Gly His Pro Asp Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu  
20 25 30

Asp Ala Leu Leu Glu Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr  
35 40 45

Val Val Thr Thr Gly Ile Val His Val Val Gly Glu Val Arg Thr Ser  
50 55 60

Ala Tyr Val Glu Ile Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile

65		70		75		80
Gly Phe Asn Ser Ser Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val						
	85			90		95
Ser Val Ser Ile Gly Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp						
	100		105		110	
Asn Ser Asp Glu Ala Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg						
	115		120		125	
Ala Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu						
	130		135		140	
Thr Glu Glu Tyr Met Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser						
	145		150		155	160
Arg Arg Leu Thr Gln Val Arg Lys Glu Gly Ile Val Pro His Leu Arg						
		165		170		175
Pro Asp Gly Lys Thr Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg						
	180		185		190	
Pro Ser His Leu Asp Thr Val Val Ile Ser Thr Gln His Asp Pro Glu						
	195		200		205	
Val Asp Arg Ala Trp Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp						
	210		215		220	
Trp Val Ile Lys Asp Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile						
	225		230		235	240
Thr Val Leu Ile Asn Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met						
		245		250		255
Gly Asp Ala Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly						
	260		265		270	
Gly Met Ala Arg His Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser						
	275		280		285	
Lys Val Asp Arg Ser Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn						
	290		295		300	
Ile Val Ala Ala Gly Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr						
	305		310		315	320
Ala Ile Gly Arg Ala Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp						
		325		330		335
Thr Asn Lys Glu Gly Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu						
	340		345		350	
Glu Val Phe Asp Leu Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu						
	355		360		365	
Leu Arg Pro Ile Tyr Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg						
	370		375		380	
Thr Asp Leu Asp Leu Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu						
	385		390		395	400

Arg Ala Ala Leu Lys Leu Ala  
405

<210> 243  
<211> 669  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(646)  
<223> RXA00780

<400> 243

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                                         Met Ile Arg Glu Asp
                                         1                               5

ctc gca aac gct cgt gaa cac gat cca gca gcc cga ggc gat tta gaa 163
Leu Ala Asn Ala Arg Glu His Asp Pro Ala Ala Arg Gly Asp Leu Glu
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aac gca gtg gtt tac tcc gga ctc cac gcc atc tgg gca cat cga gtt 211
Asn Ala Val Val Tyr Ser Gly Leu His Ala Ile Trp Ala His Arg Val
                        25                               30                               35

gcc aac agc tgg tgg aaa tcc ggt ttc cgc ggc ccc gcc cgc gta tta 259
Ala Asn Ser Trp Trp Lys Ser Gly Phe Arg Gly Pro Ala Arg Val Leu
                        40                               45                               50

gcc caa ttc acc cga ttc ctc acc ggc att gaa att cac ccc ggt gcc 307
Ala Gln Phe Thr Arg Phe Leu Thr Gly Ile Glu Ile His Pro Gly Ala
                        55                               60                               65

acc att ggt cgt cgc ttt ttt att gac cac gga atg gga atc gtc atc 355
Thr Ile Gly Arg Arg Phe Phe Ile Asp His Gly Met Gly Ile Val Ile
                        70                               75                               80                               85

ggc gaa acc gct gaa atc ggc gaa ggc gtc atg ctc tac cac ggc gtc 403
Gly Glu Thr Ala Glu Ile Gly Glu Gly Val Met Leu Tyr His Gly Val
                        90                               95                               100

acc ctc ggc gga cag gtt ctc acc caa acc aag cgc cac ccc acg ctc 451
Thr Leu Gly Gly Gln Val Leu Thr Gln Thr Lys Arg His Pro Thr Leu
                        105                               110                               115

tgc gac aac gtg aca gtc ggc gcg ggc gca aaa atc tta ggt ccc atc 499
Cys Asp Asn Val Thr Val Gly Ala Gly Ala Lys Ile Leu Gly Pro Ile
                        120                               125                               130

acc atc ggc gaa ggc tcc gca att ggc gcc aat gca gtt gtc acc aaa 547
Thr Ile Gly Glu Gly Ser Ala Ile Gly Ala Asn Ala Val Val Thr Lys
                        135                               140                               145

gac gtg ccg gca gaa cac atc gca gtc gga att cct gcg gta gca cgc 595
Asp Val Pro Ala Glu His Ile Ala Val Gly Ile Pro Ala Val Ala Arg
150                               155                               160                               165

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cca cgt ggc aag aca gag aag atc aag ctc gtc gat ccg gac tat tac 643  
 Pro Arg Gly Lys Thr Glu Lys Ile Lys Leu Val Asp Pro Asp Tyr Tyr  
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 <213> Corynebacterium glutamicum

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 Arg Gly Asp Leu Glu Asn Ala Val Val Tyr Ser Gly Leu His Ala Ile  
                   20                  25                  30  
 Trp Ala His Arg Val Ala Asn Ser Trp Trp Lys Ser Gly Phe Arg Gly  
                   35                  40                  45  
 Pro Ala Arg Val Leu Ala Gln Phe Thr Arg Phe Leu Thr Gly Ile Glu  
                   50                  55                  60  
 Ile His Pro Gly Ala Thr Ile Gly Arg Arg Phe Phe Ile Asp His Gly  
   65                  70                  75                  80  
 Met Gly Ile Val Ile Gly Glu Thr Ala Glu Ile Gly Glu Gly Val Met  
                   85                  90                  95  
 Leu Tyr His Gly Val Thr Leu Gly Gly Gln Val Leu Thr Gln Thr Lys  
                   100                  105                  110  
 Arg His Pro Thr Leu Cys Asp Asn Val Thr Val Gly Ala Gly Ala Lys  
                   115                  120                  125  
 Ile Leu Gly Pro Ile Thr Ile Gly Glu Gly Ser Ala Ile Gly Ala Asn  
                   130                  135                  140  
 Ala Val Val Thr Lys Asp Val Pro Ala Glu His Ile Ala Val Gly Ile  
   145                  150                  155                  160  
 Pro Ala Val Ala Arg Pro Arg Gly Lys Thr Glu Lys Ile Lys Leu Val  
                   165                  170                  175  
 Asp Pro Asp Tyr Tyr Ile  
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<220>  
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 <222> (101)..(1033)







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 Gln Phe Glu Asn Glu Ala Asn Pro Arg Val Asn Arg Asp Thr Thr Ala  
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 Lys Glu Ile Leu Glu Asp Thr Asp Gly Thr Val Asp Ile Phe Val Ala  
 165 170 175  
 Ser Phe Gly Thr Gly Gly Thr Val Thr Gly Val Gly Gln Val Leu Lys  
 180 185 190  
 Glu Asn Asn Ala Asp Val Gln Val Tyr Thr Val Glu Pro Glu Ala Ser  
 195 200 205  
 Pro Leu Leu Thr Ala Gly Lys Ala Gly Pro His Lys Ile Gln Gly Ile  
 210 215 220  
 Gly Ala Asn Phe Ile Pro Glu Val Leu Asp Arg Lys Val Leu Asp Asp  
 225 230 235 240  
 Val Leu Thr Val Ser Asn Glu Asp Ala Ile Ala Phe Ser Arg Lys Leu  
 245 250 255  
 Ala Thr Glu Glu Gly Ile Leu Gly Gly Ile Ser Thr Gly Ala Asn Ile  
 260 265 270  
 Lys Ala Ala Leu Asp Leu Ala Ala Lys Pro Glu Asn Ala Gly Lys Thr  
 275 280 285  
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 290 295 300  
 Leu Tyr Glu Asp Ile Arg Asp  
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 <223> RXN00402

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 gat gct gct tac cac gga ttg aag tac gca gac ctt ggt gca cca gcc 96  
 Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala  
 20 25 30  
 ttc ggc ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc tcc acc 144  
 Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr  
 35 40 45  
 ctc tcc gca ttc aac gca tgg gct gca gtc cag ggc atc gac acc ctt 192

Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu  
 50 55 60  
 tcc ctg cgc ctg gag cgc cac aac gaa aac gcc atc aag gtt gca gaa 240  
 Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu  
 65 70 75 80  
 ttc ctc aac aac cac gag aag gtg gaa aag gtt aac ttc gca ggc ctg 288  
 Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu  
 85 90 95  
 aag gat tcc cct tgg tac gca acc aag gaa aag ctt ggc ctg aag tac 336  
 Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr  
 100 105 110  
 acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat gag gct 384  
 Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala  
 115 120 125  
 tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca aac atc 432  
 Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile  
 130 135 140  
 ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc cat tca 480  
 Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser  
 145 150 155 160  
 cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag tcc acc 528  
 Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr  
 165 170 175  
 gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc gct gac 576  
 Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp  
 180 185 190  
 ctc gaa ggc ggc ttt gct gca atc tagctttaaa tagactcacc cca 623  
 Leu Glu Gly Gly Phe Ala Ala Ile  
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 <213> Corynebacterium glutamicum  
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 20 25 30  
 Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr  
 35 40 45  
 Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu  
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 Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu  
 65 70 75 80

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Val	Leu	Pro	Tyr	Phe	Val	Thr	Pro	Asp	Ala	Ala	Tyr	His	Gly	Leu	Lys	
1				5					10					15		
tac	gca	gac	ctt	ggc	gca	cca	gcc	ttc	ggc	ctc	aag	gtt	cgc	gtt	ggc	96
Tyr	Ala	Asp	Leu	Gly	Ala	Pro	Ala	Phe	Gly	Leu	Lys	Val	Arg	Val	Gly	
			20					25					30			
ctt	cta	cgc	gac	acc	ggc	tcc	acc	ctc	tcc	gca	ttc	aac	gca	tgg	gct	144
Leu	Leu	Arg	Asp	Thr	Gly	Ser	Thr	Leu	Ser	Ala	Phe	Asn	Ala	Trp	Ala	
		35					40					45				
gca	gtc	cag	ggc	atc	gac	acc	ctt	tcc	ctg	cgc	ctg	gag	cgc	cac	aac	192
Ala	Val	Gln	Gly	Ile	Asp	Thr	Leu	Ser	Leu	Arg	Leu	Glu	Arg	His	Asn	
	50					55					60					
gaa	aac	gcc	atc	aag	gtt	gca	gaa	ttc	ctc	aac	aac	cac	gag	aag	gtg	240
Glu	Asn	Ala	Ile	Lys	Val	Ala	Glu	Phe	Leu	Asn	Asn	His	Glu	Lys	Val	
65					70					75					80	
gaa	aag	gtt	aac	ttc	gca	ggc	ctg	aag	gat	tcc	cct	tgg	tac	gca	acc	288
Glu	Lys	Val	Asn	Phe	Ala	Gly	Leu	Lys	Asp	Ser	Pro	Trp	Tyr	Ala	Thr	
				85					90					95		
aag	gaa	aag	ctt	ggc	ctg	aag	tac	acc	ggc	tcc	gtt	ctc	acc	ttc	gag	336

Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu  
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atc aag ggc ggc aag gat gag gct tgg gca ttt atc gac gcc ctg aag 384  
 Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys  
 115 120 125

cta cac tcc aac ctt gca aac atc ggc gat gtt cgc tcc ctc gtt gtt 432  
 Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val  
 130 135 140

cac cca gca acc acc acc cat tca cag tcc gac gaa gct ggc ctg gca 480  
 His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala  
 145 150 155 160

cgc gcg ggc gtt acc cag tcc acc gtc cgc ctg tcc gtt ggc atc gag 528  
 Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu  
 165 170 175

acc att gat gat atc atc gct gac ctc gaa ggc ggc ttt gct gca atc 576  
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tagctttaaa tagactcacc cca 599

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Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly  
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Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala  
 35 40 45

Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn  
 50 55 60

Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val  
 65 70 75 80

Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr  
 85 90 95

Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu  
 100 105 110

Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys  
 115 120 125

Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val  
 130 135 140

His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala  
 145 150 155 160

Arg	Ala	Gly	Val	Thr	Gln	Ser	Thr	Val	Arg	Leu	Ser	Val	Gly	Ile	Glu
				165					170					175	
Thr	Ile	Asp	Asp	Ile	Ile	Ala	Asp	Leu	Glu	Gly	Gly	Phe	Ala	Ala	Ile
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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(613)  
<223> RXS00405
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Met Pro Lys Tyr Asp 5															
aat tcc aat gct gac cag tgg ggc ttt gaa acc cgc tcc att cac gca 163															
Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr Arg Ser Ile His Ala 20															
ggc cag tca gta gac gca cag acc agc gca cga aac ctt ccg atc tac 211															
Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr 35															
caa tcc acc gct ttc gtg ttc gac tcc gct gag cac gcc aag cag cgt 259															
Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu His Ala Lys Gln Arg 50															
ttc gca ctt gag gat cta ggc cct gtt tac tcc cgc ctc acc aac cca 307															
Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro 65															
acc gtt gag gct ttg gaa aac cgc atc gct tcc ctc gaa ggt ggc gtc 355															
Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser Leu Glu Gly Gly Val 85															
cac gct gta gcg ttc tcc tcc gga cag gcc gca acc acc aac gcc att 403															
His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile 100															
ctg aac ctg gca gga gcg ggc gac cac atc gtc acc tcc cca cgc ctc 451															
Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val Thr Ser Pro Arg Leu 115															
tac ggt ggc acc gag act cta ttc ctt atc act ctt aac cgc ctg ggt 499															
Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly 130															
ctc gat gtt tcc ttc gtg gaa aac ccc gac gac cct gag tcc tgg cag 547															

Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln  
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gca gcc gtt cag cca aac acc aaa gca ttc ttc ggc gag act ttc gcc 595  
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 150 155 160 165

aac cca cag gca gac gtc 613  
 Asn Pro Gln Ala Asp Val  
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<210> 252  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 252  
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Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu  
 35 40 45

His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser  
 50 55 60

Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser  
 65 70 75 80

Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala  
 85 90 95

Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val  
 100 105 110

Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr  
 115 120 125

Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp  
 130 135 140

Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe  
 145 150 155 160

Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val  
 165 170

<210> 253  
 <211> 1812  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1789)  
 <223> RXC00164

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ggccagcctg ccgcaagtgc ggcgcgaggt ggcccggcag gtg ggt cgt att ccg 115  
Val Gly Arg Ile Pro  
1 5

cgg gcg aag tgg tgg ttt tta ggc gcg ctg gtg ttg ctg agt gcg ggc 163  
Arg Ala Lys Trp Trp Phe Leu Gly Ala Leu Val Leu Leu Ser Ala Gly  
10 15 20

gct tat gcg tcg gtg ctg gtg ccg cag gtg ctg ggg cgg att gtg gat 211  
Ala Tyr Ala Ser Val Leu Val Pro Gln Val Leu Gly Arg Ile Val Asp  
25 30 35

ctg gtg tcc gat ggc gcg cag atg cgt gat ttt gtt gag ctc agt gtg 259  
Leu Val Ser Asp Gly Ala Gln Met Arg Asp Phe Val Glu Leu Ser Val  
40 45 50

att ctc att gcg gtg gca att gcc ggc gcg gtg ctc agt gcg tgc ggg 307  
Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val Leu Ser Ala Cys Gly  
55 60 65

ttc tat gtg gtg tcg cgg att tct gag aag att atc gcc aat ttg agg 355  
Phe Tyr Val Val Ser Arg Ile Ser Glu Lys Ile Ile Ala Asn Leu Arg  
70 75 80 85

gaa gat atg gtg ggc acc gcg ctt ggg ttg ccc acg cac cag gtg gaa 403  
Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro Thr His Gln Val Glu  
90 95 100

gat gcg ggc tct ggc gat ttg gtg agc cgc tcc acc gat gat gtc tcc 451  
Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser Thr Asp Asp Val Ser  
105 110 115

gag cta tcc gca gcg gtg aca gag acc gtc ccg att tta agt tcc tca 499  
Glu Leu Ser Ala Ala Val Thr Glu Thr Val Pro Ile Leu Ser Ser Ser  
120 125 130

ctg ttt acc att gcc gcg acg atc att gcg ctg ttt tct ttg gac tgg 547  
Leu Phe Thr Ile Ala Ala Thr Ile Ile Ala Leu Phe Ser Leu Asp Trp  
135 140 145

caa ttt gtg ctc att cct gtc gtg gtg gcg ccg gtg tac tac ttc gcg 595  
Gln Phe Val Leu Ile Pro Val Val Val Ala Pro Val Tyr Tyr Phe Ala  
150 155 160 165

tcc aag cac tat ttg agc aag gcg ccg gat cgg tat gcg gca gaa cgc 643  
Ser Lys His Tyr Leu Ser Lys Ala Pro Asp Arg Tyr Ala Ala Glu Arg  
170 175 180

gcg gcg atg gcg gag cgt gcg cga aag gta ctt gag gct att cgc ggg 691  
Ala Ala Met Ala Glu Arg Ala Arg Lys Val Leu Glu Ala Ile Arg Gly  
185 190 195

cgt gca act gtg cgg gcg tat tcc atg gaa gat gcc atg cat aat cag 739  
Arg Ala Thr Val Arg Ala Tyr Ser Met Glu Asp Ala Met His Asn Gln  
200 205 210

att gat cag gcg tcg tgg tct gtg gtg gtc aag ggt att cgt gcg cgc 787



Ile Asp Gln Ala Ser Trp Ser Val Val Val Lys Gly Ile Arg Ala Arg  
 215 220 225  
 acc acc atg ttg att ttg aac atg tgg atg ctg ttt gcg gaa ttc ctc 835  
 Thr Thr Met Leu Ile Leu Asn Met Trp Met Leu Phe Ala Glu Phe Leu  
 230 235 240 245  
 atg ctc gcg gtc gcg ttg gtg atc ggc tac aag ctg gtc att gat aat 883  
 Met Leu Ala Val Ala Leu Val Ile Gly Tyr Lys Leu Val Ile Asp Asn  
 250 255 260  
 gcg ctg acg atc ggc gcg gtt acc ggt gcc gtg ctg atg att att cgt 931  
 Ala Leu Thr Ile Gly Ala Val Thr Gly Ala Val Leu Met Ile Ile Arg  
 265 270 275  
 ctg cgt ggc ccg atg aat atg ttc atg cgc gtg ctc gac acc att caa 979  
 Leu Arg Gly Pro Met Asn Met Phe Met Arg Val Leu Asp Thr Ile Gln  
 280 285 290  
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 Ser Gly Tyr Ala Ser Leu Ala Arg Ile Val Gly Val Val Ala Asp Pro  
 295 300 305  
 ccg att cct gtg ccc gac agc ggt gtg aaa gca cct cag ggc aaa gtg  
 1075  
 Pro Ile Pro Val Pro Asp Ser Gly Val Lys Ala Pro Gln Gly Lys Val  
 310 315 320 325  
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 1123  
 Glu Leu Arg Asn Val Ser Phe Ser Tyr Gly Asp Ser Trp Ala Val Lys  
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 Asp Ile Asp Ile Thr Ile Asn Ser Gly Glu Thr Val Ala Leu Val Gly  
 345 350 355  
 gca tct ggc gca ggt aag acg acg gtc gcc gcc ttg ctg gcg ggc ttg  
 1219  
 Ala Ser Gly Ala Gly Lys Thr Thr Val Ala Ala Leu Leu Ala Gly Leu  
 360 365 370  
 cgg gtg cca gat caa ggg caa gtg ctt gtc gac gac ttc ccc gtc tct  
 1267  
 Arg Val Pro Asp Gln Gly Gln Val Leu Val Asp Asp Phe Pro Val Ser  
 375 380 385  
 cac ctc tct gac cgc gag cgt atc gcc cgc ttg gcc atg gtc agc cag  
 1315  
 His Leu Ser Asp Arg Glu Arg Ile Ala Arg Leu Ala Met Val Ser Gln  
 390 395 400 405  
 gag gtt cat gtt ttc tcc ggc acg ctg cgc cag gat ctc acc ttg gct  
 1363  
 Glu Val His Val Phe Ser Gly Thr Leu Arg Gln Asp Leu Thr Leu Ala  
 410 415 420  
 aaa cca gat gcc tcc gat gag gaa tta gcg cat gct ctt ggg caa gtt  
 1411

Lys Pro Asp Ala Ser Asp Glu Glu Leu Ala His Ala Leu Gly Gln Val  
 425 430 435

aat gcc ctt gac tgg ttg gag agt ctt cca gaa gga ctg gac acg gtc  
 1459

Asn Ala Leu Asp Trp Leu Glu Ser Leu Pro Glu Gly Leu Asp Thr Val  
 440 445 450

gtt ggt gcg cga gga atc cag cta gaa cca gtg gtg gct cag cag ttg  
 1507

Val Gly Ala Arg Gly Ile Gln Leu Glu Pro Val Val Ala Gln Gln Leu  
 455 460 465

gcg ttg gcc cgg gtg ttg ttg ctc aat ccg gcg atc gtc atc atg gat  
 1555

Ala Leu Ala Arg Val Leu Leu Leu Asn Pro Ala Ile Val Ile Met Asp  
 470 475 480 485

gaa gcc acg gca gaa gca gga tcg gcg ggt gcc agc gca ctg gaa gag  
 1603

Glu Ala Thr Ala Glu Ala Gly Ser Ala Gly Ala Ser Ala Leu Glu Glu  
 490 495 500

gct gca gat gca gtg agc aag aac cgt tcc gca ttg gtg gtg gcg cac  
 1651

Ala Ala Asp Ala Val Ser Lys Asn Arg Ser Ala Leu Val Val Ala His  
 505 510 515

cgg ttg gat cag gca tcg cgg gct gat cag att ctg gtg atg gat aag  
 1699

Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile Leu Val Met Asp Lys  
 520 525 530

ggg gag gtt gtg gaa tcc ggt act cac cag gag tta ttg gat cac ggg  
 1747

Gly Glu Val Val Glu Ser Gly Thr His Gln Glu Leu Leu Asp His Gly  
 535 540 545

ggt att tat cag cgt ctg tgg act gcg tgg agt gtc gga aga  
 1789

Gly Ile Tyr Gln Arg Leu Trp Thr Ala Trp Ser Val Gly Arg  
 550 555 560

tagttgactg ttcaatgcgt tga  
 1812

<210> 254

<211> 563

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

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Leu Leu Ser Ala Gly Ala Tyr Ala Ser Val Leu Val Pro Gln Val Leu  
 20 25 30

Gly Arg Ile Val Asp Leu Val Ser Asp Gly Ala Gln Met Arg Asp Phe  
 35 40 45

Val Glu Leu Ser Val Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val  
 50 55 60  
 Leu Ser Ala Cys Gly Phe Tyr Val Val Ser Arg Ile Ser Glu Lys Ile  
 65 70 75 80  
 Ile Ala Asn Leu Arg Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro  
 85 90 95  
 Thr His Gln Val Glu Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser  
 100 105 110  
 Thr Asp Asp Val Ser Glu Leu Ser Ala Ala Val Thr Glu Thr Val Pro  
 115 120 125  
 Ile Leu Ser Ser Ser Leu Phe Thr Ile Ala Ala Thr Ile Ile Ala Leu  
 130 135 140  
 Phe Ser Leu Asp Trp Gln Phe Val Leu Ile Pro Val Val Val Ala Pro  
 145 150 155 160  
 Val Tyr Tyr Phe Ala Ser Lys His Tyr Leu Ser Lys Ala Pro Asp Arg  
 165 170 175  
 Tyr Ala Ala Glu Arg Ala Ala Met Ala Glu Arg Ala Arg Lys Val Leu  
 180 185 190  
 Glu Ala Ile Arg Gly Arg Ala Thr Val Arg Ala Tyr Ser Met Glu Asp  
 195 200 205  
 Ala Met His Asn Gln Ile Asp Gln Ala Ser Trp Ser Val Val Val Lys  
 210 215 220  
 Gly Ile Arg Ala Arg Thr Thr Met Leu Ile Leu Asn Met Trp Met Leu  
 225 230 235 240  
 Phe Ala Glu Phe Leu Met Leu Ala Val Ala Leu Val Ile Gly Tyr Lys  
 245 250 255  
 Leu Val Ile Asp Asn Ala Leu Thr Ile Gly Ala Val Thr Gly Ala Val  
 260 265 270  
 Leu Met Ile Ile Arg Leu Arg Gly Pro Met Asn Met Phe Met Arg Val  
 275 280 285  
 Leu Asp Thr Ile Gln Ser Gly Tyr Ala Ser Leu Ala Arg Ile Val Gly  
 290 295 300  
 Val Val Ala Asp Pro Pro Ile Pro Val Pro Asp Ser Gly Val Lys Ala  
 305 310 315 320  
 Pro Gln Gly Lys Val Glu Leu Arg Asn Val Ser Phe Ser Tyr Gly Asp  
 325 330 335  
 Ser Trp Ala Val Lys Asp Ile Asp Ile Thr Ile Asn Ser Gly Glu Thr  
 340 345 350  
 Val Ala Leu Val Gly Ala Ser Gly Ala Gly Lys Thr Thr Val Ala Ala  
 355 360 365

Leu Leu Ala Gly Leu Arg Val Pro Asp Gln Gly Gln Val Leu Val Asp  
 370 375 380  
 Asp Phe Pro Val Ser His Leu Ser Asp Arg Glu Arg Ile Ala Arg Leu  
 385 390 395 400  
 Ala Met Val Ser Gln Glu Val His Val Phe Ser Gly Thr Leu Arg Gln  
 405 410 415  
 Asp Leu Thr Leu Ala Lys Pro Asp Ala Ser Asp Glu Glu Leu Ala His  
 420 425 430  
 Ala Leu Gly Gln Val Asn Ala Leu Asp Trp Leu Glu Ser Leu Pro Glu  
 435 440 445  
 Gly Leu Asp Thr Val Val Gly Ala Arg Gly Ile Gln Leu Glu Pro Val  
 450 455 460  
 Val Ala Gln Gln Leu Ala Leu Ala Arg Val Leu Leu Leu Asn Pro Ala  
 465 470 475 480  
 Ile Val Ile Met Asp Glu Ala Thr Ala Glu Ala Gly Ser Ala Gly Ala  
 485 490 495  
 Ser Ala Leu Glu Glu Ala Ala Asp Ala Val Ser Lys Asn Arg Ser Ala  
 500 505 510  
 Leu Val Val Ala His Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile  
 515 520 525  
 Leu Val Met Asp Lys Gly Glu Val Val Glu Ser Gly Thr His Gln Glu  
 530 535 540  
 Leu Leu Asp His Gly Gly Ile Tyr Gln Arg Leu Trp Thr Ala Trp Ser  
 545 550 555 560  
 Val Gly Arg

<210> 255  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1690)  
 <223> RXC01191

<400> 255  
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 cgtgttggtg gccgtcgcgg gggttggtagg gccctgggcg gtg ggt gga ctc gtc 115  
 Val Gly Gly Leu Val  
 1 5  
 gat aag ctc ctt gca acc ccg agc atg cgc gac gtt gta gtg ttc gcg 163  
 Asp Lys Leu Leu Ala Thr Pro Ser Met Arg Asp Val Val Val Phe Ala  
 10 15 20

ctg ctt atc gtg gct ggc ggc gtt gtt tgc agc ctg ggc acg tgg tgg	211
Leu Leu Ile Val Ala Gly Gly Val Val Ser Ser Leu Gly Thr Trp Trp	
25 30 35	
ggc agc gcg ctg atg gcg cgc gcg ttg gag ccg gcg atc gcg ggg ctg	259
Gly Ser Ala Leu Met Ala Arg Ala Leu Glu Pro Ala Ile Ala Gly Leu	
40 45 50	
cgc gag gat gtg ttg cgc gcg gcg gtg agt ttg gat gcg aac acg att	307
Arg Glu Asp Val Leu Arg Ala Val Ser Leu Asp Ala Asn Thr Ile	
55 60 65	
gaa acg gcg ggg cgc ggc gac gtg att tgc cgt atc gcg gat gat tgc	355
Glu Thr Ala Gly Arg Gly Asp Val Ile Ser Arg Ile Ala Asp Asp Ser	
70 75 80 85	
cgg gag gtg tcc act gcg gcg agc acc gtg gtg ccg ctg atg gtg cag	403
Arg Glu Val Ser Thr Ala Ala Ser Thr Val Val Pro Leu Met Val Gln	
90 95 100	
gcg ggc ttt acc gtg gtg att tcc gcg ttt ggc atg gcg gcg gtt gat	451
Ala Gly Phe Thr Val Val Ile Ser Ala Phe Gly Met Ala Ala Val Asp	
105 110 115	
tgg cgc ctc ggc ctt gtc ggt ttg gtc gcg atc ccg ctg tat tgg acc	499
Trp Arg Leu Gly Leu Val Gly Leu Val Ala Ile Pro Leu Tyr Trp Thr	
120 125 130	
acg ttg cgc gtc tat tta ccc cgc tca ggt ccg ctt tat acg cgt gag	547
Thr Leu Arg Val Tyr Leu Pro Arg Ser Gly Pro Leu Tyr Thr Arg Glu	
135 140 145	
cgc gag gcc ttt ggg gtg cgc acg cag ccg ctt gtc ggc gca gtc gaa	595
Arg Glu Ala Phe Gly Val Arg Thr Gln Arg Leu Val Gly Ala Val Glu	
150 155 160 165	
ggc gcg gaa acc ttg cgc gct ttc cgc gca gaa gat aca gaa tta aag	643
Gly Ala Glu Thr Leu Arg Ala Phe Arg Ala Glu Asp Thr Glu Leu Lys	
170 175 180	
cgt atc gac gca gcc tcc ggc gaa gcc cgc gac att tcc att tct gtt	691
Arg Ile Asp Ala Ala Ser Gly Glu Ala Arg Asp Ile Ser Ile Ser Val	
185 190 195	
ttc agg ttc ctc aca tgg gca ttt tcc cgc aac aac cgc gcg gaa tgc	739
Phe Arg Phe Leu Thr Trp Ala Phe Ser Arg Asn Asn Arg Ala Glu Cys	
200 205 210	
atc acc ctc gtg ctc atc ttg ggc acc ggc ttt tac ctg gtc aac atc	787
Ile Thr Leu Val Leu Ile Leu Gly Thr Gly Phe Tyr Leu Val Asn Ile	
215 220 225	
gat ctg gtc acc gtc ggc gca gtc tca acc gcc gca ctg atc ttc cac	835
Asp Leu Val Thr Val Gly Ala Val Ser Thr Ala Ala Leu Ile Phe His	
230 235 240 245	
cga ctc ttc ggt cca atc ggc acg ctc gtg ggc atg ttc tcc gac atc	883
Arg Leu Phe Gly Pro Ile Gly Thr Leu Val Gly Met Phe Ser Asp Ile	
250 255 260	
caa tcc gcc agc gca tgc ctg atc cgc atg gtg ggc gtt att aac gcg	931

Gln Ser Ala Ser Ala Ser Leu Ile Arg Met Val Gly Val Ile Asn Ala  
 265 270 275

gca tcg aac cag gtc agc ggc acc tcg ccg gcg tct gcc agc acc gct 979  
 Ala Ser Asn Gln Val Ser Gly Thr Ser Pro Ala Ser Ala Ser Thr Ala  
 280 285 290

tta acg ctt ttc gac gtc tcc cac cac tat cac act gca ccc gtc atc  
 1027  
 Leu Thr Leu Phe Asp Val Ser His His Tyr His Thr Ala Pro Val Ile  
 295 300 305

aag aat gca tcc gtg cag ctg gaa cca ggg gaa cac atc gcc att gtg  
 1075  
 Lys Asn Ala Ser Val Gln Leu Glu Pro Gly Glu His Ile Ala Ile Val  
 310 315 320 325

ggt gcg acc ggc gct ggt aaa agc acg ctc gcc ctc att gcg gca ggc  
 1123  
 Gly Ala Thr Gly Ala Gly Lys Ser Thr Leu Ala Leu Ile Ala Ala Gly  
 330 335 340

ctg ctc agc cca act tcc ggg cag gtg gct ctc ggc gga tcg agt ttt  
 1171  
 Leu Leu Ser Pro Thr Ser Gly Gln Val Ala Leu Gly Gly Ser Ser Phe  
 345 350 355

tct aac gtc gaa ccg gaa gca ttg cgc cag aag atc gcg atg gtc agc  
 1219  
 Ser Asn Val Glu Pro Glu Ala Leu Arg Gln Lys Ile Ala Met Val Ser  
 360 365 370

caa gaa atc cac tgc ttc cga gga tct gtt tta gat aat ctt cgt atc  
 1267  
 Gln Glu Ile His Cys Phe Arg Gly Ser Val Leu Asp Asn Leu Arg Ile  
 375 380 385

gca cgc ccc gaa gcc acc gat gcg gac atc cac gcc gtt ctc gcc gat  
 1315  
 Ala Arg Pro Glu Ala Thr Asp Ala Asp Ile His Ala Val Leu Ala Asp  
 390 395 400 405

att ggt gat tcc tgg ttg gag cgc tta ccg caa ggc ata gac acc atc  
 1363  
 Ile Gly Asp Ser Trp Leu Glu Arg Leu Pro Gln Gly Ile Asp Thr Ile  
 410 415 420

gtg ggt gat ggc gct ttc cgt tta acc tct gtg gaa aac cag atc atg  
 1411  
 Val Gly Asp Gly Ala Phe Arg Leu Thr Ser Val Glu Asn Gln Ile Met  
 425 430 435

gcg ctt gct cgc gta cat ttg gcc gac cta gca atc gtc atc ctt gat  
 1459  
 Ala Leu Ala Arg Val His Leu Ala Asp Leu Ala Ile Val Ile Leu Asp  
 440 445 450

gaa gca acg gct gaa tca ggc tct gat cat gca aaa cag ctt gaa gat  
 1507  
 Glu Ala Thr Ala Glu Ser Gly Ser Asp His Ala Lys Gln Leu Glu Asp  
 455 460 465

gca gcc ctt aaa gtc act gaa aac aga tca gcc atc atc gtg gct cac  
1555

Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala Ile Ile Val Ala His  
470 475 480 485

cgc ctc aac caa gcg aaa acc gcc gat cgc atc atc gtc atg gac tcc  
1603

Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile Ile Val Met Asp Ser  
490 495 500

gga gaa atc ata gaa tct gga acc cat gaa gag ctt cga gcg atc ggc  
1651

Gly Glu Ile Ile Glu Ser Gly Thr His Glu Glu Leu Arg Ala Ile Gly  
505 510 515

ggc cga tat gaa caa ctg tgg act gcg tgg tct gcg cgc taattagcca  
1700

Gly Arg Tyr Glu Gln Leu Trp Thr Ala Trp Ser Ala Arg  
520 525 530

cccaagacca cgc  
1713

<210> 256

<211> 530

<212> PRT

<213> Corynebacterium glutamicum

<400> 256

Val Gly Gly Leu Val Asp Lys Leu Leu Ala Thr Pro Ser Met Arg Asp  
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Val Val Val Phe Ala Leu Leu Ile Val Ala Gly Gly Val Val Ser Ser  
20 25 30

Leu Gly Thr Trp Trp Gly Ser Ala Leu Met Ala Arg Ala Leu Glu Pro  
35 40 45

Ala Ile Ala Gly Leu Arg Glu Asp Val Leu Arg Ala Ala Val Ser Leu  
50 55 60

Asp Ala Asn Thr Ile Glu Thr Ala Gly Arg Gly Asp Val Ile Ser Arg  
65 70 75 80

Ile Ala Asp Asp Ser Arg Glu Val Ser Thr Ala Ala Ser Thr Val Val  
85 90 95

Pro Leu Met Val Gln Ala Gly Phe Thr Val Val Ile Ser Ala Phe Gly  
100 105 110

Met Ala Ala Val Asp Trp Arg Leu Gly Leu Val Gly Leu Val Ala Ile  
115 120 125

Pro Leu Tyr Trp Thr Thr Leu Arg Val Tyr Leu Pro Arg Ser Gly Pro  
130 135 140

Leu Tyr Thr Arg Glu Arg Glu Ala Phe Gly Val Arg Thr Gln Arg Leu  
145 150 155 160

Val Gly Ala Val Glu Gly Ala Glu Thr Leu Arg Ala Phe Arg Ala Glu  
 165 170 175  
 Asp Thr Glu Leu Lys Arg Ile Asp Ala Ala Ser Gly Glu Ala Arg Asp  
 180 185 190  
 Ile Ser Ile Ser Val Phe Arg Phe Leu Thr Trp Ala Phe Ser Arg Asn  
 195 200 205  
 Asn Arg Ala Glu Cys Ile Thr Leu Val Leu Ile Leu Gly Thr Gly Phe  
 210 215 220  
 Tyr Leu Val Asn Ile Asp Leu Val Thr Val Gly Ala Val Ser Thr Ala  
 225 230 235 240  
 Ala Leu Ile Phe His Arg Leu Phe Gly Pro Ile Gly Thr Leu Val Gly  
 245 250 255  
 Met Phe Ser Asp Ile Gln Ser Ala Ser Ala Ser Leu Ile Arg Met Val  
 260 265 270  
 Gly Val Ile Asn Ala Ala Ser Asn Gln Val Ser Gly Thr Ser Pro Ala  
 275 280 285  
 Ser Ala Ser Thr Ala Leu Thr Leu Phe Asp Val Ser His His Tyr His  
 290 295 300  
 Thr Ala Pro Val Ile Lys Asn Ala Ser Val Gln Leu Glu Pro Gly Glu  
 305 310 315 320  
 His Ile Ala Ile Val Gly Ala Thr Gly Ala Gly Lys Ser Thr Leu Ala  
 325 330 335  
 Leu Ile Ala Ala Gly Leu Leu Ser Pro Thr Ser Gly Gln Val Ala Leu  
 340 345 350  
 Gly Gly Ser Ser Phe Ser Asn Val Glu Pro Glu Ala Leu Arg Gln Lys  
 355 360 365  
 Ile Ala Met Val Ser Gln Glu Ile His Cys Phe Arg Gly Ser Val Leu  
 370 375 380  
 Asp Asn Leu Arg Ile Ala Arg Pro Glu Ala Thr Asp Ala Asp Ile His  
 385 390 395 400  
 Ala Val Leu Ala Asp Ile Gly Asp Ser Trp Leu Glu Arg Leu Pro Gln  
 405 410 415  
 Gly Ile Asp Thr Ile Val Gly Asp Gly Ala Phe Arg Leu Thr Ser Val  
 420 425 430  
 Glu Asn Gln Ile Met Ala Leu Ala Arg Val His Leu Ala Asp Leu Ala  
 435 440 445  
 Ile Val Ile Leu Asp Glu Ala Thr Ala Glu Ser Gly Ser Asp His Ala  
 450 455 460  
 Lys Gln Leu Glu Asp Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala  
 465 470 475 480  
 Ile Ile Val Ala His Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile



485

490

495

Ile Val Met Asp Ser Gly Glu Ile Ile Glu Ser Gly Thr His Glu Glu  
                   500                                  505                                  510

Leu Arg Ala Ile Gly Gly Arg Tyr Glu Gln Leu Trp Thr Ala Trp Ser  
           515                                  520                                  525

Ala Arg  
       530

<210> 257  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1369)  
 <223> RXA02646

<400> 257  
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catgagtgaa acatacgtgt ctgagaaaag tccaggagtg atg gct agc gga gcg 115  
   Met Ala Ser Gly Ala  
   1                                  5

gag ctg att cgt gcc gcc gac att caa acg gcg cag gca cga att tcc 163  
 Glu Leu Ile Arg Ala Ala Asp Ile Gln Thr Ala Gln Ala Arg Ile Ser  
                                   10                                  15                                  20

tcc gtc att gca cca act cca ttg cag tat tgc cct cgt ctt tct gag 211  
 Ser Val Ile Ala Pro Thr Pro Leu Gln Tyr Cys Pro Arg Leu Ser Glu  
                                   25                                  30                                  35

gaa acc gga gcg gaa atc tac ctt aag cgt gag gat ctg cag gat gtt 259  
 Glu Thr Gly Ala Glu Ile Tyr Leu Lys Arg Glu Asp Leu Gln Asp Val  
                                   40                                  45                                  50

cgt tcc tac aag atc cgc ggt gcg ctg aac tct gga gcg cag ctc acc 307  
 Arg Ser Tyr Lys Ile Arg Gly Ala Leu Asn Ser Gly Ala Gln Leu Thr  
                                   55                                  60                                  65

caa gag cag cgc gat gca ggt atc gtt gcc gca tct gca ggt aac cat 355  
 Gln Glu Gln Arg Asp Ala Gly Ile Val Ala Ala Ser Ala Gly Asn His  
                                   70                                  75                                  80                                  85

gcc cag ggc gtg gcc tat gtg tgc aag tcc ttg ggc gtt cag gga cgc 403  
 Ala Gln Gly Val Ala Tyr Val Cys Lys Ser Leu Gly Val Gln Gly Arg  
                                   90                                  95                                  100

atc tat gtt cct gtg cag act cca aag caa aag cgt gac cgc atc atg 451  
 Ile Tyr Val Pro Val Gln Thr Pro Lys Gln Lys Arg Asp Arg Ile Met  
                                   105                                  110                                  115

gtt cac ggc gga gag ttt gtc tcc ttg gtg gtc act ggc aat aac ttc 499  
 Val His Gly Gly Glu Phe Val Ser Leu Val Val Thr Gly Asn Asn Phe  
                                   120                                  125                                  130

gac gaa gca tcg gct gca gcg cat gaa gat gca gag cgc acc ggc gca Asp Glu Ala Ser Ala Ala Ala His Glu Asp Ala Glu Arg Thr Gly Ala 135 140 145	547
acg ctg atc gag cct ttc gat gct cgc aac acc gtc atc ggt cag ggc Thr Leu Ile Glu Pro Phe Asp Ala Arg Asn Thr Val Ile Gly Gln Gly 150 155 160 165	595
acc gtg gct gct gag atc ttg tcg cag ctg act tcc atg ggc aag agt Thr Val Ala Ala Glu Ile Leu Ser Gln Leu Thr Ser Met Gly Lys Ser 170 175 180	643
gca gat cac gtg atg gtt cca gtc ggc ggt ggc gga ctt ctt gca ggt Ala Asp His Val Met Val Pro Val Gly Gly Gly Gly Leu Leu Ala Gly 185 190 195	691
gtg gtc agc tac atg gct gat atg gca cct cgc act gcg atc gtt ggt Val Val Ser Tyr Met Ala Asp Met Ala Pro Arg Thr Ala Ile Val Gly 200 205 210	739
atc gaa cca gcg gga gca gca tcc atg cag gct gca ttg cac aat ggt Ile Glu Pro Ala Gly Ala Ala Ser Met Gln Ala Ala Leu His Asn Gly 215 220 225	787
gga cca atc act ttg gag act gtt gat ccc ttt gtg gac ggc gca gca Gly Pro Ile Thr Leu Glu Thr Val Asp Pro Phe Val Asp Gly Ala Ala 230 235 240 245	835
gtc aaa cgt gtc gga gat ctc aac tac acc atc gtg gag aag aac cag Val Lys Arg Val Gly Asp Leu Asn Tyr Thr Ile Val Glu Lys Asn Gln 250 255 260	883
ggt cgc gtg cac atg atg agc gcg acc gag ggc gct gtg tgt act gag Gly Arg Val His Met Met Ser Ala Thr Glu Gly Ala Val Cys Thr Glu 265 270 275	931
atg ctc gat ctt tac caa aac gaa ggc atc atc gcg gag cct gct ggc Met Leu Asp Leu Tyr Gln Asn Glu Gly Ile Ile Ala Glu Pro Ala Gly 280 285 290	979
gcg ctg tct atc gct ggg ttg aag gaa atg tcc ttt gca gct cgc tct 1027 Ala Leu Ser Ile Ala Gly Leu Lys Glu Met Ser Phe Ala Ala Arg Ser 295 300 305	
gtc gtg gtg tgc atc atc tct ggt ggc aac aac gat gtg ctg cgt tat 1075 Val Val Val Cys Ile Ile Ser Gly Gly Asn Asn Asp Val Leu Arg Tyr 310 315 320 325	
gcg gaa atc gct gag cgc tcc ttg gtg cgc cgc ggt tta aag cac tac 1123 Ala Glu Ile Ala Glu Arg Ser Leu Val Arg Arg Gly Leu Lys His Tyr 330 335 340	
ttc ttg gtg aac ttc ccg caa aag cct ggt cag ttg cgt cac ttc ctg 1171 Phe Leu Val Asn Phe Pro Gln Lys Pro Gly Gln Leu Arg His Phe Leu 345 350 355	

gaa gat atc ctg gga ccg gat gat gac atc acg ctg ttt gag tac ctc  
1219

Glu Asp Ile Leu Gly Pro Asp Asp Asp Ile Thr Leu Phe Glu Tyr Leu  
360 365 370

aag cgc aac aac cgt gag acc ggt act gcg ttg gtg ggt att cac ttg  
1267

Lys Arg Asn Asn Arg Glu Thr Gly Thr Ala Leu Val Gly Ile His Leu  
375 380 385

agt gaa gca tca gga ttg gat tct ttg ctg gaa cgt atg gag gaa tcg  
1315

Ser Glu Ala Ser Gly Leu Asp Ser Leu Leu Glu Arg Met Glu Glu Ser  
390 395 400 405

gca att gat tcc cgt cgc ctc gag ccg ggc acc cct gag tac gaa tac  
1363

Ala Ile Asp Ser Arg Arg Leu Glu Pro Gly Thr Pro Glu Tyr Glu Tyr  
410 415 420

ttg acc taaacatagc tgaaggccac ctc  
1392

Leu Thr

<210> 258

<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 258

Met Ala Ser Gly Ala Glu Leu Ile Arg Ala Ala Asp Ile Gln Thr Ala  
1 5 10 15

Gln Ala Arg Ile Ser Ser Val Ile Ala Pro Thr Pro Leu Gln Tyr Cys  
20 25 30

Pro Arg Leu Ser Glu Glu Thr Gly Ala Glu Ile Tyr Leu Lys Arg Glu  
35 40 45

Asp Leu Gln Asp Val Arg Ser Tyr Lys Ile Arg Gly Ala Leu Asn Ser  
50 55 60

Gly Ala Gln Leu Thr Gln Glu Gln Arg Asp Ala Gly Ile Val Ala Ala  
65 70 75 80

Ser Ala Gly Asn His Ala Gln Gly Val Ala Tyr Val Cys Lys Ser Leu  
85 90 95

Gly Val Gln Gly Arg Ile Tyr Val Pro Val Gln Thr Pro Lys Gln Lys  
100 105 110

Arg Asp Arg Ile Met Val His Gly Gly Glu Phe Val Ser Leu Val Val  
115 120 125

Thr Gly Asn Asn Phe Asp Glu Ala Ser Ala Ala Ala His Glu Asp Ala  
130 135 140

Glu Arg Thr Gly Ala Thr Leu Ile Glu Pro Phe Asp Ala Arg Asn Thr  
145 150 155 160

Val Ile Gly Gln Gly Thr Val Ala Ala Glu Ile Leu Ser Gln Leu Thr  
 165 170 175  
 Ser Met Gly Lys Ser Ala Asp His Val Met Val Pro Val Gly Gly Gly  
 180 185 190  
 Gly Leu Leu Ala Gly Val Val Ser Tyr Met Ala Asp Met Ala Pro Arg  
 195 200 205  
 Thr Ala Ile Val Gly Ile Glu Pro Ala Gly Ala Ala Ser Met Gln Ala  
 210 215 220  
 Ala Leu His Asn Gly Gly Pro Ile Thr Leu Glu Thr Val Asp Pro Phe  
 225 230 235 240  
 Val Asp Gly Ala Ala Val Lys Arg Val Gly Asp Leu Asn Tyr Thr Ile  
 245 250 255  
 Val Glu Lys Asn Gln Gly Arg Val His Met Met Ser Ala Thr Glu Gly  
 260 265 270  
 Ala Val Cys Thr Glu Met Leu Asp Leu Tyr Gln Asn Glu Gly Ile Ile  
 275 280 285  
 Ala Glu Pro Ala Gly Ala Leu Ser Ile Ala Gly Leu Lys Glu Met Ser  
 290 295 300  
 Phe Ala Ala Arg Ser Val Val Val Cys Ile Ile Ser Gly Gly Asn Asn  
 305 310 315 320  
 Asp Val Leu Arg Tyr Ala Glu Ile Ala Glu Arg Ser Leu Val Arg Arg  
 325 330 335  
 Gly Leu Lys His Tyr Phe Leu Val Asn Phe Pro Gln Lys Pro Gly Gln  
 340 345 350  
 Leu Arg His Phe Leu Glu Asp Ile Leu Gly Pro Asp Asp Asp Ile Thr  
 355 360 365  
 Leu Phe Glu Tyr Leu Lys Arg Asn Asn Arg Glu Thr Gly Thr Ala Leu  
 370 375 380  
 Val Gly Ile His Leu Ser Glu Ala Ser Gly Leu Asp Ser Leu Leu Glu  
 385 390 395 400  
 Arg Met Glu Glu Ser Ala Ile Asp Ser Arg Arg Leu Glu Pro Gly Thr  
 405 410 415  
 Pro Glu Tyr Glu Tyr Leu Thr  
 420

<210> 259  
 <211> 966  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101) .. (943)

&lt;223&gt; RXA00766

&lt;400&gt; 259

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ctacggcggg tccatccggc aacaaaaccc caacctacca atg gtt ttt tgg gac 115  
Met Val Phe Trp Asp  
1 5

gat gca gcc tta acc cga ggc gat ggc atc ttt gaa aca ctc ctc atc 163  
Asp Ala Ala Leu Thr Arg Gly Asp Gly Ile Phe Glu Thr Leu Leu Ile  
10 15 20

cgc gac gga cat gcc tgc aac gtg cgc cga cac gga gaa cgc ttc aaa 211  
Arg Asp Gly His Ala Cys Asn Val Arg Arg His Gly Glu Arg Phe Lys  
25 30 35

gca tcg gca gca cta ttg gga ctg cca gag ccg atc ctg gaa gac tgg 259  
Ala Ser Ala Ala Leu Leu Gly Leu Pro Glu Pro Ile Leu Glu Asp Trp  
40 45 50

gaa aaa gcc acc caa atg ggc atc gaa tcc tgg tac tcc cac ccc aac 307  
Glu Lys Ala Thr Gln Met Gly Ile Glu Ser Trp Tyr Ser His Pro Asn  
55 60 65

gca ggc gag gcc tca tgc acc tgg acg ctc agc cga ggt cgt tcc tcc 355  
Ala Gly Glu Ala Ser Cys Thr Trp Thr Leu Ser Arg Gly Arg Ser Ser  
70 75 80 85

acg ggg ctg gcc tca gga tgg tta acc atc acc cca gtc tcc tcc gac 403  
Thr Gly Leu Ala Ser Gly Trp Leu Thr Ile Thr Pro Val Ser Ser Asp  
90 95 100

aaa ctg gcg caa cgt gaa cac ggt gta tcg gtc atg acc agt tca aga 451  
Lys Leu Ala Gln Arg Glu His Gly Val Ser Val Met Thr Ser Ser Arg  
105 110 115

gga tat tcc atc gac acc ggc ctc ccc gga atc gga aaa gcc acc cga 499  
Gly Tyr Ser Ile Asp Thr Gly Leu Pro Gly Ile Gly Lys Ala Thr Arg  
120 125 130

ggc gag cta tct aaa gtg gaa cga acc ccc gca cca tgg ctg aca gtc 547  
Gly Glu Leu Ser Lys Val Glu Arg Thr Pro Ala Pro Trp Leu Thr Val  
135 140 145

ggc gcc aaa aca cta gcc tac gca gca aac atg gca gcc ctg cgc tac 595  
Gly Ala Lys Thr Leu Ala Tyr Ala Ala Asn Met Ala Ala Leu Arg Tyr  
150 155 160 165

gcc aaa tca aac gga ttc gac gat gtg atc ttc acc gat ggc gac cgc 643  
Ala Lys Ser Asn Gly Phe Asp Asp Val Ile Phe Thr Asp Gly Asp Arg  
170 175 180

gtt cta gaa ggc gcc acc tcc acc gta gtg agt ttc aaa ggc gac aaa 691  
Val Leu Glu Gly Ala Thr Ser Thr Val Val Ser Phe Lys Gly Asp Lys  
185 190 195

atc cgc acc cct tca ccc ggt ggc gac att ctc ccc gga acc acc caa 739  
Ile Arg Thr Pro Ser Pro Gly Gly Asp Ile Leu Pro Gly Thr Thr Gln  
200 205 210

gca gca ctc ttt gca cac gca acc gaa aaa gga tgg cga tgt aaa gaa 787  
 Ala Ala Leu Phe Ala His Ala Thr Glu Lys Gly Trp Arg Cys Lys Glu  
 215 220 225

aaa gac tta agc att gac gat ctt ttc gga gcc gac agc gtg tgg cta 835  
 Lys Asp Leu Ser Ile Asp Asp Leu Phe Gly Ala Asp S r Val Trp Leu  
 230 235 240 245

gtg tcc tcc gtc cgc gga cca gtt cgg gtg acc agg ctc gat gga cac 883  
 Val Ser Ser Val Arg Gly Pro Val Arg Val Thr Arg Leu Asp Gly His  
 250 255 260

aaa tta cgg aaa cca gac aat gaa aaa gaa atc aag gcg ctg att acc 931  
 Lys Leu Arg Lys Pro Asp Asn Glu Lys Glu Ile Lys Ala Leu Ile Thr  
 265 270 275

aaa gct ctg ggg tagaggctgg cgctgggact tgc 966  
 Lys Ala Leu Gly  
 280

<210> 260  
 <211> 281  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 260  
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 Gly Glu Arg Phe Lys Ala Ser Ala Ala Leu Leu Gly Leu Pro Glu Pro  
 35 40 45  
 Ile Leu Glu Asp Trp Glu Lys Ala Thr Gln Met Gly Ile Glu Ser Trp  
 50 55 60  
 Tyr Ser His Pro Asn Ala Gly Glu Ala Ser Cys Thr Trp Thr Leu Ser  
 65 70 75 80  
 Arg Gly Arg Ser Ser Thr Gly Leu Ala Ser Gly Trp Leu Thr Ile Thr  
 85 90 95  
 Pro Val Ser Ser Asp Lys Leu Ala Gln Arg Glu His Gly Val Ser Val  
 100 105 110  
 Met Thr Ser Ser Arg Gly Tyr Ser Ile Asp Thr Gly Leu Pro Gly Ile  
 115 120 125  
 Gly Lys Ala Thr Arg Gly Glu Leu Ser Lys Val Glu Arg Thr Pro Ala  
 130 135 140  
 Pro Trp Leu Thr Val Gly Ala Lys Thr Leu Ala Tyr Ala Ala Asn Met  
 145 150 155 160  
 Ala Ala Leu Arg Tyr Ala Lys Ser Asn Gly Phe Asp Asp Val Ile Phe  
 165 170 175  
 Thr Asp Gly Asp Arg Val Leu Glu Gly Ala Thr Ser Thr Val Val Ser

180 185 190  
 Phe Lys Gly Asp Lys Ile Arg Thr Pro Ser Pro Gly Gly Asp Ile Leu  
 195 200 205  
 Pro Gly Thr Thr Gln Ala Ala Leu Phe Ala His Ala Thr Glu Lys Gly  
 210 215 220  
 Trp Arg Cys Lys Glu Lys Asp Leu Ser Ile Asp Asp Leu Phe Gly Ala  
 225 230 235 240  
 Asp Ser Val Trp Leu Val Ser Ser Val Arg Gly Pro Val Arg Val Thr  
 245 250 255  
 Arg Leu Asp Gly His Lys Leu Arg Lys Pro Asp Asn Glu Lys Glu Ile  
 260 265 270  
 Lys Ala Leu Ile Thr Lys Ala Leu Gly  
 275 280

<210> 261  
 <211> 1224  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1201)  
 <223> RXN01690

<400> 261  
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 Met Thr Ser Leu Glu 5  
 1  
 ttc aca gta acc cgt acc gaa aat ccg acg tca ccc gat cgt ctg aag 163  
 Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser Pro Asp Arg Leu Lys 20  
 10 15  
 gaa att ctt gcc gca ccg aag ttc ggt aag ttc ttc acc gac cac atg 211  
 Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe Phe Thr Asp His Met 35  
 25 30  
 gtg acc att gac tgg aac gag tcg gaa ggc tgg cac aac gcc caa tta 259  
 Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp His Asn Ala Gln Leu 50  
 40 45  
 gtg cca tac gcg ccg att cct atg gat cct gcc acc acc gta ttc cac 307  
 Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala Thr Thr Val Phe His 65  
 55 60  
 tac gga cag gca att ttt gag gga att aag gcc tac cgc cat tcg gac 355  
 Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala Tyr Arg His Ser Asp 85  
 70 75 80  
 gaa acc atc aag act ttc cgt cct gat gaa aac gcc gag cgt atg cag 403  
 Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn Ala Glu Arg Met Gln 100  
 90 95

cgt tca gca gct cga atg gca atg cca cag ttg cca acc gag gac ttt 451  
 Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu Pro Thr Glu Asp Phe  
 105 110 115

att aaa gca ctt gaa ctg ctg gta gac gcg gat cag gat tgg gtt cct 499  
 Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp Gln Asp Trp Val Pro  
 120 125 130

gag tac ggc gga gaa gct tcc ctc tac ctg cgc cca ttc atg atc tcc 547  
 Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg Pro Phe Met Ile Ser  
 135 140 145

acc gaa att ggc ttg ggt gtc agc cca gct gat gcc tac aag ttc ctg 595  
 Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp Ala Tyr Lys Phe Leu  
 150 155 160 165

gtc atc gca tcc cca gtc ggc gct tac ttc acc ggt gga atc aag cct 643  
 Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr Gly Gly Ile Lys Pro  
 170 175 180

gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc gct gca ccc ggc gga 691  
 Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg Ala Ala Pro Gly Gly  
 185 190 195

act ggt gac gcc aaa ttt gct ggc aac tac gcg gct tct ttg ctt gcc 739  
 Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala Ala Ser Leu Leu Ala  
 200 205 210

cag tcc cag gct gcg gaa aag ggc tgt gac cag gtc gta tgg ttg gat 787  
 Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln Val Val Trp Leu Asp  
 215 220 225

gcc atc gag cac aag tac atc gaa gaa atg ggt ggc atg aac ctt ggg 835  
 Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly Gly Met Asn Leu Gly  
 230 235 240 245

ttc atc tac cgc aac ggc gac caa gtc aag cta gtc acc cct gaa ctt 883  
 Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu Val Thr Pro Glu Leu  
 250 255 260

tcc ggc tca cta ctt cca ggc atc acc cgc aag tca ctt cta caa gta 931  
 Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys Ser Leu Leu Gln Val  
 265 270 275

gca cgc gac ttg gga tac gaa gta gaa gag cga aag atc acc acc acc 979  
 Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg Lys Ile Thr Thr Thr  
 280 285 290

gag tgg gaa gaa gac gca aag tct ggc gcc atg acc gag gca ttt gct  
 1027  
 Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met Thr Glu Ala Phe Ala  
 295 300 305

tgc ggt act gca gct gtt atc acc cct gtt ggc acc gtg aaa tca gct  
 1075  
 Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly Thr Val Lys Ser Ala  
 310 315 320 325

cac ggc acc ttc gaa gtg aac aac aat gaa gtc gga gaa atc acg atg  
 1123



His Gly Thr Phe Glu Val Asn Asn Asn Glu Val Gly Glu Ile Thr Met  
 330 335 340

aag ctt cgt gaa acc ctc acc gga att cag caa gga aac gtt gaa gac  
 1171

Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln Gly Asn Val Glu Asp  
 345 350 355

caa aac gga tgg ctt tac cca ctg gtt ggc taaatcaacc gggtttaaga  
 1221

Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly  
 360 365

ccc  
 1224

<210> 262

<211> 367

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Met Thr Ser Leu Glu Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser  
 1 5 10 15

Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe  
 20 25 30

Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp  
 35 40 45

His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala  
 50 55 60

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala  
 65 70 75 80

Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn  
 85 90 95

Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu  
 100 105 110

Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp  
 115 120 125

Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg  
 130 135 140

Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp  
 145 150 155 160

Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr  
 165 170 175

Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg  
 180 185 190

Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala  
 195 200 205

Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln  
 210 215 220

Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly  
 225 230 235 240

Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu  
 245 250 255

Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys  
 260 265 270

Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg  
 275 280 285

Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met  
 290 295 300

Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly  
 305 310 315 320

Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val  
 325 330 335

Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln  
 340 345 350

Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly  
 355 360 365

<210> 263  
 <211> 1076  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1053)  
 <223> FRXA01690

<400> 263

ccc gat cgt ctg aag gaa att ctt gcc gca ccg aag ttc ggt aag ttc	48
Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe	
1 5 10 15	
ttc acc gac cac atg gtg acc att gac tgg aac gag tcg gaa ggc tgg	96
Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp	
20 25 30	
cac aac gcc caa tta gtg cca tac gcg ccg att cct atg gat cct gcc	144
His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala	
35 40 45	
acc acc gta ttc cac tac gga cag gca att ttt gag gga att aag gcc	192
Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala	
50 55 60	
tac cgc cat tcg gac gaa acc atc aag act ttc cgt cct gat gaa aac	240
Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn	

65	70	75	80	
gcc gag cgt atg cag cgt tca gca gct cga atg gca atg cca cag ttg				288
Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu	85	90	95	
cca acc gag gac ttt att aaa gca ctt gaa ctg ctg gta gac gcg gat				336
Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp	100	105	110	
cag gat tgg gtt cct gag tac ggc gga gaa gct tcc ctc tac ctg cgc				384
Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg	115	120	125	
cca ttc atg atc tcc acc gaa att ggc ttg ggt gtc agc cca gct gat				432
Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp	130	135	140	
gcc tac aag ttc ctg gtc atc gca tcc cca gtc ggc gct tac ttc acc				480
Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr	145	150	155	160
ggt gga atc aag cct gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc				528
Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg	165	170	175	
gct gca ccc ggc gga act ggt gac gcc aaa ttt gct ggc aac tac gcg				576
Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala	180	185	190	
gct tct ttg ctt gcc cag tcc cag gct gcg gaa aag ggc tgt gac cag				624
Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln	195	200	205	
gtc gta tgg ttg gat gcc atc gag cac aag tac atc gaa gaa atg ggt				672
Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly	210	215	220	
ggc atg aac ctt ggg ttc atc tac cgc aac ggc gac caa gtc aag cta				720
Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu	225	230	235	240
gtc acc cct gaa ctt tcc ggc tca cta ctt cca ggc atc acc cgc aag				768
Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys	245	250	255	
tca ctt cta caa gta gca cgc gac ttg gga tac gaa gta gaa gag cga				816
Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg	260	265	270	
aag atc acc acc acc gag tgg gaa gaa gac gca aag tct ggc gcc atg				864
Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met	275	280	285	
acc gag gca ttt gct tgc ggt act gca gct gtt atc acc cct gtt ggc				912
Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly	290	295	300	
acc gtg aaa tca gct cac ggc acc ttc gaa gtg aac aac aat gaa gtc				960
Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val	305	310	315	320

gga gaa atc acg atg aag ctt cgt gaa acc ctc acc gga att cag caa

1008

Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln  
325 330 335

gga aac gtt gaa gac caa aac gga tgg ctt tac cca ctg gtt ggc

1053

Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly  
340 345 350

taaatacaacc gggtttaaga ccc

1076

<210> 264

<211> 351

<212> PRT

<213> Corynebacterium glutamicum

<400> 264

Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe  
1 5 10 15

Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp  
20 25 30

His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala  
35 40 45

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala  
50 55 60

Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn  
65 70 75 80

Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu  
85 90 95

Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp  
100 105 110

Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg  
115 120 125

Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp  
130 135 140

Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr  
145 150 155 160

Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg  
165 170 175

Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala  
180 185 190

Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln  
195 200 205

Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly

210	215	220	
Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu			
225	230	235	240
Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys			
	245	250	255
Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg			
	260	265	270
Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met			
	275	280	285
Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly			
	290	295	300
Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val			
305	310	315	320
Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln			
	325	330	335
Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly			
	340	345	350
<210> 265			
<211> 1782			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1759)			
<223> RXN01026			
<400> 265			
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tatagtgaga tttacagatt tttaaaggac ggtgagttcc atg acc agc ccc gtg 115			
Met Thr Ser Pro Val			
1 5			
gag aac agc acc tca act gag aag ctg acc ctg gca gag aag gtg tgg 163			
Glu Asn Ser Thr Ser Thr Glu Lys Leu Thr Leu Ala Glu Lys Val Trp			
10 15 20			
cgc gac cat gtc gtg tcc aag gga gaa aac ggc gag ccc gac ctc ctc 211			
Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp Leu Leu			
25 30 35			
tac atc gac ctg cag ctg ctg cat gaa gtg acc tca cca cag gca ttt 259			
Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln Ala Phe			
40 45 50			
gac ggc ctg cgc atg acc ggc cgt aaa ctg cgc cac cca gaa ctg cac 307			
Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu Leu His			
55 60 65			
ctg gcc acc gaa gac cac aac gtg cca acc gaa ggc atc aag act ggc 355			

Leu	Ala	Thr	Glu	Asp	His	Asn	Val	Pro	Thr	Glu	Gly	Ile	Lys	Thr	Gly	
70					75					80					85	
tca	ctg	ctg	gaa	atc	aac	gac	aag	att	tcc	cgc	ctg	cag	gta	tct	act	403
Ser	Leu	Leu	Glu	Ile	Asn	Asp	Lys	Ile	Ser	Arg	Leu	Gln	Val	Ser	Thr	
				90					95					100		
ctg	cgc	gac	aac	tgt	gaa	gaa	ttc	ggc	gtg	cgc	ctg	cac	cca	atg	ggc	451
Leu	Arg	Asp	Asn	Cys	Glu	Glu	Phe	Gly	Val	Arg	Leu	His	Pro	Met	Gly	
			105					110					115			
gat	gtc	cga	cag	ggc	atc	gtg	cac	acc	gtc	ggc	cca	cag	ctc	ggc	gca	499
Asp	Val	Arg	Gln	Gly	Ile	Val	His	Thr	Val	Gly	Pro	Gln	Leu	Gly	Ala	
			120				125						130			
acc	cag	cca	ggc	atg	acc	att	gtg	tgc	ggc	gac	tcc	cac	acc	tcc	acc	547
Thr	Gln	Pro	Gly	Met	Thr	Ile	Val	Cys	Gly	Asp	Ser	His	Thr	Ser	Thr	
			135			140					145					
cac	ggc	gct	ttt	ggc	tcc	atg	gca	ttc	ggc	atc	ggc	acc	tca	gag	gtt	595
His	Gly	Ala	Phe	Gly	Ser	Met	Ala	Phe	Gly	Ile	Gly	Thr	Ser	Glu	Val	
150					155					160					165	
gag	cac	gtc	atg	gct	act	caa	acc	ctg	cca	ctg	aag	cct	ttc	aag	acc	643
Glu	His	Val	Met	Ala	Thr	Gln	Thr	Leu	Pro	Leu	Lys	Pro	Phe	Lys	Thr	
				170				175						180		
atg	gcc	att	gaa	gtt	act	ggc	gaa	ctg	cag	cca	ggc	gtt	tcc	tcc	aag	691
Met	Ala	Ile	Glu	Val	Thr	Gly	Glu	Leu	Gln	Pro	Gly	Val	Ser	Ser	Lys	
			185					190					195			
gac	ctg	att	ctg	gcg	att	atc	gcc	aag	atc	ggc	acc	ggc	ggc	gga	cag	739
Asp	Leu	Ile	Leu	Ala	Ile	Ile	Ala	Lys	Ile	Gly	Thr	Gly	Gly	Gly	Gln	
			200				205					210				
ggc	tac	gtt	ctg	gaa	tac	cgc	ggc	gaa	gca	atc	cgt	aag	atg	tcc	atg	787
Gly	Tyr	Val	Leu	Glu	Tyr	Arg	Gly	Glu	Ala	Ile	Arg	Lys	Met	Ser	Met	
	215					220					225					
gat	gca	cgc	atg	acc	atg	tgc	aac	atg	tcc	atc	gaa	gct	ggc	gca	cgt	835
Asp	Ala	Arg	Met	Thr	Met	Cys	Asn	Met	Ser	Ile	Glu	Ala	Gly	Ala	Arg	
230					235					240				245		
gcc	ggc	atg	atc	gcc	cca	gac	caa	acc	acc	ttc	gac	tac	gtt	gaa	ggc	883
Ala	Gly	Met	Ile	Ala	Pro	Asp	Gln	Thr	Thr	Phe	Asp	Tyr	Val	Glu	Gly	
				250					255					260		
cgc	gaa	atg	gca	cca	aag	ggc	gcc	gac	tgg	gac	gaa	gca	gtt	gct	tac	931
Arg	Glu	Met	Ala	Pro	Lys	Gly	Ala	Asp	Trp	Asp	Glu	Ala	Val	Ala	Tyr	
			265				270						275			
tgg	aag	acc	ctg	cca	acc	gac	gaa	ggc	gca	acc	ttt	gac	aag	gtc	gta	979
Trp	Lys	Thr	Leu	Pro	Thr	Asp	Glu	Gly	Ala	Thr	Phe	Asp	Lys	Val	Val	
		280					285					290				
gaa	atc	gat	ggc	tcg	gca	ctg	acc	cca	ttc	atc	acc	tgg	ggc	acc	aac	
1027																
Glu	Ile	Asp	Gly	Ser	Ala	Leu	Thr	Pro	Phe	Ile	Thr	Trp	Gly	Thr	Asn	
	295					300					305					

cca ggc cag ggc ctg cca ctg ggc gaa tcc gta cca agc cca gaa gac  
 1075  
 Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro Glu Asp  
 310 315 320 325

ttc acc aac gac aac gac aag gca gca gcc gaa aag gca ctg cag tac  
 1123  
 Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu Gln Tyr  
 330 335 340

atg gac ctg gta cca gga acc cca ctg cgc gac atc aag atc gac acc  
 1171  
 Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile Asp Thr  
 345 350 355

gtc ttc ctg gga tcc tgc acc aac gcc cgc atc gaa gac ctg cag atc  
 1219  
 Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu Gln Ile  
 360 365 370

gcc gct gac atc ctc aag ggc cac aaa atc gcc gac ggc atg cgc atg  
 1267  
 Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met Arg Met  
 375 380 385

atg gtc gtg cct tcc tcc acc tgg atc aag caa gag gca gaa gcg ctc  
 1315  
 Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu Ala Leu  
 390 395 400 405

gga ctg gac aaa atc ttc acc gac gct ggc gct gaa tgg cgt acc gca  
 1363  
 Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg Thr Ala  
 410 415 420

ggc tgc tcc atg tgc ctg ggc atg aac cca gac caa ctg aag cca ggc  
 1411  
 Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys Pro Gly  
 425 430 435

gag cgc tcc gca ttc acc tcc aac cga aac ttc gaa gga cgc caa gga  
 1459  
 Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg Gln Gly  
 440 445 450

cca gga ggc cgc acc cac ctg gta tcc cca gca gtc gca gcc gcc acc  
 1507  
 Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala Ala Thr  
 455 460 465

gaa tcc gcg gac cct gtc ctc acc tgc aga tat cta agg aag gct aga  
 1555  
 Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys Ala Arg  
 470 475 480 485

aaa caa tgg aaa aat tta cca cct aca ccg gcg ttg gcg ttc cac tgc  
 1603  
 Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe His Cys  
 490 495 500

agc gat cca acg tgg aca ccg acc aga tca tcc cag ccg tct acc tca  
1651

Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser Thr Ser  
505 510 515

agc gcg tca ccc gga ccg gct tcg aag acg gac tgt ttt cca act ggc  
1699

Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro Thr Gly  
520 525 530

gcc aaa acg acc cca act ttg tcc tca aca ccg aca cct aca aga acg  
1747

Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr Arg Thr  
535 540 545

gct ccg ttc tcg tagcaggccc tgactttggc acc  
1782

Ala Pro Phe Ser  
550

<210> 266

<211> 553

<212> PRT

<213> Corynebacterium glutamicum

<400> 266

Met Thr Ser Pro Val Glu Asn Ser Thr Ser Thr Glu Lys Leu Thr Leu  
1 5 10 15

Ala Glu Lys Val Trp Arg Asp His Val Val Ser Lys Gly Glu Asn Gly  
20 25 30

Glu Pro Asp Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr  
35 40 45

Ser Pro Gln Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg  
50 55 60

His Pro Glu Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu  
65 70 75 80

Gly Ile Lys Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg  
85 90 95

Leu Gln Val Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg  
100 105 110

Leu His Pro Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly  
115 120 125

Pro Gln Leu Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp  
130 135 140

Ser His Thr Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile  
145 150 155 160

Gly Thr Ser Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu  
165 170 175

Lys Pro Phe Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro



180	185	190
Gly Val Ser Ser Lys Asp Leu Ile Leu Ala Ile Ile Ala Lys Ile Gly 195 200 205		
Thr Gly Gly Gly Gln Gly Tyr Val Leu Glu Tyr Arg Gly Glu Ala Ile 210 215 220		
Arg Lys Met Ser Met Asp Ala Arg Met Thr Met Cys Asn Met Ser Ile 225 230 235 240		
Glu Ala Gly Ala Arg Ala Gly Met Ile Ala Pro Asp Gln Thr Thr Phe 245 250 255		
Asp Tyr Val Glu Gly Arg Glu Met Ala Pro Lys Gly Ala Asp Trp Asp 260 265 270		
Glu Ala Val Ala Tyr Trp Lys Thr Leu Pro Thr Asp Glu Gly Ala Thr 275 280 285		
Phe Asp Lys Val Val Glu Ile Asp Gly Ser Ala Leu Thr Pro Phe Ile 290 295 300		
Thr Trp Gly Thr Asn Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val 305 310 315 320		
Pro Ser Pro Glu Asp Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu 325 330 335		
Lys Ala Leu Gln Tyr Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp 340 345 350		
Ile Lys Ile Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile 355 360 365		
Glu Asp Leu Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala 370 375 380		
Asp Gly Met Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln 385 390 395 400		
Glu Ala Glu Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala 405 410 415		
Glu Trp Arg Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp 420 425 430		
Gln Leu Lys Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe 435 440 445		
Glu Gly Arg Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala 450 455 460		
Val Ala Ala Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr 465 470 475 480		
Leu Arg Lys Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala 485 490 495		
Leu Ala Phe His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser 500 505 510		

Gln Pro Ser Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp  
 515 520 525

Cys Phe Pro Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro  
 530 535 540

Thr Pro Thr Arg Thr Ala Pro Phe Ser  
 545 550

<210> 267

<211> 1625

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1602)

<223> FRXA01026

<400> 267

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Val Trp Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp	
1 5 10 15	
ctc ctc tac atc gac ctg cag ctg ctg cat gaa gtg acc tca cca cag	96
Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln	
20 25 30	
gca ttt gac ggc ctg cgc atg acc ggc cgt aaa ctg cgc cac cca gaa	144
Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu	
35 40 45	
ctg cac ctg gcc acc gaa gac cac aac gtg cca acc gaa ggc atc aag	192
Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu Gly Ile Lys	
50 55 60	
act ggc tca ctg ctg gaa atc aac gac aag att tcc cgc ctg cag gta	240
Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg Leu Gln Val	
65 70 75 80	
tct act ctg cgc gac aac tgt gaa gaa ttc ggc gtg cgc ctg cac cca	288
Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg Leu His Pro	
85 90 95	
atg ggt gat gtc cga cag ggc atc gtg cac acc gtc ggc cca cag ctc	336
Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly Pro Gln Leu	
100 105 110	
ggc gca acc cag cca ggc atg acc att gtg tgc ggt gac tcc cac acc	384
Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp Ser His Thr	
115 120 125	
tcc acc cac ggt gct ttt ggc tcc atg gca ttc ggc atc ggt acc tca	432
Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile Gly Thr Ser	
130 135 140	
gag gtt gag cac gtc atg gct act caa acc ctg cca ctg aag cct ttc	480
Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu Lys Pro Phe	
145 150 155 160	

aag acc atg gcc att gaa gtt act ggt gaa ctg cag cca ggt gtt tcc 528  
Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro Gly Val Ser  
165 170 175

tcc aag gac ctg att ctg gcg att atc gcc aag atc ggc acc ggc ggc 576  
Ser Lys Asp Leu Ile Leu Ala Ile Ile Ala Lys Ile Gly Thr Gly Gly  
180 185 190

gga cag ggc tac gtt ctg gaa tac cgc ggc gaa gca atc cgt aag atg 624  
Gly Gln Gly Tyr Val Leu Glu Tyr Arg Gly Glu Ala Ile Arg Lys Met  
195 200 205

tcc atg gat gca cgc atg acc atg tgc aac atg tcc atc gaa gct ggc 672  
Ser Met Asp Ala Arg Met Thr Met Cys Asn Met Ser Ile Glu Ala Gly  
210 215 220

gca cgt gcc ggc atg atc gcc cca gac caa acc acc ttc gac tac gtt 720  
Ala Arg Ala Gly Met Ile Ala Pro Asp Gln Thr Thr Phe Asp Tyr Val  
225 230 235 240

gaa ggc cgc gaa atg gca cca aag ggc gcc gac tgg gac gaa gca gtt 768  
Glu Gly Arg Glu Met Ala Pro Lys Gly Ala Asp Trp Asp Glu Ala Val  
245 250 255

gct tac tgg aag acc ctg cca acc gac gaa ggc gca acc ttt gac aag 816  
Ala Tyr Trp Lys Thr Leu Pro Thr Asp Glu Gly Ala Thr Phe Asp Lys  
260 265 270

gtc gta gaa atc gat ggc tgc gca ctg acc cca ttc atc acc tgg ggc 864  
Val Val Glu Ile Asp Gly Ser Ala Leu Thr Pro Phe Ile Thr Trp Gly  
275 280 285

acc aac cca ggc cag ggc ctg cca ctg ggc gaa tcc gta cca agc cca 912  
Thr Asn Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro  
290 295 300

gaa gac ttc acc aac gac aac gac aag gca gca gcc gaa aag gca ctg 960  
Glu Asp Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu  
305 310 315 320

cag tac atg gac ctg gta cca gga acc cca ctg cgc gac atc aag atc  
1008  
Gln Tyr Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile  
325 330 335

gac acc gtc ttc ctg gga tcc tgc acc aac gcc cgc atc gaa gac ctg  
1056  
Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu  
340 345 350

cag atc gcc gct gac atc ctc aag ggc cac aaa atc gcc gac ggc atg  
1104  
Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met  
355 360 365

cgc atg atg gtc gtg cct tcc tcc acc tgg atc aag caa gag gca gaa  
1152  
Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu  
370 375 380

gcg ctc gga ctg gac aaa atc ttc acc gac gct ggc gct gaa tgg cgt  
1200

Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg  
385 390 395 400

acc gca ggc tgc tcc atg tgc ctg ggc atg aac cca gac caa ctg aag  
1248

Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys  
405 410 415

cca ggc gag cgc tcc gca ttc acc tcc aac cga aac ttc gaa gga cgc  
1296

Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg  
420 425 430

caa gga cca gga ggc cgc acc cac ctg gta tcc cca gca gtc gca gcc  
1344

Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala  
435 440 445

gcc acc gaa tcc gcg gac cct gtc ctc acc tgc aga tat cta agg aag  
1392

Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys  
450 455 460

gct aga aaa caa tgg aaa aat tta cca cct aca ccg gcg ttg gcg ttc  
1440

Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe  
465 470 475 480

cac tgc agc gat cca acg tgg aca ccg acc aga tca tcc cag ccg tct  
1488

His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser  
485 490 495

acc tca agc gcg tca ccc gga ccg gct tcg aag acg gac tgt ttt cca  
1536

Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro  
500 505 510

act ggc gcc aaa acg acc cca act ttg tcc tca aca ccg aca cct aca  
1584

Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr  
515 520 525

aga acg gct ccg ttc tcg tagcaggccc tgactttggc acc  
1625

Arg Thr Ala Pro Phe Ser  
530

<210> 268

<211> 534

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

Val Trp Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp  
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Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln

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Ala	Phe	Asp	Gly	Leu	Arg	Met	Thr	Gly	Arg	Lys	Leu	Arg	His	Pro	Glu				
		35					40					45							
Leu	His	Leu	Ala	Thr	Glu	Asp	His	Asn	Val	Pro	Thr	Glu	Gly	Ile	Lys				
	50					55					60								
Thr	Gly	Ser	Leu	Leu	Glu	Ile	Asn	Asp	Lys	Ile	Ser	Arg	Leu	Gln	Val				
	65				70				75					80					
Ser	Thr	Leu	Arg	Asp	Asn	Cys	Glu	Glu	Phe	Gly	Val	Arg	Leu	His	Pro				
			85						90					95					
Met	Gly	Asp	Val	Arg	Gln	Gly	Ile	Val	His	Thr	Val	Gly	Pro	Gln	Leu				
		100						105					110						
Gly	Ala	Thr	Gln	Pro	Gly	Met	Thr	Ile	Val	Cys	Gly	Asp	Ser	His	Thr				
	115						120					125							
Ser	Thr	His	Gly	Ala	Phe	Gly	Ser	Met	Ala	Phe	Gly	Ile	Gly	Thr	Ser				
	130				135						140								
Glu	Val	Glu	His	Val	Met	Ala	Thr	Gln	Thr	Leu	Pro	Leu	Lys	Pro	Phe				
	145				150				155					160					
Lys	Thr	Met	Ala	Ile	Glu	Val	Thr	Gly	Glu	Leu	Gln	Pro	Gly	Val	Ser				
			165					170						175					
Ser	Lys	Asp	Leu	Ile	Leu	Ala	Ile	Ile	Ala	Lys	Ile	Gly	Thr	Gly	Gly				
		180					185						190						
Gly	Gln	Gly	Tyr	Val	Leu	Glu	Tyr	Arg	Gly	Glu	Ala	Ile	Arg	Lys	Met				
	195						200					205							
Ser	Met	Asp	Ala	Arg	Met	Thr	Met	Cys	Asn	Met	Ser	Ile	Glu	Ala	Gly				
	210					215					220								
Ala	Arg	Ala	Gly	Met	Ile	Ala	Pro	Asp	Gln	Thr	Thr	Phe	Asp	Tyr	Val				
	225			230					235					240					
Glu	Gly	Arg	Glu	Met	Ala	Pro	Lys	Gly	Ala	Asp	Trp	Asp	Glu	Ala	Val				
			245					250					255						
Ala	Tyr	Trp	Lys	Thr	Leu	Pro	Thr	Asp	Glu	Gly	Ala	Thr	Phe	Asp	Lys				
		260					265						270						
Val	Val	Glu	Ile	Asp	Gly	Ser	Ala	Leu	Thr	Pro	Phe	Ile	Thr	Trp	Gly				
	275						280					285							
Thr	Asn	Pro	Gly	Gln	Gly	Leu	Pro	Leu	Gly	Glu	Ser	Val	Pro	Ser	Pro				
	290					295					300								
Glu	Asp	Phe	Thr	Asn	Asp	Asn	Asp	Lys	Ala	Ala	Ala	Glu	Lys	Ala	Leu				
	305			310					315					320					
Gln	Tyr	Met	Asp	Leu	Val	Pro	Gly	Thr	Pro	Leu	Arg	Asp	Ile	Lys	Ile				
			325					330					335						
Asp	Thr	Val	Phe	Leu	Gly	Ser	Cys	Thr	Asn	Ala	Arg	Ile	Glu	Asp	Leu				
		340						345					350						

Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met  
 355 360 365  
 Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu  
 370 375 380  
 Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg  
 385 390 395 400  
 Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys  
 405 410 415  
 Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg  
 420 425 430  
 Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala  
 435 440 445  
 Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys  
 450 455 460  
 Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe  
 465 470 475 480  
 His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser  
 485 490 495  
 Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro  
 500 505 510  
 Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr  
 515 520 525  
 Arg Thr Ala Pro Phe Ser  
 530

<210> 269  
 <211> 1143  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1120)  
 <223> RXN01127

<400> 269  
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 Met Lys Leu Ala Val  
 1 5  
 att ggt gga gat ggt atc ggc cca gag gtt act gca gaa gcc ctc aag 163  
 Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr Ala Glu Ala Leu Lys  
 10 15 20  
 gtt cta aac gct gtc cgc gac gac atc gag acc acc gat tat gac ctt 211  
 Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr Thr Asp Tyr Asp Leu

25	30	35	
ggc gca cgc cgt tac ctc aaa aat ggc gag ctg ctc acc gac gag gat Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu Leu Thr Asp Glu Asp 40 45 50			259
ctg gca tcc ctg cgc gag cat gac gcg atc ctt ctt ggc gct atc ggt Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu Leu Gly Ala Ile Gly 55 60 65			307
gca cca ggt tcc gtc cct cca gga att ctc gag cgt ggt ttg ctg ctg Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu Arg Gly Leu Leu Leu 70 75 80 85			355
aag atg cga ttc gca ctg gat cac cac gtg aac ctg cgc cca tcc aag Lys Met Arg Phe Ala Leu Asp His His Val Asn Leu Arg Pro Ser Lys 90 95 100			403
ctg tac gac ggc gtg gag tcc cca ctg cgt aac cca ggc aag att gat Leu Tyr Asp Gly Val Glu Ser Pro Leu Arg Asn Pro Gly Lys Ile Asp 105 110 115			451
ttc gtt gtg gtc cgc gaa ggt acc gaa ggc gcc tac act ggc aac ggt Phe Val Val Val Arg Glu Gly Thr Glu Gly Ala Tyr Thr Gly Asn Gly 120 125 130			499
gga gca atc cgc gtg gga acc cct cac gag att gcc aat gaa acc tcc Gly Ala Ile Arg Val Gly Thr Pro His Glu Ile Ala Asn Glu Thr Ser 135 140 145			547
gtg aac act cgc tac ggc gct gag cgc gtt att cgc tac gca ttc gag Val Asn Thr Arg Tyr Gly Ala Glu Arg Val Ile Arg Tyr Ala Phe Glu 150 155 160 165			595
ctg gca cag agc cgc cgc aag aag ctc acc ctc gtg cac aag acc aac Leu Ala Gln Ser Arg Arg Lys Lys Leu Thr Leu Val His Lys Thr Asn 170 175 180			643
gtc ctg gtt cac ggt ggt ggc ctg tgg cag cgc acc gta gat gag gtt Val Leu Val His Gly Gly Gly Leu Trp Gln Arg Thr Val Asp Glu Val 185 190 195			691
gca aag gaa tac cca gag gta gcc gtc gat tac aac cac atc gat gca Ala Lys Glu Tyr Pro Glu Val Ala Val Asp Tyr Asn His Ile Asp Ala 200 205 210			739
gca acc atc tat ctg gtc act gat cct tcc cgc ttc gat gtg att gtt Ala Thr Ile Tyr Leu Val Thr Asp Pro Ser Arg Phe Asp Val Ile Val 215 220 225			787
acc gat aac ctc ttc ggc gac atc ctc acc gat gag gca ggc gca gtc Thr Asp Asn Leu Phe Gly Asp Ile Leu Thr Asp Glu Ala Gly Ala Val 230 235 240 245			835
tct ggc gga att ggc ctc gca gca tcc ggc aac atc gat gcc acg ggc Ser Gly Gly Ile Gly Leu Ala Ala Ser Gly Asn Ile Asp Ala Thr Gly 250 255 260			883
acc aac cct tcc atg ttc gag cca gtc cac ggc tct gca cca gat atc Thr Asn Pro Ser Met Phe Glu Pro Val His Gly Ser Ala Pro Asp Ile 265 270 275			931

gca ggc cag gga atc gca gac cca acg gca gca atc cta tcc gct gcg 979  
 Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala Ile Leu Ser Ala Ala  
           280                                  285                                  290

atg ctg ctg cgt cac tta ggt gat gaa gac aac gca gta cgt att gaa  
 1027  
 Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn Ala Val Arg Ile Glu  
           295                                  300                                  305

aca gcc atc gca gct gat gtg gct ggc cga gat aac tct cag ccg att  
 1075  
 Thr Ala Ile Ala Ala Asp Val Ala Gly Arg Asp Asn Ser Gln Pro Ile  
           310                                  315                                  320                                  325

tct acc act gag gtg gga gac cgc atc gtc aag gcg ctg caa agc  
 1120  
 Ser Thr Thr Glu Val Gly Asp Arg Ile Val Lys Ala Leu Gln Ser  
                                   330                                  335                                  340

taaatttcaa cgccgacccc ctt  
 1143

<210> 270  
 <211> 340  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 270

Met Lys Leu Ala Val Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr  
   1                                  5                                  10                                  15

Ala Glu Ala Leu Lys Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr  
           20                                  25                                  30

Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu  
           35                                  40                                  45

Leu Thr Asp Glu Asp Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu  
           50                                  55                                  60

Leu Gly Ala Ile Gly Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu  
           65                                  70                                  75                                  80

Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn  
                                   85                                  90                                  95

Leu Arg Pro Ser Lys Leu Tyr Asp Gly Val Glu Ser Pro Leu Arg Asn  
           100                                  105                                  110

Pro Gly Lys Ile Asp Phe Val Val Val Arg Glu Gly Thr Glu Gly Ala  
           115                                  120                                  125

Tyr Thr Gly Asn Gly Gly Ala Ile Arg Val Gly Thr Pro His Glu Ile  
           130                                  135                                  140

Ala Asn Glu Thr Ser Val Asn Thr Arg Tyr Gly Ala Glu Arg Val Ile  
           145                                  150                                  155                                  160

Arg Tyr Ala Phe Glu Leu Ala Gln Ser Arg Arg Lys Lys Leu Thr Leu



165 170 175  
 Val His Lys Thr Asn Val Leu Val His Gly Gly Gly Leu Trp Gln Arg  
 180 185 190  
 Thr Val Asp Glu Val Ala Lys Glu Tyr Pro Glu Val Ala Val Asp Tyr  
 195 200 205  
 Asn His Ile Asp Ala Ala Thr Ile Tyr Leu Val Thr Asp Pro Ser Arg  
 210 215 220  
 Phe Asp Val Ile Val Thr Asp Asn Leu Phe Gly Asp Ile Leu Thr Asp  
 225 230 235 240  
 Glu Ala Gly Ala Val Ser Gly Gly Ile Gly Leu Ala Ala Ser Gly Asn  
 245 250 255  
 Ile Asp Ala Thr Gly Thr Asn Pro Ser Met Phe Glu Pro Val His Gly  
 260 265 270  
 Ser Ala Pro Asp Ile Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala  
 275 280 285  
 Ile Leu Ser Ala Ala Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn  
 290 295 300  
 Ala Val Arg Ile Glu Thr Ala Ile Ala Ala Asp Val Ala Gly Arg Asp  
 305 310 315 320  
 Asn Ser Gln Pro Ile Ser Thr Thr Glu Val Gly Asp Arg Ile Val Lys  
 325 330 335  
 Ala Leu Gln Ser  
 340

<210> 271  
 <211> 403  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(403)  
 <223> FRXA01132

<400> 271  
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 cactagtga gttccatatag tgagaaggga atcccacaac atg aaa ctt gct gtt 115  
 Met Lys Leu Ala Val  
 1 5  
 att ggt gga gat ggt atc ggc cca gag gtt act gca gaa gcc ctc aag 163  
 Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr Ala Glu Ala Leu Lys  
 10 15 20  
 gtt cta aac gct gtc cgc gac gac atc gag acc acc gat tat gac ctt 211  
 Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr Thr Asp Tyr Asp Leu  
 25 30 35

ggc gca cgc cgt tac ctc aaa aat ggc gag ctg ctc acc gac gag gat 259  
Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu Leu Thr Asp Glu Asp  
40 45 50

ctg gca tcc ctg cgc gag cat gac gcg atc ctt ctt ggc gct atc ggt 307  
Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu Leu Gly Ala Ile Gly  
55 60 65

gca	cca	ggt	tcc	gtc	cct	cca	gga	att	ctc	gag	cgt	ggt	ttg	ctg	ctg	355
Ala	Pro	Gly	Ser	Val	Pro	Pro	Gly	Ile	Leu	Glu	Arg	Gly	Leu	Leu	Leu	
70					75					80					85	

aag atg cga ttc gca ctg gat cac cac gtg aac ctg cgc cca tcc aag 403  
Lys Met Arg Phe Ala Leu Asp His His Val Asn Leu Arg Pro Ser Lys  
90 95 100

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<210> 272
<211> 101
<212> PRT
<213> Corynebacterium glutamicum
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<400> 272
Met Lys Leu Ala Val Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr
  1                               10                      15
Ala Glu Ala Leu Lys Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr
                20                          25                      30
Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu
          35                                40                      45
Leu Thr Asp Glu Asp Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu
      50                              55                      60
Leu Gly Ala Ile Gly Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu
   65                             70                      75                      80
Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn
              85                                90                      95
Leu Arg Pro Ser Lys
            100
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<210> 273
<211> 1494
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (101)..(1471)  
<223> RXN00536
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tcgtggacct acccaaaact ttttaagaag gttgaacaca atg tct cct aac gat 115  
Met Ser Pro Asn Asp  
1 5
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gca ttc atc tcc gca cct gcc aag atc gaa acc cca gtt ggg cct cgc	163
Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr Pro Val Gly Pro Arg	
10 15 20	
aac gaa ggc cag cca gca tgg aat aag cag cgt ggc tcc tca atg cca	211
Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg Gly Ser Ser Met Pro	
25 30 35	
gtt aac cgc tac atg cct ttc gag gtt gag gta gaa gat att tct ctg	259
Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val Glu Asp Ile Ser Leu	
40 45 50	
ccg gac cgc act tgg cca gat aaa aaa atc acc gtt gca cct cag tgg	307
Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr Val Ala Pro Gln Trp	
55 60 65	
tgt gct gtt gac ctg cgt gac ggc aac cag gct ctg att gat ccg atg	355
Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala Leu Ile Asp Pro Met	
70 75 80 85	
tct cct gag cgt aag cgc cgc atg ttt gag ctg ctg gtt cag atg ggc	403
Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu Leu Val Gln Met Gly	
90 95 100	
ttc aaa gaa atc gag gtc ggt ttc cct tca gct tcc cag act gat ttt	451
Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala Ser Gln Thr Asp Phe	
105 110 115	
gat ttc gtt cgt gag atc atc gaa aag ggc atg atc cct gac gat gtc	499
Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met Ile Pro Asp Asp Val	
120 125 130	
acc att cag gtt ctg gtt cag gct cgt gag cac ctg att cgc cgt act	547
Thr Ile Gln Val Leu Val Gln Ala Arg Glu His Leu Ile Arg Arg Thr	
135 140 145	
ttt gaa gct tgc gaa ggc gca aaa aac gtt atc gtg cac ttc tac aac	595
Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile Val His Phe Tyr Asn	
150 155 160 165	
tcc acc tcc atc ctg cag cgc aac gtg gtg ttc cgc atg gac aag gtg	643
Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe Arg Met Asp Lys Val	
170 175 180	
cag gtg aag aag ctg gct acc gat gcc gct gaa cta atc aag acc atc	691
Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu Leu Ile Lys Thr Ile	
185 190 195	
gct cag gat tac cca gac acc aac tgg cgc tgg cag tac tcc cct gag	739
Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp Gln Tyr Ser Pro Glu	
200 205 210	
tcc ttc acc ggc act gag gtt gag tac gcc aag gaa gtt gtg gac gca	787
Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys Glu Val Val Asp Ala	
215 220 225	
gtt gtt gag gtc atg gat cca act cct gag aac cca atg atc atc aac	835
Val Val Glu Val Met Asp Pro Thr Pro Glu Asn Pro Met Ile Ile Asn	
230 235 240 245	

ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc 883  
 Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser  
 250 255 260

att gaa tgg atg cac cgc aat cta aac cgt cgt gat tcc att atc ctg 931  
 Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu  
 265 270 275

tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag 979  
 Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu  
 280 285 290

ctg ggc tac atg gct ggc gct gac cgc atc gaa ggc tgc ctg ttc ggc  
 1027  
 Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu Gly Cys Leu Phe Gly  
 295 300 305

aac ggc gag cgc acc ggc aac gtc tgc ctg gtc acc ctg gca ctg aac  
 1075  
 Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val Thr Leu Ala Leu Asn  
 310 315 320 325

atg ctg acc cag ggc gtt gac cct cag ctg gac ttc acc gat ata cgc  
 1123  
 Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp Phe Thr Asp Ile Arg  
 330 335 340

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 Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln Leu Arg Val Pro Glu  
 345 350 355

cgc cac cca tac ggc ggt gac ctg gtc ttc acc gct ttc tcc ggt tcc  
 1219  
 Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr Ala Phe Ser Gly Ser  
 360 365 370

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 1267  
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 375 380 385

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 1315  
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 390 395 400 405

acc cga atg gga ggt tcc tta cct gcc tat cga tcc aaa gga tgt cgg  
 1363  
 Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg Ser Lys Gly Cys Arg  
 410 415 420

tcg cga cta cga ggc tgt tat ccg cgt gaa ctc cca gtc cgg caa ggg  
 1411  
 Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu Pro Val Arg Gln Gly  
 425 430 435

cgg cgt tgc tta cat cat gaa gac cga tca cgg tct gca gat ccc tcg  
 1459  
 Arg Arg Cys Leu His His Glu Asp Arg Ser Arg Ser Ala Asp Pro Ser  
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1494

Leu His Ala Gly  
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<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

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Gly	Ser	Ser	Met	Pro	Val	Asn	Arg	Tyr	Met	Pro	Phe	Glu	Val	Glu	Val	35	40	45	
Glu	Asp	Ile	Ser	Leu	Pro	Asp	Arg	Thr	Trp	Pro	Asp	Lys	Lys	Ile	Thr	50	55	60	
Val	Ala	Pro	Gln	Trp	Cys	Ala	Val	Asp	Leu	Arg	Asp	Gly	Asn	Gln	Ala	65	70	75	80
Leu	Ile	Asp	Pro	Met	Ser	Pro	Glu	Arg	Lys	Arg	Arg	Met	Phe	Glu	Leu	85	90	95	
Leu	Val	Gln	Met	Gly	Phe	Lys	Glu	Ile	Glu	Val	Gly	Phe	Pro	Ser	Ala	100	105	110	
Ser	Gln	Thr	Asp	Phe	Asp	Phe	Val	Arg	Glu	Ile	Ile	Glu	Lys	Gly	Met	115	120	125	
Ile	Pro	Asp	Asp	Val	Thr	Ile	Gln	Val	Leu	Val	Gln	Ala	Arg	Glu	His	130	135	140	
Leu	Ile	Arg	Arg	Thr	Phe	Glu	Ala	Cys	Glu	Gly	Ala	Lys	Asn	Val	Ile	145	150	155	160
Val	His	Phe	Tyr	Asn	Ser	Thr	Ser	Ile	Leu	Gln	Arg	Asn	Val	Val	Phe	165	170	175	
Arg	Met	Asp	Lys	Val	Gln	Val	Lys	Lys	Leu	Ala	Thr	Asp	Ala	Ala	Glu	180	185	190	
Leu	Ile	Lys	Thr	Ile	Ala	Gln	Asp	Tyr	Pro	Asp	Thr	Asn	Trp	Arg	Trp	195	200	205	
Gln	Tyr	Ser	Pro	Glu	Ser	Phe	Thr	Gly	Thr	Glu	Val	Glu	Tyr	Ala	Lys	210	215	220	
Glu	Val	Val	Asp	Ala	Val	Val	Glu	Val	Met	Asp	Pro	Thr	Pro	Glu	Asn	225	230	235	240
Pro	Met	Ile	Ile	Asn	Leu	Pro	Ser	Thr	Val	Glu	Met	Ile	Thr	Pro	Asn	245	250	255	

Val Tyr Ala Asp Ser Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg  
 260 265 270

Asp Ser Ile Ile Leu Ser Leu His Pro His Asn Asp Arg Gly Thr Gly  
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Val Gly Ala Ala Glu Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu  
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Gly Cys Leu Phe Gly Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val  
 305 310 315 320

Thr Leu Ala Leu Asn Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp  
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Phe Thr Asp Ile Arg Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln  
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Leu Arg Val Pro Glu Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr  
 355 360 365

Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala  
 370 375 380

Met Ala Ala Lys Val Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp  
 385 390 395 400

Glu Gln Leu Arg Asp Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg  
 405 410 415

Ser Lys Gly Cys Arg Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu  
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Ser Ala Asp Pro Ser Leu His Ala Gly  
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<210> 275

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1333)

<223> FRXA00536

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 Met Ser Pro Asn Asp  
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 Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr Pro Val Gly Pro Arg  
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Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg Gly Ser Ser Met Pro	
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Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val Glu Asp Ile Ser Leu	
40 45 50	
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Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr Val Ala Pro Gln Trp	
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Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala Leu Ile Asp Pro Met	
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Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu Leu Val Gln Met Gly	
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Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala Ser Gln Thr Asp Phe	
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Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met Ile Pro Asp Asp Val	
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Thr Ile Gln Val Leu Val Gln Ala Arg Glu His Leu Ile Arg Arg Thr	
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Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile Val His Phe Tyr Asn	
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Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe Arg Met Asp Lys Val	
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Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu Leu Ile Lys Thr Ile	
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gct cag gat tac cca gac acc aac tgg cgc tgg cag tac tcc cct gag	739
Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp Gln Tyr Ser Pro Glu	
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tcc ttc acc ggc act gag gtt gag tac gcc aag gaa gtt gtg gac gca	787
Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys Glu Val Val Asp Ala	
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ggt gtt gag gtc atg gat cca act cct gag aac cca atg atc atc aac	835
Val Val Glu Val Met Asp Pro Thr Pro Glu Asn Pro Met Ile Ile Asn	
230 235 240 245	
ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc	883
Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser	
250 255 260	
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Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu  
 265 270 275

tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag 979  
 Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu  
 280 285 290

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 330 335 340

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 360 365 370

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 His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala Met Ala Ala Lys Val  
 375 380 385

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 <213> Corynebacterium glutamicum

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Leu	Ile	Asp	Pro	Met	Ser	Pro	Glu	Arg	Lys	Arg	Arg	Met	Phe	Glu	Leu	
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Leu	Ile	Arg	Arg	Thr	Phe	Glu	Ala	Cys	Glu	Gly	Ala	Lys	Asn	Val	Ile	
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225					230					235					240	
Pro	Met	Ile	Ile	Asn	Leu	Pro	Ser	Thr	Val	Glu	Met	Ile	Thr	Pro	Asn	
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Asp	Ser	Ile	Ile	Leu	Ser	Leu	His	Pro	His	Asn	Asp	Arg	Gly	Thr	Gly	
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305					310					315					320	
Thr	Leu	Ala	Leu	Asn	Met	Leu	Thr	Gln	Gly	Val	Asp	Pro	Gln	Leu	Asp	
325					330					335						
Phe	Thr	Asp	Ile	Arg	Gln	Ile	Arg	Ser	Thr	Val	Glu	Tyr	Cys	Asn	Gln	
340					345					350						
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Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala  
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<211> 714

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(691)

<223> RXN02965

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 Thr Tyr Thr Gly Val Gly Val Pro Leu Gln Arg Ser Asn Val Asp Thr  
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 Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg Val Thr Arg Thr Gly  
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 Phe Glu Asp Gly Leu Phe Ser Asn Trp Arg Gln Asn Asp Pro Asn Phe  
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 Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser Val Leu Val Ala Gly  
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 Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His Ala Val Trp Ala Leu  
 70 75 80 85

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 Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser Arg Phe Ala Asp Ile  
 90 95 100

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 Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu Thr Gly Ile Met Glu  
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 Gln S r Asp Ile Glu Leu Leu Trp Lys Leu Met Glu Gln Thr Pro Gly  
 120 125 130

ctc gaa ctg acc gtg aac ctg gaa aag cag atc gtc acc gca ggc gac 547

Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile Val Thr Ala Gly Asp  
 135 140 145  
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 Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile Arg Trp Arg Leu Met  
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 Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg Lys Leu Asp Glu Ile  
 170 175 180  
 gaa gac tac gag gct aag cgc cct gcg ttt aag cca cgc act aac gct 691  
 Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys Pro Arg Thr Asn Ala  
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 Asn Asp Pro Asn Phe Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser  
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 Val Leu Val Ala Gly Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His  
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 Arg Phe Ala Asp Ile Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu  
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 Glu Gln Thr Pro Gly Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile  
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 Val Thr Ala Gly Asp Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile  
 145 150 155 160  
 Arg Trp Arg Leu Met Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg  
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 Lys Leu Asp Glu Ile Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys  
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195

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<220>  
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 <223> RXN01929

<400> 279

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Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val
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Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala
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Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser
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Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg
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Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro
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Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala
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Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg
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cgc att gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc 547
Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr
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ccg cag tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc 595
Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly
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gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg 643

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 Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg  
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gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc 739  
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 200 205 210

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 215 220 225

aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc 835  
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 230 235 240 245

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 Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala  
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<400> 280

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 35 40 45

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 50 55 60

Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr  
 65 70 75 80

Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr  
 85 90 95

Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met  
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Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile  
 115 120 125

Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly

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His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val		
145	150	155 160
Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg		
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Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro		
	180	185 190
Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile		
	195	200 205
Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln		
	210	215 220
Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu		
	225	230 235 240
Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile		
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 <223> FRXA01929

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 Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly  
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 Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile  
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 Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala  
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 Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu  
 55 60 65  
 atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt 355

Met	Ile	Val	Leu	Ala	Lys	Ala	Val	Thr	Il	Ala	Thr	Lys	Arg	Ala	Leu	
70					75					80					85	
gtg	gtg	gtt	gat	ctg	ccg	ttt	ggg	acc	tat	gag	gtg	agc	cca	aat	cag	403
Val	Val	Val	Asp	Leu	Pro	Phe	Gly	Thr	Tyr	Glu	Val	Ser	Pro	Asn	Gln	
				90					95					100		
gcg	gtg	gag	tcc	gcg	atc	cgg	gtc	atg	cgt	gaa	acg	ggg	gcg	gct	gcg	451
Ala	Val	Glu	Ser	Ala	Ile	Arg	Val	Met	Arg	Glu	Thr	Gly	Ala	Ala	Ala	
			105					110					115			
gtg	aag	atc	gag	ggg	ggc	gtg	gag	atc	gcg	cag	acg	att	cga	cgc	att	499
Val	Lys	Ile	Glu	Gly	Gly	Val	Glu	Ile	Ala	Gln	Thr	Ile	Arg	Arg	Ile	
		120					125					130				
gtt	gat	gct	gga	att	ccg	gtt	gtc	ggc	cac	atc	ggg	tac	acc	ccg	cag	547
Val	Asp	Ala	Gly	Ile	Pro	Val	Val	Gly	His	Ile	Gly	Tyr	Thr	Pro	Gln	
	135					140					145					
tcc	gag	cat	tcc	ttg	ggc	ggc	cac	gtg	gtt	cag	ggg	cgt	ggc	gcg	agt	595
Ser	Glu	His	Ser	Leu	Gly	Gly	His	Val	Val	Gln	Gly	Arg	Gly	Ala	Ser	
150					155					160					165	
tct	gga	aag	ctc	atc	gcc	gat	gcc	cgc	gcg	ttg	gag	cag	gcg	ggg	gcg	643
Ser	Gly	Lys	Leu	Ile	Ala	Asp	Ala	Arg	Ala	Leu	Glu	Gln	Ala	Gly	Ala	
			170					175						180		
ttt	gcg	gtt	gtg	ttg	gag	atg	gtt	cca	gca	gag	gca	gcg	cgc	gag	gtt	691
Phe	Ala	Val	Val	Leu	Glu	Met	Val	Pro	Ala	Glu	Ala	Ala	Arg	Glu	Val	
			185					190					195			
acc	gag	gat	ctt	tcc	atc	acc	act	atc	gga	atc	ggg	gcc	ggc	aat	ggc	739
Thr	Glu	Asp	Leu	Ser	Ile	Thr	Thr	Ile	Gly	Ile	Gly	Ala	Gly	Asn	Gly	
		200					205					210				
aca	gat	ggg	cag	gtt	ttg	gtg	tgg	cag	gat	gcc	ttc	ggc	ctc	aac	cgc	787
Thr	Asp	Gly	Gln	Val	Leu	Val	Trp	Gln	Asp	Ala	Phe	Gly	Leu	Asn	Arg	
	215					220					225					
ggc	aag	aag	cca	cgc	ttc	gtc	cgc	gag	tac	gcc	acc	ttg	ggc	gat	tcc	835
Gly	Lys	Lys	Pro	Arg	Phe	Val	Arg	Glu	Tyr	Ala	Thr	Leu	Gly	Asp	Ser	
230				235				240						245		
ttg	cac	gac	gcc	gcg	cag	gcc	tac	atc	gcc	gat	atc	cac	gcg	ggg	acc	883
Leu	His	Asp	Ala	Ala	Gln	Ala	Tyr	Ile	Ala	Asp	Ile	His	Ala	Gly	Thr	
			250					255					260			
ttc	cca	ggc	gaa	gcg	gag	tcc	ttt	taatgcaggt	agcaaccaca	aag						930
Phe	Pro	Gly	Glu	Ala	Glu	Ser	Phe									
			265													

&lt;210&gt; 282

&lt;211&gt; 269

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 282

Met	Ser	Gly	Ile	Asp	Ala	Lys	Lys	Ile	Arg	Thr	Arg	His	Phe	Arg	Glu
1				5				10						15	

Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala  
                   20                                  25                                  30  
 Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val  
                   35                                  40                                  45  
 Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser  
                   50                                  55                                  60  
 Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala  
                   65                                  70                                  75                                  80  
 Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu  
                                   85                                  90                                  95  
 Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu  
                                  100                                 105                                 110  
 Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln  
                  115                                 120                                 125  
 Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile  
                  130                                 135                                 140  
 Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln  
                  145                                 150                                 155                                 160  
 Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu  
                                  165                                 170                                 175  
 Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu  
                                  180                                 185                                 190  
 Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile  
                  195                                 200                                 205  
 Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala  
                  210                                 215                                 220  
 Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala  
                  225                                 230                                 235                                 240  
 Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp  
                                  245                                 250                                 255  
 Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe  
                  260                                 265

&lt;210&gt; 283

&lt;211&gt; 1065

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1042)

&lt;223&gt; RXN01420

&lt;400&gt; 283

cgaagttcac gactacaggc attacctggg tgctgatttt gcgcgagtaa agctgtggct 60



gcggaatgcg	ctgctcatcc	acacgtggaa	tcctgattgg	gtg	acg	ctg	ggt	gga		115						
				Val	Thr	Leu	Gly	Gly								
				1				5								
ttg	aat	gta	cca	tcg	tgg	tcg	ctg	ggc	gcg	gaa	atg	ctg	ttc	tac	ctg	163
Leu	Asn	Val	Pro	Ser	Trp	Ser	Leu	Gly	Ala	Glu	Met	Leu	Phe	Tyr	Leu	
				10				15						20		
acg	ttc	ccg	ctg	ttt	att	ccg	tta	gtg	cgc	aaa	gtg	aag	ggc	gtg	ggc	211
Thr	Phe	Pro	Leu	Phe	Ile	Pro	Leu	Val	Arg	Lys	Val	Lys	Gly	Val	Gly	
			25					30					35			
aac	tgg	tgg	gca	ttt	ggc	atc	acc	ttt	gcc	gtg	agc	ctg	gcg	ctg	att	259
Asn	Trp	Trp	Ala	Phe	Gly	Ile	Thr	Phe	Ala	Val	Ser	Leu	Ala	Leu	Ile	
		40					45					50				
aca	gtg	att	cac	ttt	tat	gcg	gac	gga	cca	aag	ggg	att	gag	aac	ttc	307
Thr	Val	Ile	His	Phe	Tyr	Ala	Asp	Gly	Pro	Lys	Gly	Ile	Glu	Asn	Phe	
	55					60					65					
ttt	gtt	cct	cgc	ctg	tgg	gac	acc	aat	gtg	tca	ccg	gtc	gcg	gaa	gtt	355
Phe	Val	Pro	Arg	Leu	Trp	Asp	Thr	Asn	Val	Ser	Pro	Val	Ala	Glu	Val	
	70				75					80					85	
cac	gcc	gat	cca	gtg	tgg	ttt	atg	cag	gaa	gaa	att	ccc	gtg	ctg	gaa	403
His	Ala	Asp	Pro	Val	Trp	Phe	Met	Gln	Glu	Glu	Ile	Pro	Val	Leu	Glu	
				90				95						100		
tct	tac	tgg	ctg	tct	tac	tac	ttc	ccg	ctg	acc	aga	ctc	atc	gag	ttc	451
Ser	Tyr	Trp	Leu	Ser	Tyr	Tyr	Phe	Pro	Leu	Thr	Arg	Leu	Ile	Glu	Phe	
			105					110					115			
tac	ctc	ggt	gtg	ttt	ggc	gcg	aag	ctg	gtt	gct	gaa	ggc	atg	ttt	aaa	499
Tyr	Leu	Gly	Val	Phe	Gly	Ala	Lys	Leu	Val	Ala	Glu	Gly	Met	Phe	Lys	
		120					125					130				
aac	acc	aac	atc	acc	atc	ccg	ctg	atc	gca	ctg	gct	gtt	tct	ttt	gtt	547
Asn	Thr	Asn	Ile	Thr	Ile	Pro	Leu	Ile	Ala	Leu	Ala	Val	Ser	Phe	Val	
		135				140					145					
gct	act	tgg	ttt	gtg	cca	ctg	gca	ttc	aag	atg	tct	gtc	atc	atg	tcc	595
Ala	Thr	Trp	Phe	Val	Pro	Leu	Ala	Phe	Lys	Met	Ser	Val	Ile	Met	Ser	
	150				155					160					165	
ctg	cca	atg	gct	ttt	gtt	gtg	gca	acg	ctt	gcg	gtg	aga	gac	att	gaa	643
Leu	Pro	Met	Ala	Phe	Val	Val	Ala	Thr	Leu	Ala	Val	Arg	Asp	Ile	Glu	
				170				175						180		
ggc	aag	agt	ggg	gaa	atc	gcc	tcg	cct	cgc	gca	gtt	ttg	ttg	ggt	aat	691
Gly	Lys	Ser	Gly	Glu	Ile	Ala	Ser	Pro	Arg	Ala	Val	Leu	Leu	Gly	Asn	
			185				190						195			
att	tcc	ttt	gcc	ttc	tac	atg	gtg	caa	ttc	ccc	gtc	atg	gtg	ttt	gtg	739
Ile	Ser	Phe	Ala	Phe	Tyr	Met	Val	Gln	Phe	Pro	Val	Met	Val	Phe	Val	
		200					205					210				
cag	cgc	tat	ttc	att	gct	ggc	aaa	gaa	tac	ggc	ttc	ctt	ggc	tgg	gca	787
Gln	Arg	Tyr	Phe	Ile	Ala	Gly	Lys	Glu	Tyr	Gly	Phe	Leu	Gly	Trp	Ala	
	215					220					225					

ttc tat gca gtg gtg tgt ttc atc gtg tcg gtc att ctc gcg tgg gtg 835  
 Phe Tyr Ala Val Val Cys Phe Ile Val Ser Val Ile Leu Ala Trp Val  
 230 235 240 245

ctg ttt acc ttc gtt gat gat cct ttg atg aag gcc acg gcg cgc aag 883  
 Leu Phe Thr Phe Val Asp Asp Pro Leu Met Lys Ala Thr Ala Arg Lys  
 250 255 260

aag ggg agt agg cgc ttg aag cag tcc aat att ttg gtc cgt gac ctg 931  
 Lys Gly Ser Arg Arg Leu Lys Gln Ser Asn Ile Leu Val Arg Asp Leu  
 265 270 275

aaa gtt ctc ttc ggc aaa agc ccc gaa aag ccg tta aaa gtt gag act 979  
 Lys Val Leu Phe Gly Lys Ser Pro Glu Lys Pro Leu Lys Val Glu Thr  
 280 285 290

cgc gct gag aat ctc aca gaa aac tcc gaa gct ccc gct aag gta gct  
 1027  
 Arg Ala Glu Asn Leu Thr Glu Asn Ser Glu Ala Pro Ala Lys Val Ala  
 295 300 305

acc gga atc aaa tct tagggaagga aaacatatgg cta  
 1065  
 Thr Gly Ile Lys Ser  
 310

<210> 284  
 <211> 314  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 284  
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Met Leu Phe Tyr Leu Thr Phe Pro Leu Phe Ile Pro Leu Val Arg Lys  
 20 25 30

Val Lys Gly Val Gly Asn Trp Trp Ala Phe Gly Ile Thr Phe Ala Val  
 35 40 45

Ser Leu Ala Leu Ile Thr Val Ile His Phe Tyr Ala Asp Gly Pro Lys  
 50 55 60

Gly Ile Glu Asn Phe Phe Val Pro Arg Leu Trp Asp Thr Asn Val Ser  
 65 70 75 80

Pro Val Ala Glu Val His Ala Asp Pro Val Trp Phe Met Gln Glu Glu  
 85 90 95

Ile Pro Val Leu Glu Ser Tyr Trp Leu Ser Tyr Tyr Phe Pro Leu Thr  
 100 105 110

Arg Leu Ile Glu Phe Tyr Leu Gly Val Phe Gly Ala Lys Leu Val Ala  
 115 120 125

Glu Gly Met Phe Lys Asn Thr Asn Ile Thr Ile Pro Leu Ile Ala Leu  
 130 135 140

Ala Val Ser Phe Val Ala Thr Trp Phe Val Pro Leu Ala Phe Lys Met

145		150		155		160
Ser Val Ile Met	Ser Leu Pro Met Ala Phe Val Val Ala Thr Leu Ala					
	165			170		175
Val Arg Asp Ile Glu Gly Lys Ser Gly Glu Ile Ala Ser Pro Arg Ala						
	180		185			190
Val Leu Leu Gly Asn Ile Ser Phe Ala Phe Tyr Met Val Gln Phe Pro						
	195		200			205
Val Met Val Phe Val Gln Arg Tyr Phe Ile Ala Gly Lys Glu Tyr Gly						
	210		215			220
Phe Leu Gly Trp Ala Phe Tyr Ala Val Val Cys Phe Ile Val Ser Val						
	225		230		235	240
Ile Leu Ala Trp Val Leu Phe Thr Phe Val Asp Asp Pro Leu Met Lys						
	245		250			255
Ala Thr Ala Arg Lys Lys Gly Ser Arg Arg Leu Lys Gln Ser Asn Ile						
	260		265			270
Leu Val Arg Asp Leu Lys Val Leu Phe Gly Lys Ser Pro Glu Lys Pro						
	275		280			285
Leu Lys Val Glu Thr Arg Ala Glu Asn Leu Thr Glu Asn Ser Glu Ala						
	290		295			300
Pro Ala Lys Val Ala Thr Gly Ile Lys Ser						
	305		310			

<210> 285  
 <211> 1137  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101) .. (1114)  
 <223> RXS01145

<400> 285  
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 cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115  
 Met Ala Ile Glu Leu  
 1 5  
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163  
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val  
 10 15 20  
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211  
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu  
 25 30 35  
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259  
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys  
 40 45 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct	307
Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala	
55 60 65	
gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc	355
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr	
70 75 80 85	
tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca	403
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala	
90 95 100	
ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg	451
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu	
105 110 115	
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc	499
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly	
120 125 130	
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct	547
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro	
135 140 145	
tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg	595
Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu	
150 155 160 165	
acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc	643
Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile	
170 175 180	
cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag	691
Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln	
185 190 195	
gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag	739
Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu	
200 205 210	
gtt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt	787
Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val	
215 220 225	
ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc	835
Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile	
230 235 240 245	
agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac	883
Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr	
250 255 260	
ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag	931
Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys	
265 270 275	
gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc	979
Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile	
280 285 290	

gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc  
1027

Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser  
295 300 305

tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc  
1075

Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu  
310 315 320 325

atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtttcac  
1124

Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala  
330 335

ccctttgacg gct  
1137

<210> 286

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 286

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile  
1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala  
20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu  
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu  
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu  
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp  
130 135 140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly  
145 150 155 160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala  
165 170 175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp  
180 185 190

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val  
 195 200 205

Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met  
 210 215 220

Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met  
 225 230 235 240

Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala  
 245 250 255

Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr  
 260 265 270

Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe  
 275 280 285

Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu  
 290 295 300

Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala  
 305 310 315 320

Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu  
 325 330 335

Thr Ala

<210> 287

<211> 556

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> FRXA01145

<400> 287

taatgtagtt gtctgccc aa gcgagttaaa ctcccacgat ttacagtggg gggcagacat 60

cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115  
 Met Ala Ile Glu Leu  
 1 5

ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163  
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val  
 10 15 20

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211  
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu  
 25 30 35

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259  
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys  
 40 45 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

S r Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala  
 55 60 65  
 gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355  
 Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr  
 70 75 80 85  
 tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403  
 Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala  
 90 95 100  
 ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451  
 Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu  
 105 110 115  
 atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499  
 Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly  
 120 125 130  
 cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547  
 Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro  
 135 140 145  
 tgc ctc atc  
 Cys Leu Ile 556  
 150

&lt;210&gt; 288

&lt;211&gt; 152

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 288

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile  
 1 5 10 15  
 Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala  
 20 25 30  
 His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu  
 35 40 45  
 Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
 50 55 60  
 Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu  
 65 70 75 80  
 Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu  
 85 90 95  
 Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
 100 105 110  
 Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
 115 120 125  
 Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp  
 130 135 140

Gly Lys Gly Val Pro Cys Leu Ile  
145 150

<210> 289  
<211> 1350  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101) .. (1327)  
<223> RXA02375

<400> 289  
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aagcgttcga ttacgggata atctcccaac gccaacccaa atg gcg ccg gtg aca 115  
Met Ala Pro Val Thr  
1 5  
ggg ctt cct gtc acc ccc tac agc cag gaa gca agc atc ggt gcg agc 163  
Gly Leu Pro Val Thr Pro Tyr Ser Gln Glu Ala Ser Ile Gly Ala Ser  
10 15 20  
ttc ccg gca gtg gat ccg gac acc aaa gac agc gcc gca tac gga cat 211  
Phe Pro Ala Val Asp Pro Asp Thr Lys Asp Ser Ala Ala Tyr Gly His  
25 30 35  
gaa tcc gga atg cgt gag cgc atc tcc aac gct aag cga gtg gtg gtg 259  
Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala Lys Arg Val Val Val  
40 45 50  
aaa att ggt tcg tcc tca ttg act aac gat gag gac gga cac acc gtc 307  
Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu Asp Gly His Thr Val  
55 60 65  
gat ccc aac cgc atc aac act att gtc aat gcc ttg caa gca cgc atg 355  
Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala Leu Gln Ala Arg Met  
70 75 80 85  
gaa gct ggc tcg gac ctc atc gtt gtg tcc tct ggc gca gtg gcc gcg 403  
Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser Gly Ala Val Ala Ala  
90 95 100  
gga atg gcc ccg ctt gga ttg agc acc cgg ccc acg gaa ttg gca gtc 451  
Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro Thr Glu Leu Ala Val  
105 110 115  
aag cag gct gca gca gca gtg ggg caa gtt cac ctc atg cac cag tgg 499  
Lys Gln Ala Ala Ala Ala Val Gly Gln Val His Leu Met His Gln Trp  
120 125 130  
gga cgt tct ttt gcc cgg tat ggt cgc ccc atc ggc cag gtg ctt ctt 547  
Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile Gly Gln Val Leu Leu  
135 140 145  
acc gca gct gat gca gga aag cgt gat cgt gcg agg aat gcg cag cgt 595  
Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala Arg Asn Ala Gln Arg  
150 155 160 165



acc atc gac aag ctg cgc att ttg ggc gcg gtt cct atc gtc aat gaa 643  
 Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val Pro Ile Val Asn Glu  
 170 175 180

aat gac acc gtg gca acc acc ggt gtg aat ttt ggt gac aac gac cga 691  
 Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe Gly Asp Asn Asp Arg  
 185 190 195

ctt gct gca att gtg gcg cac ctg gtg tcg gct gat gct ttg gtg ctg 739  
 Leu Ala Ala Ile Val Ala His Leu Val Ser Ala Asp Ala Leu Val Leu  
 200 205 210

ctc agt gac gtg gat gga ctt ttt gat aaa aac cct act gat ccc acc 787  
 Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn Pro Thr Asp Pro Thr  
 215 220 225

gcg aag ttt att tcc gag gtt cgt gac ggc aat gat ttg aaa ggt gtc 835  
 Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn Asp Leu Lys Gly Val  
 230 235 240 245

att gcc ggc gac ggc gga aaa gtg ggc acc ggt ggc atg gca tca aag 883  
 Ile Ala Gly Asp Gly Gly Lys Val Gly Thr Gly Gly Met Ala Ser Lys  
 250 255 260

gtg tct gct gca cgt ttg gct tcc cga agt ggc gtg cct gtg ctg ttg 931  
 Val Ser Ala Ala Arg Leu Ala Ser Arg Ser Gly Val Pro Val Leu Leu  
 265 270 275

acc tct gcg gca aac att ggc cca gca ctg gaa gac gcc cag gtg ggc 979  
 Thr Ser Ala Ala Asn Ile Gly Pro Ala Leu Glu Asp Ala Gln Val Gly  
 280 285 290

act gta ttc cac ccc aag gac aac cgc ctc tcc gcg tgg aag ttc tgg  
 1027  
 Thr Val Phe His Pro Lys Asp Asn Arg Leu Ser Ala Trp Lys Phe Trp  
 295 300 305

gct ttg tat gcc gca gat act gca gga aag atc cga ctc gat gac ggc  
 1075  
 Ala Leu Tyr Ala Ala Asp Thr Ala Gly Lys Ile Arg Leu Asp Asp Gly  
 310 315 320 325

gcg gtg gaa gca gtg acc tcc ggt ggt aaa tct ttg ctg gct gtg ggc  
 1123  
 Ala Val Glu Ala Val Thr Ser Gly Gly Lys Ser Leu Leu Ala Val Gly  
 330 335 340

att act gaa atc att ggt gat ttc cag cag ggt gag atc gtg gag atc  
 1171  
 Ile Thr Glu Ile Ile Gly Asp Phe Gln Gln Gly Glu Ile Val Glu Ile  
 345 350 355

ttg gga cct gcc ggc caa atc atc ggg cga ggc gag gtg tcc tac gat  
 1219  
 Leu Gly Pro Ala Gly Gln Ile Ile Gly Arg Gly Glu Val Ser Tyr Asp  
 360 365 370

tct gat acc ttg caa tca atg gtt ggt atg caa acg cag gac ctt cca  
 1267  
 Ser Asp Thr Leu Gln Ser Met Val Gly Met Gln Thr Gln Asp Leu Pro  
 375 380 385

gat ggc atg cag cgc ccg gta gtg cat gca gat tat ctg tcc aac tac  
1315

Asp Gly Met Gln Arg Pro Val Val His Ala Asp Tyr Leu Ser Asn Tyr  
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gcc agc cgc gcg taaagcgcgg gcctgctggt ggc  
1350

Ala Ser Arg Ala

<210> 290

<211> 409

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

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Ser Ile Gly Ala Ser Phe Pro Ala Val Asp Pro Asp Thr Lys Asp Ser  
20 25 30

Ala Ala Tyr Gly His Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala  
35 40 45

Lys Arg Val Val Val Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu  
50 55 60

Asp Gly His Thr Val Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala  
65 70 75 80

Leu Gln Ala Arg Met Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser  
85 90 95

Gly Ala Val Ala Ala Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro  
100 105 110

Thr Glu Leu Ala Val Lys Gln Ala Ala Ala Ala Val Gly Gln Val His  
115 120 125

Leu Met His Gln Trp Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile  
130 135 140

Gly Gln Val Leu Leu Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala  
145 150 155 160

Arg Asn Ala Gln Arg Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val  
165 170 175

Pro Ile Val Asn Glu Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe  
180 185 190

Gly Asp Asn Asp Arg Leu Ala Ala Ile Val Ala His Leu Val Ser Ala  
195 200 205

Asp Ala Leu Val Leu Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn  
210 215 220

Pro Thr Asp Pro Thr Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn

225		230		235		240
Asp Leu Lys Gly Val Ile Ala Gly Asp Gly Gly Lys Val Gly Thr Gly						
	245		250		255	
Gly Met Ala Ser Lys Val Ser Ala Ala Arg Leu Ala Ser Arg Ser Gly						
	260		265		270	
Val Pro Val Leu Leu Thr Ser Ala Ala Asn Ile Gly Pro Ala Leu Glu						
	275		280		285	
Asp Ala Gln Val Gly Thr Val Phe His Pro Lys Asp Asn Arg Leu Ser						
	290		295		300	
Ala Trp Lys Phe Trp Ala Leu Tyr Ala Ala Asp Thr Ala Gly Lys Ile						
	305		310		315	320
Arg Leu Asp Asp Gly Ala Val Glu Ala Val Thr Ser Gly Gly Lys Ser						
	325		330		335	
Leu Leu Ala Val Gly Ile Thr Glu Ile Ile Gly Asp Phe Gln Gln Gly						
	340		345		350	
Glu Ile Val Glu Ile Leu Gly Pro Ala Gly Gln Ile Ile Gly Arg Gly						
	355		360		365	
Glu Val Ser Tyr Asp Ser Asp Thr Leu Gln Ser Met Val Gly Met Gln						
	370		375		380	
Thr Gln Asp Leu Pro Asp Gly Met Gln Arg Pro Val Val His Ala Asp						
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Tyr Leu Ser Asn Tyr Ala Ser Arg Ala						
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXN02382

<400> 291  
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 Met Ser Ser Thr Thr  
 1 5  
 cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163  
 Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala  
 10 15 20  
 aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211  
 Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly  
 25 30 35

acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt	259
Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val	
40 45 50	
gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg	307
Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala	
55 60 65	
ggt cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt	355
Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu	
70 75 80 85	
gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct	403
Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala	
90 95 100	
ggc ctg acc gac cca gtg ggt gaa gta ctg cgc gga cat gtc atg gaa	451
Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg Gly His Val Met Glu	
105 110 115	
aac ggc att cag atg aag cag gtc cgt gtg cct ttg ggc gtg atg ggc	499
Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly	
120 125 130	
atg gtc tat gaa gcc cgc cct aac gtc acc gtc gac gcc ttc ggc ctg	547
Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu	
135 140 145	
gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct	595
Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala	
150 155 160 165	
gtg cat tcc aac acc aag ctc gtg gaa atc ctg cag gac gtc ctc gag	643
Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu	
170 175 180	
cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg cct tgc caa acc	691
Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Pro Cys Gln Thr	
185 190 195	
cgc gga tcc gtc caa gat ttg atc acc gca cgc ggc ctc gtt gac gtg	739
Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg Gly Leu Val Asp Val	
200 205 210	
gtc atc cca cgc ggc ggc gca gga cta atc aac gca gtg gtc acc ggt	787
Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn Ala Val Val Thr Gly	
215 220 225	
gcg acc gtg ccc acc att gaa acc ggc acc ggc aac tgc cac ttc tac	835
Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr	
230 235 240 245	
atc gat gcc gaa gcc aag ctt gat cag gca atc gcc atg gtc atc aac	883
Ile Asp Ala Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn	
250 255 260	
ggc aag acc cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt	931
Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu	
265 270 275	
ctc gac gcc gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg	979

Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala  
 280 285 290

ctc cag gaa gca gga gtc aca att cat gga cgg gtg gcc gaa ttg gaa  
 1027

Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu  
 295 300 305

gca ttc ggt gca acc gac gtg gtg gaa gca act gaa act gac tgg gat  
 1075

Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp  
 310 315 320 325

tct gag tac ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg  
 1123

Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val  
 330 335 340

gat gga gct ctg gca cac atc gct aag tac agc acc aag cac acc gaa  
 1171

Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu  
 345 350 355

gcg atc gcc acc caa aac att gaa acc gct cag cgc ttt gca gat cgc  
 1219

Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg  
 360 365 370

gtc gat gca gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat  
 1267

Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp  
 375 380 385

ggg gag cag tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa  
 1315

Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys  
 390 395 400 405

ctg cat gca cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag  
 1363

Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys  
 410 415 420

tgg att ctg cag ggc aca gga caa att agg cct taagtttgaa gaagtaatca  
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Trp Ile Leu Gln Gly Thr Gly Gln Ile Arg Pro  
 425 430

agc  
 1419

<210> 292

<211> 432

<212> PRT

<213> Corynebacterium glutamicum

<400> 292

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Thr Glu Val Leu Ala Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp  
 20 25 30  
 Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala  
 35 40 45  
 Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala  
 50 55 60  
 Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile  
 65 70 75 80  
 Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly  
 85 90 95  
 Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg  
 100 105 110  
 Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro  
 115 120 125  
 Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val  
 130 135 140  
 Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg  
 145 150 155 160  
 Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu  
 165 170 175  
 Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu  
 180 185 190  
 Leu Pro Cys Gln Thr Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg  
 195 200 205  
 Gly Leu Val Asp Val Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn  
 210 215 220  
 Ala Val Val Thr Gly Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly  
 225 230 235 240  
 Asn Cys His Phe Tyr Ile Asp Ala Glu Ala Lys Leu Asp Gln Ala Ile  
 245 250 255  
 Ala Met Val Ile Asn Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala  
 260 265 270  
 Thr Glu Thr Ala Leu Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu  
 275 280 285  
 Ala Val Val Gln Ala Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg  
 290 295 300  
 Val Ala Glu Leu Glu Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr  
 305 310 315 320  
 Glu Thr Asp Trp Asp Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala  
 325 330 335  
 Val Val Asp Gly Val Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser

340	345	350
Thr Lys His Thr Glu Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln		
355	360	365
Arg Phe Ala Asp Arg Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser		
370	375	380
Thr Ala Tyr Thr Asp Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly		
385	390	395
Ile Ser Thr Gln Lys Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu		
405	410	415
Leu Thr Ser Thr Lys Trp Ile Leu Gln Gly Thr Gly Gln Ile Arg Pro		
420	425	430

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> FRXA02378

<400> 293  
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 cgacactgtt gcttcttaag ggtctgtata gtgggcaacc atg agt tca acg acc 115  
 Met Ser Ser Thr Thr  
 1 5  
 cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163  
 Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala  
 10 15 20  
 aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211  
 Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly  
 25 30 35  
 acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt 259  
 Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val  
 40 45 50  
 gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg 307  
 Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala  
 55 60 65  
 ggt cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt 355  
 Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu  
 70 75 80 85  
 gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct 403  
 Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala  
 90 95 100

ggc ctg acc gac cca gtg ggt gaa gta ctg cgc gga cat gtc atg gaa 451  
 Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg Gly His Val Met Glu  
 105 110 115  
  
 aac ggc att cag atg aag cag gtc cgt gtg cct ttg ggc gtg atg ggc 499  
 Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly  
 120 125 130  
  
 atg gtc tat gaa gcc cgc cct aac gtc acc gtc gac gcc ttc ggc ctg 547  
 Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu  
 135 140 145  
  
 gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct 595  
 Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala  
 150 155 160 165  
  
 gtg cat tcc aac acc aag ctc gtg gaa atc ctg cag gac gta ctc gag 643  
 Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu  
 170 175 180  
  
 cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg ctt gcc aaa ccc 691  
 Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Leu Ala Lys Pro  
 185 190 195  
  
 gcg gat ccg tcc aag att tgatcaccgg acgcg 724  
 Ala Asp Pro Ser Lys Ile  
 200

&lt;210&gt; 294

&lt;211&gt; 203

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 294

Met Ser Ser Thr Thr Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg  
 1 5 10 15  
  
 Thr Glu Val Leu Ala Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp  
 20 25 30  
  
 Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala  
 35 40 45  
  
 Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala  
 50 55 60  
  
 Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile  
 65 70 75 80  
  
 Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly  
 85 90 95  
  
 Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg  
 100 105 110  
  
 Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro  
 115 120 125  
  
 Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val



130	135	140
Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg		
145	150	155 160
Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu		
	165	170 175
Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu		
	180	185 190
Leu Leu Ala Lys Pro Ala Asp Pro Ser Lys Ile		
195	200	

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 <213> Corynebacterium glutamicum

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 <222> (1)..(600)  
 <223> FRXA02382

<400> 295

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Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr Ile Asp Ala	
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gaa gcc aag ctt gat cag gca atc gcc atg gtc atc aac ggc aag acc	96
Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn Gly Lys Thr	
20 25 30	
cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt ctc gac gcc	144
Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala	
35 40 45	
gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg ctc cag gaa	192
Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu	
50 55 60	
gca gga gtc aca att cat gga cgg gtg gcc gaa ttg gaa gca ttc ggt	240
Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly	
65 70 75 80	
gca acc gac gtg gtg gaa gca act gaa act gac tgg gat tct gag tac	288
Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr	
85 90 95	
ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg gat gga gct	336
Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala	
100 105 110	
ctg gca cac atc gct aag tac agc acc aag cac acc gaa gcg atc gcc	384
Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala	
115 120 125	
acc caa aac att gaa acc gct cag cgc ttt gca gat cgc gtc gat gca	432
Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala	
130 135 140	

gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat ggg gag cag 480  
 Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln  
 145 150 155 160

tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa ctg cat gca 528  
 Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala  
 165 170 175

cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag tgg att ctg 576  
 Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu  
 180 185 190

cag ggc aca gga caa att agg cct taagtttgaa gaagtaatca agc 623  
 Gln Gly Thr Gly Gln Ile Arg Pro  
 195 200

<210> 296

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 296

Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr Ile Asp Ala  
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Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn Gly Lys Thr  
 20 25 30

Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala  
 35 40 45

Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu  
 50 55 60

Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly  
 65 70 75 80

Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr  
 85 90 95

Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala  
 100 105 110

Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala  
 115 120 125

Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala  
 130 135 140

Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln  
 145 150 155 160

Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala  
 165 170 175

Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu  
 180 185 190

Gln Gly Thr Gly Gln Ile Arg Pro

195

200

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<212> DNA
<213> Corynebacterium glutamicum
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<223> RXA02499
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				Met	Thr	Thr	Ile	Ala		5						
				1												
gta	atc	ggc	ggc	gga	caa	atc	ggc	gag	gct	tta	gtc	tca	ggg	ttg	atc	163
Val	Ile	Gly	Gly	Gly	Gln	Ile	Gly	Glu	Ala	Leu	Val	Ser	Gly	Leu	Ile	
				10				15						20		
gcg	gcc	aac	atg	aat	cca	caa	aat	att	cgc	gtc	acc	aac	cgt	tcg	gaa	211
Ala	Ala	Asn	Met	Asn	Pro	Gln	Asn	Ile	Arg	Val	Thr	Asn	Arg	Ser	Glu	
			25					30					35			
gag	cgc	ggc	caa	gag	ctg	cgt	gac	cgc	tac	ggc	atc	ctc	aac	atg	acg	259
Glu	Arg	Gly	Gln	Glu	Leu	Arg	Asp	Arg	Tyr	Gly	Ile	Leu	Asn	Met	Thr	
		40					45					50				
gat	aat	tcc	caa	gcc	gca	gac	gaa	gcc	gac	gtg	gtg	ttc	ctg	tgc	gtg	307
Asp	Asn	Ser	Gln	Ala	Ala	Asp	Glu	Ala	Asp	Val	Val	Phe	Leu	Cys	Val	
	55					60					65					
aag	ccg	aaa	ttt	atc	gtc	gaa	gtg	ctc	tcc	gaa	atc	acc	ggc	act	ttg	355
Lys	Pro	Lys	Phe	Ile	Val	Glu	Val	Leu	Ser	Glu	Ile	Thr	Gly	Thr	Leu	
70					75			80							85	
gat	aac	aac	tcc	gca	caa	agt	gtt	gtg	gtc	agc	atg	gcc	gca	ggc	atc	403
Asp	Asn	Asn	Ser	Ala	Gln	Ser	Val	Val	Val	Ser	Met	Ala	Ala	Gly	Ile	
				90					95					100		
agc	atc	gct	gcc	atg	gaa	gaa	agc	gcc	tct	gcg	ggg	ctc	ccc	gtc	gtg	451
Ser	Ile	Ala	Ala	Met	Glu	Glu	Ser	Ala	Ser	Ala	Gly	Leu	Pro	Val	Val	
			105					110					115			
cgc	gtc	atg	ccg	aac	act	cca	atg	ctc	gtg	ggc	aag	ggc	atg	tcg	act	499
Arg	Val	Met	Pro	Asn	Thr	Pro	Met	Leu	Val	Gly	Lys	Gly	Met	Ser	Thr	
		120					125					130				
gtc	acc	aaa	ggc	cgc	tac	gtt	gac	gcg	gaa	cag	ttg	gaa	caa	gtc	aag	547
Val	Thr	Lys	Gly	Arg	Tyr	Val	Asp	Ala	Glu	Gln	Leu	Glu	Gln	Val	Lys	
	135					140					145					
gac	ttg	ttg	agc	acc	gtt	gga	gac	gtc	ctc	gaa	gtc	gcg	gaa	tca	gac	595
Asp	Leu	Leu	Ser	Thr	Val	Gly	Asp	Val	Leu	Glu	Val	Ala	Glu	Ser	Asp	
150					155					160					165	
atc	gac	gca	gtc	acc	gcg	atg	tcc	gga	tcc	tcc	cct	gca	tac	ctg	ttc	643

Ile Asp Ala Val Thr Ala Met Ser Gly Ser Ser Pro Ala Tyr Leu Phe  
 170 175 180

ctt gtg acc gaa gcg ctc att gag gca gga gtt aat cta ggc ctg ccc 691  
 Leu Val Thr Glu Ala Leu Ile Glu Ala Gly Val Asn Leu Gly Leu Pro  
 185 190 195

cgc gcg acc gct aaa aag ctc gct gtg gcc tca ttc gaa ggt gct gca 739  
 Arg Ala Thr Ala Lys Lys Leu Ala Val Ala Ser Phe Glu Gly Ala Ala  
 200 205 210

acc atg atg aag gaa acc ggc aaa gaa ccc tca gaa ttg cgc gca ggc 787  
 Thr Met Met Lys Glu Thr Gly Lys Glu Pro Ser Glu Leu Arg Ala Gly  
 215 220 225

gtt tcc tca ccc gca ggc acc acc gtc gca gcc atc cga gaa ctc gaa 835  
 Val Ser Ser Pro Ala Gly Thr Thr Val Ala Ala Ile Arg Glu Leu Glu  
 230 235 240 245

gaa agc gga atc cga ggc gct ttc tac cgc gca gcc caa gct tgc gcc 883  
 Glu Ser Gly Ile Arg Gly Ala Phe Tyr Arg Ala Ala Gln Ala Cys Ala  
 250 255 260

gac cga tct gaa gaa ctc gga aag cgc tagaaaccgt tattttcccg 930  
 Asp Arg Ser Glu Glu Leu Gly Lys Arg  
 265 270

tta 933

&lt;210&gt; 298

&lt;211&gt; 270

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 298

Met Thr Thr Ile Ala Val Ile Gly Gly Gly Gln Ile Gly Glu Ala Leu  
 1 5 10 15

Val Ser Gly Leu Ile Ala Ala Asn Met Asn Pro Gln Asn Ile Arg Val  
 20 25 30

Thr Asn Arg Ser Glu Glu Arg Gly Gln Glu Leu Arg Asp Arg Tyr Gly  
 35 40 45

Ile Leu Asn Met Thr Asp Asn Ser Gln Ala Ala Asp Glu Ala Asp Val  
 50 55 60

Val Phe Leu Cys Val Lys Pro Lys Phe Ile Val Glu Val Leu Ser Glu  
 65 70 75 80

Ile Thr Gly Thr Leu Asp Asn Asn Ser Ala Gln Ser Val Val Val Ser  
 85 90 95

Met Ala Ala Gly Ile Ser Ile Ala Ala Met Glu Glu Ser Ala Ser Ala  
 100 105 110

Gly Leu Pro Val Val Arg Val Met Pro Asn Thr Pro Met Leu Val Gly  
 115 120 125

Lys Gly Met Ser Thr Val Thr Lys Gly Arg Tyr Val Asp Ala Glu Gln

130	135	140
Leu Glu Gln Val Lys Asp	Leu Leu Ser Thr Val Gly Asp Val Leu Glu	
145	150	155 160
Val Ala Glu Ser Asp Ile Asp Ala Val Thr Ala Met Ser Gly Ser Ser		
	165	170 175
Pro Ala Tyr Leu Phe Leu Val Thr Glu Ala Leu Ile Glu Ala Gly Val		
	180	185 190
Asn Leu Gly Leu Pro Arg Ala Thr Ala Lys Lys Leu Ala Val Ala Ser		
	195	200 205
Phe Glu Gly Ala Ala Thr Met Met Lys Glu Thr Gly Lys Glu Pro Ser		
	210	215 220
Glu Leu Arg Ala Gly Val Ser Ser Pro Ala Gly Thr Thr Val Ala Ala		
225	230	235 240
Ile Arg Glu Leu Glu Glu Ser Gly Ile Arg Gly Ala Phe Tyr Arg Ala		
	245	250 255
Ala Gln Ala Cys Ala Asp Arg Ser Glu Glu Leu Gly Lys Arg		
	260	265 270

<210> 299  
 <211> 1296  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1273)  
 <223> RXS02157

<400> 299  
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 caccgtttttt agaaaagacg acaaggatgg ggaactgtaa atg agc acg ctg gaa 115  
 Met Ser Thr Leu Glu 5  
 act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag 163  
 Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu 20  
 ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc 211  
 Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val 35  
 tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc 259  
 Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala 50  
 cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt 307  
 His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly 65  
 cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag 355

His 70	Val	Ser	Asn	Leu	Phe 75	Ala	Ser	Arg	Pro	Val 80	Val	Glu	Val	Ala	Glu 85	
gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa 403																
Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln																
90 95 100																
acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct 451																
Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala																
105 110 115																
ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt 499																
Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val																
120 125 130																
cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag 547																
His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln																
135 140 145																
cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc 595																
Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe																
150 155 160 165																
tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac 643																
Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn																
170 175 180																
cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg 691																
Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr																
185 190 195																
ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg 739																
Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu																
200 205 210																
tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc 787																
Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly																
215 220 225																
gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt 835																
Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val																
230 235 240 245																
ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc 883																
Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile																
250 255 260																
ggg gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc 931																
Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly																
265 270 275																
aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc 979																
Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala																
280 285 290																
aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc																
1027																
Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala																
295 300 305																

cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt  
 1075  
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val  
 310 315 320 325

gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc  
 1123  
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg  
 330 335 340

gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att  
 1171  
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile  
 345 350 355

ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg  
 1219  
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val  
 360 365 370

atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca  
 1267  
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr  
 375 380 385

atc gca taaaggactc aaacttatga ctt  
 1296  
 Ile Ala  
 390

<210> 300  
 <211> 391  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 300  
 Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly  
 1 5 10 15  
 Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp  
 20 25 30  
 Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn  
 35 40 45  
 Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln  
 50 55 60  
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val  
 65 70 75 80  
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala  
 85 90 95  
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu  
 100 105 110  
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg  
 115 120 125

11 Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu  
 130 135 140  
 Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro  
 145 150 155 160  
 Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys  
 165 170 175  
 Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro  
 180 185 190  
 Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys  
 195 200 205  
 Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp  
 210 215 220  
 Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln  
 225 230 235 240  
 His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly  
 245 250 255  
 Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu  
 260 265 270  
 Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val  
 275 280 285  
 Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe  
 290 295 300  
 Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala  
 305 310 315 320  
 Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly  
 325 330 335  
 Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe  
 340 345 350  
 Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu  
 355 360 365  
 Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys  
 370 375 380  
 Ala Ile Ala Glu Thr Ile Ala  
 385 390

&lt;210&gt; 301

&lt;211&gt; 1269

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1246)

&lt;223&gt; RXS02262



&lt;400&gt; 301

gcaccaattt cggacctgaa atccccgagg aaaccgtgcc cgacgccgtg caggtgggcg 60

tcgataagca aaaaatcgct gataactcgaa aggcctcaaa atg acc gca acc tac 115  
Met Thr Ala Thr Tyr  
1 5

acc act gaa acc gcc atc aat ttc ttg ttc ttg agc gaa ccg gac atg 163  
Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu Ser Glu Pro Asp Met  
10 15 20

atc gcg gcc gga gtc aaa gac gtc gcg caa tgc gtc gat gtc atg gag 211  
Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys Val Asp Val Met Glu  
25 30 35

gaa acg ctc gtg ctc ttg gcg cag ggc gac tac aaa atg gcc ggt ttg 259  
Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr Lys Met Ala Gly Leu  
40 45 50

aac tcc aac tcg cat ggc gcg atg atc acc ttc ccg gaa aac cca gaa 307  
Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe Pro Glu Asn Pro Glu  
55 60 65

ttt gaa ggc atg ccc aag gac ggc ccc gac cgc cga ttc atg gcg atg 355  
Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg Arg Phe Met Ala Met  
70 75 80 85

ccc gca tac ctc ggc ggg cga ttc aaa aac acc ggc gtg aag tgg tac 403  
Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr Gly Val Lys Trp Tyr  
90 95 100

gga tcc aac gcg gaa aac aag gcc tca ggc ttg cct cgc tcg atc cac 451  
Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu Pro Arg Ser Ile His  
105 110 115

acc ttc gtc ctc aac gac acg gtc acc ggt gca ccg aag gcc atc atg 499  
Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala Pro Lys Ala Ile Met  
120 125 130

tcc gcg aac ctg ctg tcc gcc tac cgc acc ggc gcg gtt ccc ggc gtg 547  
Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly Ala Val Pro Gly Val  
135 140 145

ggc gtg aag cac tta gcg gtc gcc gac gcg aca acc ttg gct gtc gtc 595  
Gly Val Lys His Leu Ala Val Ala Asp Ala Thr Thr Leu Ala Val Val  
150 155 160 165

gga cct ggt gtc atg gcg aaa acc atc acc gaa gcg tgc atc gca gag 643  
Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu Ala Cys Ile Ala Glu  
170 175 180

cgc cca gga atc acc acc atc aag atc aag gga cgc agc gaa cgc ggc 691  
Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly Arg Ser Glu Arg Gly  
185 190 195

atc aac gcc ttt gca aca tgg gcg ttg gaa aaa ttc ccc gag atc gaa 739  
Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys Phe Pro Glu Ile Glu  
200 205 210

gtg gtc gcc gtc gga tct gaa gaa gac gtg gtc aaa gac gcc gac atc 787

Val Val Ala Val Gly Ser Glu Glu Asp Val Val Lys Asp Ala Asp Ile  
 215 220 225  
 gtc atc gcc gcc acc acc acg gac gcc gcc ggc tcc tcc gcc ttc cca 835  
 Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly Ser Ser Ala Phe Pro  
 230 235 240 245  
 tac ttc aaa aaa gaa tgg ctc aag ccg ggc gca ttg ctg ctg ctt cca 883  
 Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala Leu Leu Leu Leu Pro  
 250 255 260  
 gcc gcc ggt cgc ttc gac gac gct tat ttg ctt gac gac gcc cgc ctc 931  
 Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu Asp Asp Ala Arg Leu  
 265 270 275  
 gtt gtt gac tac atg ggg ctc tac gaa gcc tgg gca gaa gaa tac ggc 979  
 Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp Ala Glu Glu Tyr Gly  
 280 285 290  
 cca cag gcc tac caa cta ctc ggc att cca gga acc cac tgg tac gac  
 1027  
 Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly Thr His Trp Tyr Asp  
 295 300 305  
 ctg gcg ctg caa gga aaa ctc gac ctt gca aag att tcc cag att ggc  
 1075  
 Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys Ile Ser Gln Ile Gly  
 310 315 320 325  
 gat atc tgc tcc ggc aag cta ccc gga cgc acc aac gat gag gaa atc  
 1123  
 Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr Asn Asp Glu Glu Ile  
 330 335 340  
 atc ctc tat tcc gtc ggc ggc atg cca gta gaa gac gtc gcc tgg gca  
 1171  
 Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu Asp Val Ala Trp Ala  
 345 350 355  
 acc caa gtg tat gaa aac gcc ctg gaa aaa ggc gtc ggc acc aca ttg  
 1219  
 Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly Val Gly Thr Thr Leu  
 360 365 370  
 aac ctg tgg gaa tca ccc gca ctg gct tgagagaaga aacaacaatg  
 1266  
 Asn Leu Trp Glu Ser Pro Ala Leu Ala  
 375 380  
 aaa  
 1269

&lt;210&gt; 302

&lt;211&gt; 382

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 302

Met Thr Ala Thr Tyr Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu  
 1 5 10 15

Ser Glu Pro Asp Met Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys  
 20 25 30  
 Val Asp Val Met Glu Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr  
 35 40 45  
 Lys Met Ala Gly Leu Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe  
 50 55 60  
 Pro Glu Asn Pro Glu Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg  
 65 70 75 80  
 Arg Phe Met Ala Met Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr  
 85 90 95  
 Gly Val Lys Trp Tyr Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu  
 100 105 110  
 Pro Arg Ser Ile His Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala  
 115 120 125  
 Pro Lys Ala Ile Met Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly  
 130 135 140  
 Ala Val Pro Gly Val Gly Val Lys His Leu Ala Val Ala Asp Ala Thr  
 145 150 155 160  
 Thr Leu Ala Val Val Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu  
 165 170 175  
 Ala Cys Ile Ala Glu Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly  
 180 185 190  
 Arg Ser Glu Arg Gly Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys  
 195 200 205  
 Phe Pro Glu Ile Glu Val Val Ala Val Gly Ser Glu Glu Asp Val Val  
 210 215 220  
 Lys Asp Ala Asp Ile Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly  
 225 230 235 240  
 Ser Ser Ala Phe Pro Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala  
 245 250 255  
 Leu Leu Leu Leu Pro Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu  
 260 265 270  
 Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp  
 275 280 285  
 Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly  
 290 295 300  
 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys  
 305 310 315 320  
 Ile Ser Gln Ile Gly Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr  
 325 330 335

Asn Asp Glu Glu Ile Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu  
 340 345 350

Asp Val Ala Trp Ala Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly  
 355 360 365

Val Gly Thr Thr Leu Asn Leu Trp Glu Ser Pro Ala Leu Ala  
 370 375 380

<210> 303

<211> 1491

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1468)

<223> RXS02970

<400> 303

aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60

ttattttaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115  
 Leu Ala Leu Lys Gly  
 1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163  
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala  
 10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211  
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
 25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259  
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala  
 40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307  
 Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp  
 55 60 65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355  
 Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg  
 70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403  
 Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn  
 90 95 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451  
 Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val  
 105 110 115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499  
 Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly  
 120 125 130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547  
 Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly

135	140	145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly 150 155 160 165			595
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr 170 175 180			643
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser 185 190 195			691
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys 200 205 210			739
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala 215 220 225			787
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro 230 235 240 245			835
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile 250 255 260			883
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys 265 270 275			931
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile 280 285 290			979
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc 1027 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile 295 300 305			
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc 1075 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser 310 315 320 325			
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag 1123 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys 330 335 340			
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct 1171 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala 345 350 355			
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 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
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 1363  
 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His  
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 1411  
 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu  
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 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
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 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
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 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
 65 70 75 80  
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
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 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
 100 105 110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe

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His	Gly	Ala	Thr	Gly	Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg	Arg
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Leu	Gly	Asn	Pro	Thr	Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro
			180					185					190		
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Glu	Arg	Ala	Leu	Lys	His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala
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Ile	Ile	Leu	Pro	Pro	Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys
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Gln	Pro	Asp	Met	Ile	Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala
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Pro	Leu	Gly	Gly	Ile	Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly
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Ser	Glu	Ala	Tyr	Ser	Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala
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Ile	Pro	Arg	Val	Ala	Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu
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Arg	Glu	Leu	Ala	Glu	Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile
	370					375					380				
Gly	Phe	Phe	Trp	Ala	Val	Glu	Phe	Asn	Ala	Asp	Ala	Thr	Ala	Met	Ala
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Ala	Gly	Ala	Ala	Glu	Phe	Lys	Glu	Arg	Gly	Val	Trp	Pro	Met	Ile	Ser
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Gly	Asn	Arg	Phe	His	Ile	Ala	Pro	Pro	Leu	Thr	Thr	Thr	Asp	Asp	Glu
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Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala  
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Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
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His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala  
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Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp  
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Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg  
70 75 80 85  
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Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn  
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Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val  
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Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly  
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Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly  
135 140 145  
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Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly  
150 155 160 165



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Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
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Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
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Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
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His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
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Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
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Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
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Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
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 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
 35                      40                      45  
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
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 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
 65                      70                      75                      80  
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
 85                      90                      95  
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
 100                      105                      110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
 115                      120                      125  
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
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 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
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 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
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 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
 210                      215                      220

Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
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 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
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 325 330 335  
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 Met Thr Ser Met Asn  
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Thr Val Gly Phe Val Asp Arg Val Val Arg Thr Glu Asp Arg Glu Ala	
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Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg	
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Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys	
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Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu	
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Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Ile	
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Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp	
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200 205 210	
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Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser	
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Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile Val Leu Gln Ala Tyr	
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Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu Ala Gln Phe Gly Arg	
265 270 275	

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 Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys Val Arg Leu Val Lys  
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 1027  
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 295 300 305

cca gtt gcc aca gaa cct tcc aaa caa gcc acc gat gcc aat tac aag  
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 Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr Asp Ala Asn Tyr Lys  
 310 315 320 325

cgc gtc ctc tat tgg acg atg cgc aaa gaa aac atg gag ggc ctg cgc  
 1123  
 Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn Met Glu Gly Leu Arg  
 330 335 340

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 1171  
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 345 350 355

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 1219  
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 1267  
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 1507  
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 455 460 465

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 1555

Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro Phe Ile Asn Glu Pro  
 470 475 480 485

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 1603

Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln Trp Ala Thr Lys Ala  
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 1651

Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu Lys Gln Thr Lys Pro  
 505 510 515

gag gtg ttg gaa gag ggg gac gtc gac aag cta att aac gat gtg cgc  
 1699

Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu Ile Asn Asp Val Arg  
 520 525 530

gac gct gct gaa gcg tgg gca gcg cgc cca gcc cgt gaa cgc gct gag  
 1747

Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala Arg Glu Arg Ala Glu  
 535 540 545

att ttg tac aag acc gcc gag att ttg cgc gtg cga cgc gga cac ctg  
 1795

Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val Arg Arg Gly His Leu  
 550 555 560 565

atc tca gtg acg gcc gcg gag gtg ggc aaa gct gtg gaa caa acc gac  
 1843

Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala Val Glu Gln Thr Asp  
 570 575 580

ccg gaa atc tct gaa gcc att gat ttc gcc cgc tac tac gcg cat ttg  
 1891

Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg Tyr Tyr Ala His Leu  
 585 590 595

gcc ctg gaa ttg gac gac gta gac aat gcg gaa ttc acc cca gat cgc  
 1939

Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu Phe Thr Pro Asp Arg  
 600 605 610

gtc gtt gtg gtg acc ccg ccc tgg aat ttc ccc atc gcg atc ccc gct  
 1987

Val Val Val Val Thr Pro Pro Trp Asn Phe Pro Ile Ala Ile Pro Ala  
 615 620 625

gga tcg act ttc gca gca ctc gcg gcg ggc gct ggc gtg atc cac aaa  
 2035

Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala Gly Val Ile His Lys  
 630 635 640 645

ccc tca aag cct agc caa cat tgc tcc gct gca gtg gtc gaa gcc ctc  
 2083

Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala Val Val Glu Ala Leu  
 650 655 660

tgg gaa gcc ggc gtt ccc cgc gag gtt ctg cat tgc att tac cca gct  
 2131

Trp Glu Ala Gly Val Pro Arg Glu Val Leu His Cys Ile Tyr Pro Ala

665	670	675
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Asn Arg Asp Val Gly Cys Ala Leu Ile Ser His Glu His Val Asp Arg 680	685	690
gtc att ttg acc ggc tcc tcc gag acc gcc gcg atg ttc tcc tcc tgg 2227		
Val Ile Leu Thr Gly Ser Ser Glu Thr Ala Ala Met Phe Ser Ser Trp 695	700	705
cga cca gaa ctc acc atc aac ggc gaa acc tcc ggc aaa aac gcc atc 2275		
Arg Pro Glu Leu Thr Ile Asn Gly Glu Thr Ser Gly Lys Asn Ala Ile 710	715	720 725
gtg gtc acc cca tct gcc gac cgc gac ctc gcc gtc gcc gac ctg gtg 2323		
Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala Val Ala Asp Leu Val 730	735	740
aaa tcc gcc ttc ggc cat gca gga caa aaa tgt tcc gca gcc tcc ctc 2371		
Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys Ser Ala Ala Ser Leu 745	750	755
ggc atc ttg gta ggc agc gtc tac gaa tca gaa cgc ttc cgg aaa cag 2419		
Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu Arg Phe Arg Lys Gln 760	765	770
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Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp Trp Pro Thr Asn Pro 775	780	785
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Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro Ser Asp Lys Leu His 790	795	800 805
cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc 2563		
His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser Trp Leu Leu Lys Pro 810	815	820
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Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser Pro Gly Ile Lys Glu 825	830	835
ggc gtc aaa cca gga acc ttc ttc cac ctc aca gaa gta ttc gga cca 2659		
Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr Glu Val Phe Gly Pro 840	845	850
gtc ctc ggc ctg atg aaa gcc acc gac ctc aat gaa gcc atc gaa ttc 2707		
Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn Glu Ala Ile Glu Phe 855	860	865

caa aac ggc aac gac ttc gga ctc acc ggc gga ctc caa tcc ctc gac  
2755

Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly Leu Gln Ser Leu Asp  
870 875 880 885

gcc gac gaa gtc cgc acc tgg ctt gac cac gtc gat gtc gga aac gcc  
2803

Ala Asp Glu Val Arg Thr Trp Leu Asp His Val Asp Val Gly Asn Ala  
890 895 900

tac gtc aac cgc ggc atc acc ggc gcc att gtc caa cgc caa tcc ttc  
2851

Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val Gln Arg Gln Ser Phe  
905 910 915

gga ggc tgg aaa aaa tcc tcc gtc ggc ctc gga tcc aaa gcc gga gga  
2899

Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly Ser Lys Ala Gly Gly  
920 925 930

ccc aac tat gtc atg ctc atg gga acc tgg gcc gac gcg cca agc cac  
2947

Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His  
935 940 945

cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc  
2995

His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro  
950 955 960 965

gga gaa gag ctc gaa tgg ctc gaa aaa gcc aac gcc agc gat gaa aca  
3043

Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr  
970 975 980

gca tgg aac acg gaa ttc ggc agc cca cgc gac ccc tcc ggc ctc gat  
3091

Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp  
985 990 995

gta gaa gcc aac att ttc cgc tac cga cca gca gag gta gta ctc cga  
3139

Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala Glu Val Val Leu Arg  
1000 1005 1010

ctc gac gat tcc gcc aca ccc cga gaa act gcc cgc gca ttg ttg gca  
3187

Leu Asp Asp Ser Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala  
1015 1020 1025

gcc cgt cgc gcc ggg gtt act ccg cga gtt ctt caa aca cca ggt gtt  
3235

Ala Arg Arg Ala Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val  
1030 1035 1040 1045

tca gag caa gtc cgc gaa gta ttg tcc gct gct gga gtg agt gca gaa  
3283

Ser Glu Gln Val Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu  
1050 1055 1060



aca gtc gat gat tcg gta ttt att tcc aac gtg ttg cgc ggc gaa tac  
3331

Thr Val Asp Asp Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr  
1065 1070 1075

gac gag aac tcc agc gtc cga gtc cgc tac ctg ggc aaa gtt agc gac  
3379

Asp Glu Asn Ser Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp  
1080 1085 1090

act gtc cgt gaa cgc cta tct gta cgg ccc gaa gtt gtt ctg ctt gac  
3427

Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp  
1095 1100 1105

gat gca gta act gcc tcc ggt cga gtt gaa tta cgt tac tgg ctc aaa  
3475

Asp Ala Val Thr Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys  
1110 1115 1120 1125

gaa caa gca att tcc atg acg ttg cac cgt ttt gga aac cca gtt gcg  
3523

Glu Gln Ala Ile Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala  
1130 1135 1140

gcc ttc cac gag ttg gcg gag gaa ctt aaa cgt tgatcgtttt gcgcatgggt  
3576

Ala Phe His Glu Leu Ala Glu Glu Leu Lys Arg  
1145 1150

cgc  
3579

<210> 308

<211> 1152

<212> PRT

<213> Corynebacterium glutamicum

<400> 308

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Ala Val Asp Lys Val Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser  
20 25 30

Val Pro Asn Ala Asp Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro  
35 40 45

Asn Gly Leu Glu Phe Thr Val Gly Phe Val Asp Arg Val Val Arg Thr  
50 55 60

Glu Asp Arg Glu Ala Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile  
65 70 75 80

Ala Pro Ser Thr Met Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly  
85 90 95

Ser Leu Val Gly Arg Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg  
100 105 110

Ala Arg Ile Arg Gln Met Val Gly His Met Ile Val Asp Ala Arg Asp  
 115 120 125  
 Lys Gln Phe Ala Lys Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg  
 130 135 140  
 Leu Asn Ile Asn Leu Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala  
 145 150 155 160  
 Ala Lys His Leu Asp Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val  
 165 170 175  
 Glu Tyr Val Ser Ile Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met  
 180 185 190  
 Trp Gly Phe Glu Asp Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro  
 195 200 205  
 Leu Tyr Ile Glu Ala Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn  
 210 215 220  
 Leu Asp Met Glu Glu Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe  
 225 230 235 240  
 Lys Arg Leu Leu Ser Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile  
 245 250 255  
 Val Leu Gln Ala Tyr Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu  
 260 265 270  
 Ala Gln Phe Gly Arg Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys  
 275 280 285  
 Val Arg Leu Val Lys Gly Ala Asn Leu Pro Met Glu His Val His Ala  
 290 295 300  
 Gln Ile Thr Gly Trp Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr  
 305 310 315 320  
 Asp Ala Asn Tyr Lys Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn  
 325 330 335  
 Met Glu Gly Leu Arg Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile  
 340 345 350  
 Ala Phe Ala His Leu Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val  
 355 360 365  
 Glu Phe Glu Met Leu Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val  
 370 375 380  
 Ser Val Asp Val Gly Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro  
 385 390 395 400  
 Gln Glu Phe Asp Val Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu  
 405 410 415  
 Asn Ala Ala Ser Glu Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala  
 420 425 430  
 Asp Asn Pro Ser Phe Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile

435	440	445
Ser Asp Leu Ala Thr Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His		
450	455	460
Thr Gln Asp Arg Ser Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro		
465	470	475
Phe Ile Asn Glu Pro Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln		
	485	490
Trp Ala Thr Lys Ala Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu		
	500	505
Lys Gln Thr Lys Pro Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu		
	515	520
Ile Asn Asp Val Arg Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala		
	530	535
Arg Glu Arg Ala Glu Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val		
	545	550
Arg Arg Gly His Leu Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala		
	565	570
Val Glu Gln Thr Asp Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg		
	580	585
Tyr Tyr Ala His Leu Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu		
	595	600
Phe Thr Pro Asp Arg Val Val Val Val Thr Pro Pro Trp Asn Phe Pro		
	610	615
Ile Ala Ile Pro Ala Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala		
	625	630
Gly Val Ile His Lys Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala		
	645	650
Val Val Glu Ala Leu Trp Glu Ala Gly Val Pro Arg Glu Val Leu His		
	660	665
Cys Ile Tyr Pro Ala Asn Arg Asp Val Gly Cys Ala Leu Ile Ser His		
	675	680
Glu His Val Asp Arg Val Ile Leu Thr Gly Ser Ser Glu Thr Ala Ala		
	690	695
Met Phe Ser Ser Trp Arg Pro Glu Leu Thr Ile Asn Gly Glu Thr Ser		
	705	710
Gly Lys Asn Ala Ile Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala		
	725	730
Val Ala Asp Leu Val Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys		
	740	745
Ser Ala Ala Ser Leu Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu		
	755	760
		765

Arg Phe Arg Lys Gln Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp  
 770 775 780  
 Trp Pro Thr Asn Pro Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro  
 785 790 795 800  
 Ser Asp Lys Leu His His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser  
 805 810 815  
 Trp Leu Leu Lys Pro Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser  
 820 825 830  
 Pro Gly Ile Lys Glu Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr  
 835 840 845  
 Glu Val Phe Gly Pro Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn  
 850 855 860  
 Glu Ala Ile Glu Phe Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly  
 865 870 875 880  
 Leu Gln Ser Leu Asp Ala Asp Glu Val Arg Thr Trp Leu Asp His Val  
 885 890 895  
 Asp Val Gly Asn Ala Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val  
 900 905 910  
 Gln Arg Gln Ser Phe Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly  
 915 920 925  
 Ser Lys Ala Gly Gly Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala  
 930 935 940  
 Asp Ala Pro Ser His His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser  
 945 950 955 960  
 Lys Leu Asp Leu Pro Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn  
 965 970 975  
 Ala Ser Asp Glu Thr Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp  
 980 985 990  
 Pro Ser Gly Leu Asp Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala  
 995 1000 1005  
 Glu Val Val Leu Arg Leu Asp Asp Ser Ala Thr Pro Arg Glu Thr Ala  
 1010 1015 1020  
 Arg Ala Leu Leu Ala Ala Arg Arg Ala Gly Val Thr Pro Arg Val Leu  
 1025 1030 1035 1040  
 Gln Thr Pro Gly Val Ser Glu Gln Val Arg Glu Val Leu Ser Ala Ala  
 1045 1050 1055  
 Gly Val Ser Ala Glu Thr Val Asp Asp Ser Val Phe Ile Ser Asn Val  
 1060 1065 1070  
 Leu Arg Gly Glu Tyr Asp Glu Asn Ser Ser Val Arg Val Arg Tyr Leu  
 1075 1080 1085

Gly Lys Val Ser Asp Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu  
 1090 1095 1100

Val Val Leu Leu Asp Asp Ala Val Thr Ala Ser Gly Arg Val Glu Leu  
 1105 1110 1115 1120

Arg Tyr Trp Leu Lys Glu Gln Ala Ile Ser Met Thr Leu His Arg Phe  
 1125 1130 1135

Gly Asn Pro Val Ala Ala Phe His Glu Leu Ala Glu Glu Leu Lys Arg  
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<211> 476

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(453)

<223> FRXA00023

<400> 309

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 His Phe Pro Leu Arg Pro Ala Glu Val Val Leu Arg Leu Asp Asp Ser  
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gcc aca ccc cga gaa act gcc cgc gca ttg ttg gca gcc cgt cgc gcc 96  
 Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala Ala Arg Arg Ala  
 20 25 30

ggg gtt act ccg cga gtt ctt caa aca cca ggt gtt tca gag caa gtc 144  
 Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val Ser Glu Gln Val  
 35 40 45

cgc gaa gta ttg tcc gct gct gga gtg agt gca gaa aca gtc gat gat 192  
 Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu Thr Val Asp Asp  
 50 55 60

tcg gta ttt att tcc aac gtg ttg cgc ggc gaa tac gac gag aac tcc 240  
 Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr Asp Glu Asn Ser  
 65 70 75 80

agc gtc cga gtc cgc tac ctg ggc aaa gtt agc gac act gtc cgt gaa 288  
 Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp Thr Val Arg Glu  
 85 90 95

cgc cta tct gta cgg ccc gaa gtt gtt ctg ctt gac gat gca gta act 336  
 Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp Asp Ala Val Thr  
 100 105 110

gcc tcc ggt cga gtt gaa tta cgt tac tgg ctc aaa gaa caa gca att 384  
 Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys Glu Gln Ala Ile  
 115 120 125

tcc atg acg ttg cac cgt ttt gga aac cca gtt gcg gcc ttc cac gag 432  
 Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala Ala Phe His Glu

130 135 140  
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 Leu Ala Glu Glu Leu Lys Arg  
 145 150

<210> 310  
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 <213> Corynebacterium glutamicum

<400> 310  
 His Phe Pro Leu Arg Pro Ala Glu Val Val Leu Arg Leu Asp Asp Ser  
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 Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala Ala Arg Arg Ala  
 20 25 30  
 Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val Ser Glu Gln Val  
 35 40 45  
 Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu Thr Val Asp Asp  
 50 55 60  
 Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr Asp Glu Asn Ser  
 65 70 75 80  
 Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp Thr Val Arg Glu  
 85 90 95  
 Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp Asp Ala Val Thr  
 100 105 110  
 Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys Glu Gln Ala Ile  
 115 120 125  
 Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala Ala Phe His Glu  
 130 135 140  
 Leu Ala Glu Glu Leu Lys Arg  
 145 150

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 Met Thr Ser Met Asn  
 1 5

ctg cct att gag ttg gct acg ctg tct gac cag gct gtg gac aag gtg	163
Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln Ala Val Asp Lys Val	
10 15 20	
cgc tcc tgg ctg gag tac agc aaa aag gaa agc gtg ccc aat gcc gat	211
Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser Val Pro Asn Ala Asp	
25 30 35	
gcg aag cgt cta gct gca gtg ttg cag gat cct aat ggt ttg gaa ttc	259
Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro Asn Gly Leu Glu Phe	
40 45 50	
acg gtt ggt ttc gtg gat cga gtg gtt cga act gag gat cgt gaa gcg	307
Thr Val Gly Phe Val Asp Arg Val Val Arg Thr Glu Asp Arg Glu Ala	
55 60 65	
gca gcg cat gcg ttg tat gag ttg ggc aag att gct ccg tcg acg atg	355
Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile Ala Pro Ser Thr Met	
70 75 80 85	
tcc ttt ttg gat cgg gcg cag att cag gcc ggt tct ttg gtg ggg cgg	403
Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg	
90 95 100	
gcg ttg ccg cag gtt gtg gtt cct gcg gcg cgg gct cga atc cgg cag	451
Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg Ala Arg Ile Arg Gln	
105 110 115	
atg gtt ggg cac atg att gtg gat gcc cgc gac aag cag ttc gcc aag	499
Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys	
120 125 130	
gct gtc gct gag att cag tcg gat ggg cac cgc ctg aac atc aat ttg	547
Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu	
135 140 145	
cta ggt gaa gcg gtg ttg ggc cga aag gaa gca gcg aag cat ttg gat	595
Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala Ala Lys His Leu Asp	
150 155 160 165	
gac acg gtg cgg ttg ttg cgc cgt ccg gat gtg gaa tat gtg tcn nnn	643
Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Xaa	
170 175 180	
nnn ntc tct tcg gtg gca tcg cag att tcg atg tgg ggt ttc gaa gac	691
Xaa Xaa Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp	
185 190 195	
acc gtt aat tat gtt gtg gaa cag ctg aca cct tta tat ata gag ccc	739
Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Pro	
200 205 210	
gcg cgg gcg ccg aaa ggc acg aag ttc atc aac ctg gac atg gag gaa	787
Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn Leu Asp Met Glu Glu	
215 220 225	
tac cgc gat ctg cgc ctg act atg gag gtg ttc aag cgg ctg ctc tcc	835
Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser	
230 235 240 245	
aat cca gag ctg cat gaa cta gaa gcc gga att gtg ttg cag gcg tac	883

Asn	Pro	Glu	Leu	His	Glu	Leu	Glu	Ala	Gly	Ile	Val	Leu	Gln	Ala	Tyr	
				250					255					260		
ctt	ccc	gat	gcc	ctc	ggg	gca	atc	cag	gac	ttg	gcg	cag	ttc	ggc	cgc	931
Leu	Pro	Asp	Ala	Leu	Gly	Ala	Ile	Gln	Asp	Leu	Ala	Gln	Phe	Gly	Arg	
			265					270					275			
gag	cgc	gtc	aac	aca	ggc	ggg	gcg	ggc	gtt	aag	gtt	cgc	ctg	gtc	aag	979
Glu	Arg	Val	Asn	Thr	Gly	Gly	Ala	Gly	Val	Lys	Val	Arg	Leu	Val	Lys	
		280					285					290				
ggg	gct	aat	ttg	cct	atg	gag	cac	gtc	cac	gcg	cag	atc	acc	ggc	tgg	
1027																
Gly	Ala	Asn	Leu	Pro	Met	Glu	His	Val	His	Ala	Gln	Ile	Thr	Gly	Trp	
	295					300					305					
cca	gtt	gcc	aca	gaa	cct	tcc	aaa	caa	gcc	acc	gat	gcc	aat	tac	aag	
1075																
Pro	Val	Ala	Thr	Glu	Pro	Ser	Lys	Gln	Ala	Thr	Asp	Ala	Asn	Tyr	Lys	
310					315					320					325	
cgc	gtc	ctc	tat	tgg	acg	atg	cgc	aaa	gaa	aac	atg	gag	ggc	ctg	cgc	
1123																
Arg	Val	Leu	Tyr	Trp	Thr	Met	Arg	Lys	Glu	Asn	Met	Glu	Gly	Leu	Arg	
				330					335					340		
ctg	ggc	gtt	gcc	ggc	cac	aac	ctt	ttc	gac	ata	gca	ttc	gca	cat	ttg	
1171																
Leu	Gly	Val	Ala	Gly	His	Asn	Leu	Phe	Asp	Ile	Ala	Phe	Ala	His	Leu	
			345					350					355			
ctc	tct	gtg	gag	cgt	ggg	gta	gcg	gac	cgt	gtg	gag	ttc	gaa	atg	ctg	
1219																
Leu	Ser	Val	Glu	Arg	Gly	Val	Ala	Asp	Arg	Val	Glu	Phe	Glu	Met	Leu	
		360					365					370				
cag	ggc	atg	gcg	tcc	gat	cag	gcg	cgc	gcc	gtc	agc	gtt	gac	gtc	ggg	
1267																
Gln	Gly	Met	Ala	Ser	Asp	Gln	Ala	Arg	Ala	Val	Ser	Val	Asp	Val	Gly	
	375					380					385					
gag	ctg	ctg	ctt	tac	gta	cca	gcc	gtg	cgc	cca	caa	gaa	ttc	gac	gtg	
1315																
Glu	Leu	Leu	Leu	Tyr	Val	Pro	Ala	Val	Arg	Pro	Gln	Glu	Phe	Asp	Val	
390					395					400					405	
gcc	att	tct	tac	ctc	gtg	cgc	cgc	ctc	gag	gaa	aac	gcc	gcg	agc	gaa	
1363																
Ala	Ile	Ser	Tyr	Leu	Val	Arg	Arg	Leu	Glu	Glu	Asn	Ala	Ala	Ser	Glu	
				410					415					420		
aac	ttc	atg	tcc	gcc	atc	ttc	gac	ctc	gac	gcc	gac	aac	ccg	tcc	ttc	
1411																
Asn	Phe	Met	Ser	Ala	Ile	Phe	Asp	Leu	Asp	Ala	Asp	Asn	Pro	Ser	Phe	
			425					430					435			
aag	cga	gag	gag	agc	cgc	ttc	cgc	gcc	tcc	ata	tct	gac	ctc	gcc	acg	
1459																
Lys	Arg	Glu	Glu	Ser	Arg	Phe	Arg	Ala	Ser	Ile	Ser	Asp	Leu	Ala	Thr	
		440					445					450				



ctc atc gac gtg ccc gcg ccc ggc ccc aac cac aca caa gac cgc agc  
1507

Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His Thr Gln Asp Arg Ser  
455 460 465

aaa gag acg ctt ctc gac gcc ccc ctc gtc cca ttt atc aac gag ccc  
1555

Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro Phe Ile Asn Glu Pro  
470 475 480 485

gac acc aac cca gcg ctc atc caa aac caa cag tgg gcc aca aaa gcc  
1603

Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln Trp Ala Thr Lys Ala  
490 495 500

gtc gcc acc gca gca gag ccc ggt tgg ttg gaa aaa caa aca aag ccg  
1651

Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu Lys Gln Thr Lys Pro  
505 510 515

gag gtg ttg gaa gag ggg gac gtc gac aag cta att aac gat gtg cgc  
1699

Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu Ile Asn Asp Val Arg  
520 525 530

gac gct gct gaa gcg tgg gca gcg cgc cca gcc cgt gaa cgc gct gag  
1747

Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala Arg Glu Arg Ala Glu  
535 540 545

att ttg tac aag acc gcc gag att ttg cgc gtg cga cgc gga cac ctg  
1795

Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val Arg Arg Gly His Leu  
550 555 560 565

atc tca gtg acg gcc gcg gag gtg ggc aaa gct gtg gaa caa acc gac  
1843

Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala Val Glu Gln Thr Asp  
570 575 580

ccg gaa atc tct gaa gcc att gat ttc gcc cgc tac tac gcg cat ttg  
1891

Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg Tyr Tyr Ala His Leu  
585 590 595

gcc ctg gaa ttg gac gac gta gac aat gcg gaa ttc acc cca gat cgc  
1939

Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu Phe Thr Pro Asp Arg  
600 605 610

gtc gtt gtg gtg acc ccg ccc tgg aat ttc ccc atc gcg atc ccc gct  
1987

Val Val Val Val Thr Pro Pro Trp Asn Phe Pro Ile Ala Ile Pro Ala  
615 620 625

gga tcg act ttc gca gca ctc gcg gcg ggc gct ggc gtg atc cac aaa  
2035

Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala Gly Val Ile His Lys  
630 635 640 645

ccc tca aag cct agc caa cat tgc tcc gct gca gtg gtc gaa gcc ctc  
2083

Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala Val Val Glu Ala Leu  
650 655 660

tgg gaa gcc ggc gtt ccc cgc gag gtt ctg cat tgc att tac cca gct  
2131

Trp Glu Ala Gly Val Pro Arg Glu Val Leu His Cys Ile Tyr Pro Ala  
665 670 675

aat cgc gat gtt gga tgt gcg ttg atc agc cat gaa cac gtc gac cgc  
2179

Asn Arg Asp Val Gly Cys Ala Leu Ile Ser His Glu His Val Asp Arg  
680 685 690

gtc att ttg acc ggc tcc tcc gag acc gcc gcg atg ttc tcc tcc tgg  
2227

Val Ile Leu Thr Gly Ser Ser Glu Thr Ala Ala Met Phe Ser Ser Trp  
695 700 705

cga cca gaa ctc acc atc aac ggc gaa acc tcc ggc aaa aac gcc atc  
2275

Arg Pro Glu Leu Thr Ile Asn Gly Glu Thr Ser Gly Lys Asn Ala Ile  
710 715 720 725

gtg gtc acc cca tct gcc gac cgc gac ctc gcc gtc gcc gac ctg gtg  
2323

Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala Val Ala Asp Leu Val  
730 735 740

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2371

Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys Ser Ala Ala Ser Leu  
745 750 755

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2419

Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu Arg Phe Arg Lys Gln  
760 765 770

ctg gta gac gcc gca tcc tca ctc atc gtc gac tgg cct acc aac ccc  
2467

Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp Trp Pro Thr Asn Pro  
775 780 785

tcc gca acc gtc gga cca ctc acc gaa ctc ccc agc gat aaa ctc cac  
2515

Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro Ser Asp Lys Leu His  
790 795 800 805

cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc  
2563

His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser Trp Leu Leu Lys Pro  
810 815 820

cga caa ctc gac gac acc ggc cga ctc tgg tca ccc ggc atc aaa gaa  
2611

Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser Pro Gly Ile Lys Glu  
825 830 835

ggc gtc aaa cca gga acc ttc ttc cac ctc aca gaa gta ttc gga cca  
2659

Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr Glu Val Phe Gly Pro  
840 845 850

gtc ctc ggc ctg atg aaa gcc acc gac ctc aat gaa gcc atc gaa ttc  
2707

Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn Glu Ala Ile Glu Phe  
855 860 865

caa aac ggc aac gac ttc gga ctc acc ggc gga ctc caa tcc ctc gac  
2755

Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly Leu Gln Ser Leu Asp  
870 875 880 885

gcc gac gaa gtc cgc acc tgg ctt gac cac gtc gat gtc gga aac gcc  
2803

Ala Asp Glu Val Arg Thr Trp Leu Asp His Val Asp Val Gly Asn Ala  
890 895 900

tac gtc aac cgc ggc atc acc ggc gcc att gtc caa cgc caa tcc ttc  
2851

Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val Gln Arg Gln Ser Phe  
905 910 915

gga ggc tgg aaa aaa tcc tcc gtc ggc ctc gga tcc aaa gcc gga gga  
2899

Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly Ser Lys Ala Gly Gly  
920 925 930

ccc aac tat gtc atg ctc atg gga acc tgg gcc gac gcg cca agc cac  
2947

Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His  
935 940 945

cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc  
2995

His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro  
950 955 960 965

gga gaa gag ctc gaa tgg ctc gaa aaa gcc aac gcc agc gat gaa aca  
3043

Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr  
970 975 980

gca tgg aac acg gaa ttc ggc agc cca cgc gac ccc tcc ggc ctc gat  
3091

Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp  
985 990 995

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3124

Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala  
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<210> 312

<211> 1008

<212> PRT

<213> Corynebacterium glutamicum

&lt;400&gt; 312

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Val	Pro	Asn	Ala	Asp	Ala	Lys	Arg	Leu	Ala	Ala	Val	Leu	Gln	Asp	Pro
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Asn	Gly	Leu	Glu	Phe	Thr	Val	Gly	Phe	Val	Asp	Arg	Val	Val	Arg	Thr
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Glu	Asp	Arg	Glu	Ala	Ala	Ala	His	Ala	Leu	Tyr	Glu	Leu	Gly	Lys	Ile
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Ala	Lys	His	Leu	Asp	Asp	Thr	Val	Arg	Leu	Leu	Arg	Arg	Pro	Asp	Val
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Glu	Tyr	Val	Ser	Xaa	Xaa	Xaa	Ser	Ser	Val	Ala	Ser	Gln	Ile	Ser	Met
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Trp	Gly	Phe	Glu	Asp	Thr	Val	Asn	Tyr	Val	Val	Glu	Gln	Leu	Thr	Pro
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Leu	Tyr	Ile	Glu	Pro	Ala	Arg	Ala	Pro	Lys	Gly	Thr	Lys	Phe	Ile	Asn
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Leu	Asp	Met	Glu	Glu	Tyr	Arg	Asp	Leu	Arg	Leu	Thr	Met	Glu	Val	Phe
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Lys	Arg	Leu	Leu	Ser	Asn	Pro	Glu	Leu	His	Glu	Leu	Glu	Ala	Gly	Ile
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Val	Leu	Gln	Ala	Tyr	Leu	Pro	Asp	Ala	Leu	Gly	Ala	Ile	Gln	Asp	Leu
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Ala	Gln	Phe	Gly	Arg	Glu	Arg	Val	Asn	Thr	Gly	Gly	Ala	Gly	Val	Lys
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Gln	Ile	Thr	Gly	Trp	Pro	Val	Ala	Thr	Glu	Pro	Ser	Lys	Gln	Ala	Thr
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 325 330 335  
 Met Glu Gly Leu Arg Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile  
 340 345 350  
 Ala Phe Ala His Leu Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val  
 355 360 365  
 Glu Phe Glu Met Leu Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val  
 370 375 380  
 Ser Val Asp Val Gly Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro  
 385 390 395 400  
 Gln Glu Phe Asp Val Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu  
 405 410 415  
 Asn Ala Ala Ser Glu Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala  
 420 425 430  
 Asp Asn Pro Ser Phe Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile  
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 Ser Asp Leu Ala Thr Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His  
 450 455 460  
 Thr Gln Asp Arg Ser Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro  
 465 470 475 480  
 Phe Ile Asn Glu Pro Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln  
 485 490 495  
 Trp Ala Thr Lys Ala Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu  
 500 505 510  
 Lys Gln Thr Lys Pro Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu  
 515 520 525  
 Ile Asn Asp Val Arg Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala  
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 545 550 555 560  
 Arg Arg Gly His Leu Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala  
 565 570 575  
 Val Glu Gln Thr Asp Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg  
 580 585 590  
 Tyr Tyr Ala His Leu Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu  
 595 600 605  
 Phe Thr Pro Asp Arg Val Val Val Val Thr Pro Pro Trp Asn Phe Pro  
 610 615 620  
 Ile Ala Ile Pro Ala Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala  
 625 630 635 640  
 Gly Val Ile His Lys Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala

645						650						655					
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Cys	Ile	Tyr	Pro	Ala	Asn	Arg	Asp	Val	Gly	Cys	Ala	Leu	Ile	Ser	His		
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Glu	His	Val	Asp	Arg	Val	Ile	Leu	Thr	Gly	Ser	Ser	Glu	Thr	Ala	Ala		
	690						695				700						
Met	Phe	Ser	Ser	Trp	Arg	Pro	Glu	Leu	Thr	Ile	Asn	Gly	Glu	Thr	Ser		
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Gly	Lys	Asn	Ala	Ile	Val	Val	Thr	Pro	Ser	Ala	Asp	Arg	Asp	Leu	Ala		
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Ser	Ala	Ala	Ser	Leu	Gly	Ile	Leu	Val	Gly	Ser	Val	Tyr	Glu	Ser	Glu		
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Arg	Phe	Arg	Lys	Gln	Leu	Val	Asp	Ala	Ala	Ser	Ser	Leu	Ile	Val	Asp		
	770						775				780						
Trp	Pro	Thr	Asn	Pro	Ser	Ala	Thr	Val	Gly	Pro	Leu	Thr	Glu	Leu	Pro		
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Ser	Asp	Lys	Leu	His	His	Ala	Leu	Thr	Thr	Leu	Glu	Glu	Gly	Glu	Ser		
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			820					825					830				
Pro	Gly	Ile	Lys	Glu	Gly	Val	Lys	Pro	Gly	Thr	Phe	Phe	His	Leu	Thr		
		835					840					845					
Glu	Val	Phe	Gly	Pro	Val	Leu	Gly	Leu	Met	Lys	Ala	Thr	Asp	Leu	Asn		
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Glu	Ala	Ile	Glu	Phe	Gln	Asn	Gly	Asn	Asp	Phe	Gly	Leu	Thr	Gly	Gly		
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			900					905					910				
Gln	Arg	Gln	Ser	Phe	Gly	Gly	Trp	Lys	Lys	Ser	Ser	Val	Gly	Leu	Gly		
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Ser	Lys	Ala	Gly	Gly	Pro	Asn	Tyr	Val	Met	Leu	Met	Gly	Thr	Trp	Ala		
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Asp	Ala	Pro	Ser	His	His	Ala	Pro	Arg	Glu	Thr	Asn	Pro	Leu	Ile	Ser		
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Lys	Leu	Asp	Leu	Pro	Gly	Glu	Glu	Leu	Glu	Trp	Leu	Glu	Lys	Ala	Asn		
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101) .. (904)

<223> RXC02498

<400> 313

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 Met Ser Glu Glu Lys  
 1 5  
 ctc aca gtc gct gag ctg atg gcg cgt gcc gcg aaa gag gga cgc tcc 163  
 Leu Thr Val Ala Glu Leu Met Ala Arg Ala Ala Lys Glu Gly Arg Ser  
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 acc gat gct ccc cga cga cgc agg cgc cgc agc atc gaa gac ggt ggc 211  
 Thr Asp Ala Pro Arg Arg Arg Arg Arg Arg Ser Ile Glu Asp Gly Gly  
 25 30 35  
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 Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro Ala Val Lys Glu Lys  
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 ccc gcg gag tcc aag cac tcc agc gtg ccc atc gat gca cca gca gaa 307  
 Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile Asp Ala Pro Ala Glu  
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 cct gag gtt gtt gag gcc ccc aag cct gag ccc gcc gaa gaa gta gaa 355  
 Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro Ala Glu Glu Val Glu  
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 Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln Glu Thr Pro Glu Arg  
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 Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu Arg Ile Val Asp Glu  
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 aaa gat cca att agc ttg acg acg ggc gcg ttc ccc gtg gtt ccg gca 499  
 Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe Pro Val Val Pro Ala  
 120 125 130  
 gtt gcc gcc aag ccg gcg ccc gta gtg cgc gcg gag aag gac gcc gat 547

Val Ala Ala Lys Pro Ala Pro Val Val Arg Ala Glu Lys Asp Ala Asp  
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 Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu Val Glu Val Asp Asn  
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 act gac acc acg cag atg gct gtg gtg gaa gaa gtt gac gag gag cca 643  
 Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu Val Asp Glu Glu Pro  
 170 175 180  
 gag caa gaa aac aaa atg tcc gta ttc gcg atc atc atg atg gcg atc 691  
 Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile Ile Met Met Ala Ile  
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 Val Gly Val Val Leu Gly Val Val Val Phe Leu Gly Phe Glu Met Leu  
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 Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val Leu Ala Val Gly Val  
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 Thr Leu Gly Met Val Gly Ile Ile His Ala Leu Arg Thr Ser Arg Asp  
 230 235 240 245  
 ggt ttc agc atg gtt ctc gca gga atc gtg ggc ctg gtc atg acg ttc 883  
 Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly Leu Val Met Thr Phe  
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 Gly Pro Leu Ala Ile Val Met  
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 <213> Corynebacterium glutamicum

<400> 314

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 Ile Glu Asp Gly Gly Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro  
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 Ala Val Lys Glu Lys Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile  
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 Asp Ala Pro Ala Glu Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro  
 65 70 75 80  
 Ala Glu Glu Val Glu Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln  
 85 90 95  
 Glu Thr Pro Glu Arg Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu



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Val	Asp	Glu	Glu	Pro	Glu	Gln	Glu	Asn	Lys	Met	Ser	Val	Phe	Ala	Ile	
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Ile	Met	Met	Ala	Ile	Val	Gly	Val	Val	Leu	Gly	Val	Val	Val	Phe	Leu	
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 <223> RXA01491

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 Met Leu Asp Glu Ser 5  
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 ttg ttt cca aat tcg gca aag ttt tct ttc att aaa act ggc gat gct 163  
 Leu Phe Pro Asn Ser Ala Lys Phe Ser Phe Ile Lys Thr Gly Asp Ala 20  
 10 15  
 gtt aat tta gac cat ttc cat cag ttg cat ccg ttg gaa aag gca ctg 211  
 Val Asn Leu Asp His Phe His Gln Leu His Pro Leu Glu Lys Ala Leu 35  
 25 30  
 gta gcg cac tcg gtt gat att aga aaa gca gag ttt gga gat gcc agg 259  
 Val Ala His Ser Val Asp Ile Arg Lys Ala Glu Phe Gly Asp Ala Arg 50  
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 Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly Arg Asp Ser Gly Asp  
 55 60 65  
 ccc att ttg cgt ggg gaa cga gga atg cca ttg tgg cct tct tcg gtg 355  
 Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu Trp Pro Ser Ser Val  
 70 75 80 85  
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 Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg Ala Ala Val Val Ala  
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 cca cga ttg ttg gtg cgt tct atg gga ttg gat gcc gaa cct gcg gag 451  
 Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp Ala Glu Pro Ala Glu  
 105 110 115  
 ccg ttg ccc aag gat gtt ttg ggt tca atc gct cgg gtg ggg gag att 499  
 Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala Arg Val Gly Glu Ile  
 120 125 130  
 cct caa ctt aag cgc ttg gag gaa caa ggt gtg cac tgc gcg gat cgc 547  
 Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val His Cys Ala Asp Arg  
 135 140 145  
 ctg ctg ttt tgt gcc aag gaa gca aca tac aaa gcg tgg ttc ccg ctg 595  
 Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys Ala Trp Phe Pro Leu  
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 Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu Ile Asp Leu Arg Asp  
 170 175 180  
 gat ggc act ttt gtg tcc tat ttg ctg gtt cga cca act cca gtg ccg 691  
 Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg Pro Thr Pro Val Pro  
 185 190 195  
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 Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly Tyr Val Ile Ala Ala  
 200 205 210  
 act gca gtg act tgaactggat ggagaggata cct 774  
 Thr Ala Val Thr  
 215

&lt;210&gt; 316

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 316

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 Lys Thr Gly Asp Ala Val Asn Leu Asp His Phe His Gln Leu His Pro  
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 Leu Glu Lys Ala Leu Val Ala His Ser Val Asp Ile Arg Lys Ala Glu  
 35 40 45

Phe Gly Asp Ala Arg Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly  
 50 55 60  
 Arg Asp Ser Gly Asp Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu  
 65 70 75 80  
 Trp Pro Ser Ser Val Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg  
 85 90 95  
 Ala Ala Val Val Ala Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp  
 100 105 110  
 Ala Glu Pro Ala Glu Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala  
 115 120 125  
 Arg Val Gly Glu Ile Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val  
 130 135 140  
 His Cys Ala Asp Arg Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys  
 145 150 155 160  
 Ala Trp Phe Pro Leu Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu  
 165 170 175  
 Ile Asp Leu Arg Asp Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg  
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 Met Ala Glu Lys Gly 5  
 att acc gcg ccg aaa ggc ttc gtt gct tct gca acg acc gcg ggt att 163  
 Ile Thr Ala Pro Lys Gly Phe Val Ala Ser Ala Thr Thr Ala Gly Ile 20  
 aaa gct tct ggc aat cct gac atg gcg ttg gtg gtt aac cag ggt cca 211  
 Lys Ala Ser Gly Asn Pro Asp Met Ala Leu Val Val Asn Gln Gly Pro 35  
 gag ttt tcc gca gcg gcc gtg ttt aca cgt aac cga gtt ttc gca gcg 259  
 Glu Phe Ser Ala Ala Ala Val Phe Thr Arg Asn Arg Val Phe Ala Ala

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gtt ttg tac aac gct ggt aat gct aat gcg tgt aat ggt ctg cag ggt Val Leu Tyr Asn Ala Gly Asn Ala Asn Ala Cys Asn Gly Leu Gln Gly 70 75 80 85			355
gag aag gat gct cgt gag tct gtt tct cat cta gct caa aat ttg ggc Glu Lys Asp Ala Arg Glu Ser Val Ser His Leu Ala Gln Asn Leu Gly 90 95 100			403
ttg gag gat tcc gat att ggt gtg tgt tcc act ggt ctt att ggt gag Leu Glu Asp Ser Asp Ile Gly Val Cys Ser Thr Gly Leu Ile Gly Glu 105 110 115			451
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gag ggc gct ttg ggt gac aat ggt gca gct gct gcc aag gcg atc atg Glu Gly Ala Leu Gly Asp Asn Gly Ala Ala Ala Lys Ala Ile Met 135 140 145			547
acc act gac acg gtg gat aag gaa acc gtc gtg ttt gct gat ggt tgg Thr Thr Asp Thr Val Asp Lys Glu Thr Val Val Phe Ala Asp Gly Trp 150 155 160 165			595
act gtc ggc gga atg ggc aag ggc gtg ggc atg atg gcg ccg tct ctt Thr Val Gly Gly Met Gly Lys Gly Val Gly Met Met Ala Pro Ser Leu 170 175 180			643
gcc acc atg ctg gtc tgc ttg acc act gat gca tcc gtt act cag gaa Ala Thr Met Leu Val Cys Leu Thr Thr Asp Ala Ser Val Thr Gln Glu 185 190 195			691
atg gct cag atc gcg ctg gct aat gct acg gcc gtt acg ttt gac acc Met Ala Gln Ile Ala Leu Ala Asn Ala Thr Ala Val Thr Phe Asp Thr 200 205 210			739
ctg gat att gat gga tca acc tcc acc aat gac acc gtg ttc ctg ctg Leu Asp Ile Asp Gly Ser Thr Ser Thr Asn Asp Thr Val Phe Leu Leu 215 220 225			787
gca tct ggc gct agc gga atc acc cca act cag gat gaa ctc aac gat Ala Ser Gly Ala Ser Gly Ile Thr Pro Thr Gln Asp Glu Leu Asn Asp 230 235 240 245			835
gcg gtg tac gca gct tgt tct gat atc gca gcg aag ctt cag gct gat Ala Val Tyr Ala Ala Cys Ser Asp Ile Ala Ala Lys Leu Gln Ala Asp 250 255 260			883
gca gag ggt gtg acc aag cgc gtt gct gtg aca gtg gtg gga acc acc Ala Glu Gly Val Thr Lys Arg Val Ala Val Thr Val Val Gly Thr Thr 265 270 275			931
aac aac gag cag gcg att aat gcg gct cgc act gtt gct cgt gac aat Asn Asn Glu Gln Ala Ile Asn Ala Ala Arg Thr Val Ala Arg Asp Asn 280 285 290			979

ttg ttc aag tgc gca atg ttt gga tct gat cca aac tgg ggt cgc gtg  
1027

Leu Phe Lys Cys Ala Met Phe Gly Ser Asp Pro Asn Trp Gly Arg Val  
295 300 305

ttg gct gca gtc ggc atg gct gat gct gat atg gaa cca gag aag att  
1075

Leu Ala Ala Val Gly Met Ala Asp Ala Asp Met Glu Pro Glu Lys Ile  
310 315 320 325

tct gtg ttc ttc aat ggt caa gca gta tgc ctt gat tcc act ggc gct  
1123

Ser Val Phe Phe Asn Gly Gln Ala Val Cys Leu Asp Ser Thr Gly Ala  
330 335 340

cct ggt gct cgt gag gtg gat ctt tcc ggc gct gac att gat gtc cga  
1171

Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala Asp Ile Asp Val Arg  
345 350 355

att gat ttg ggc acc agt ggg gaa ggc cag gca aca gtt cga acc act  
1219

Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala Thr Val Arg Thr Thr  
360 365 370

gac ctg agc ttc tcc tac gtg gag atc aac tcc gcg tac agc tct  
1264

Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser Ala Tyr Ser Ser  
375 380 385

taaaaagaaa cagcactcca act  
1287

<210> 318

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

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20 25 30

Val Asn Gln Gly Pro Glu Phe Ser Ala Ala Ala Val Phe Thr Arg Asn  
35 40 45

Arg Val Phe Ala Ala Pro Val Lys Val Ser Arg Glu Asn Val Ala Asp  
50 55 60

Gly Gln Ile Arg Ala Val Leu Tyr Asn Ala Gly Asn Ala Asn Ala Cys  
65 70 75 80

Asn Gly Leu Gln Gly Glu Lys Asp Ala Arg Glu Ser Val Ser His Leu  
85 90 95

Ala Gln Asn Leu Gly Leu Glu Asp Ser Asp Ile Gly Val Cys Ser Thr  
100 105 110

Gly Leu Ile Gly Glu Leu Leu Pro Met Asp Lys Leu Asn Ala Gly Ile  
 115 120 125  
 Asp Gln Leu Thr Ala Glu Gly Ala Leu Gly Asp Asn Gly Ala Ala Ala  
 130 135 140  
 Ala Lys Ala Ile Met Thr Thr Asp Thr Val Asp Lys Glu Thr Val Val  
 145 150 155 160  
 Phe Ala Asp Gly Trp Thr Val Gly Gly Met Gly Lys Gly Val Gly Met  
 165 170 175  
 Met Ala Pro Ser Leu Ala Thr Met Leu Val Cys Leu Thr Thr Asp Ala  
 180 185 190  
 Ser Val Thr Gln Glu Met Ala Gln Ile Ala Leu Ala Asn Ala Thr Ala  
 195 200 205  
 Val Thr Phe Asp Thr Leu Asp Ile Asp Gly Ser Thr Ser Thr Asn Asp  
 210 215 220  
 Thr Val Phe Leu Leu Ala Ser Gly Ala Ser Gly Ile Thr Pro Thr Gln  
 225 230 235 240  
 Asp Glu Leu Asn Asp Ala Val Tyr Ala Ala Cys Ser Asp Ile Ala Ala  
 245 250 255  
 Lys Leu Gln Ala Asp Ala Glu Gly Val Thr Lys Arg Val Ala Val Thr  
 260 265 270  
 Val Val Gly Thr Thr Asn Asn Glu Gln Ala Ile Asn Ala Ala Arg Thr  
 275 280 285  
 Val Ala Arg Asp Asn Leu Phe Lys Cys Ala Met Phe Gly Ser Asp Pro  
 290 295 300  
 Asn Trp Gly Arg Val Leu Ala Ala Val Gly Met Ala Asp Ala Asp Met  
 305 310 315 320  
 Glu Pro Glu Lys Ile Ser Val Phe Phe Asn Gly Gln Ala Val Cys Leu  
 325 330 335  
 Asp Ser Thr Gly Ala Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala  
 340 345 350  
 Asp Ile Asp Val Arg Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala  
 355 360 365  
 Thr Val Arg Thr Thr Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser  
 370 375 380  
 Ala Tyr Ser Ser  
 385

&lt;210&gt; 319

&lt;211&gt; 1074

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1051)  
 <223> RXA02156

<400> 319

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aacagcactc caactaacaa gcagggaaaa gggcacaggc atg aat gac ttg atc 115
                                         Met Asn Asp Leu Ile
                                         1                               5

aaa gat tta ggc tct gag gtg cgc gca aat gtc ctc gct gag gcg ttg 163
Lys Asp Leu Gly Ser Glu Val Arg Ala Asn Val Leu Ala Glu Ala Leu
                               10                               15                               20

cca tgg ttg cag cac ttc cgc gac aag att gtt gtc gtg aaa tat ggc 211
Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val Val Val Lys Tyr Gly
                               25                               30                               35

gga aac gcc atg gtg gat gat gat ctc aag gct gct ttt gct gcc gac 259
Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala Ala Phe Ala Ala Asp
                               40                               45                               50

atg gtc ttc ttg cgc acc gtg ggc gca aaa cca gtg gtg gtg cac ggt 307
Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro Val Val Val His Gly
                               55                               60                               65

ggt gga cct cag att tct gag atg cta aac cgt gtg ggt ctc cag ggc 355
Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg Val Gly Leu Gln Gly
                               70                               75                               80                               85

gag ttc aag ggt ggt ttc cgt gtg acc act cct gag gtc atg gac att 403
Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro Glu Val Met Asp Ile
                               90                               95                               100

gtg cgc atg gtg ctc ttt ggt cag gtc ggt cgc gat tta gtt ggt ttg 451
Val Arg Met Val Leu Phe Gly Gln Val Gly Arg Asp Leu Val Gly Leu
                               105                               110                               115

atc aac tct cat ggc cct tac gct gtg gga acc tcc ggt gag gat gcc 499
Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr Ser Gly Glu Asp Ala
                               120                               125                               130

ggc ctg ttt acc gcg cag aag cgc atg gtc aac atc gat ggc gta ccc 547
Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn Ile Asp Gly Val Pro
                               135                               140                               145

act gat att ggt ttg gtc gga gac atc att aat gtc gat gcc tct tcc 595
Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn Val Asp Ala Ser Ser
150                               155                               160                               165

ttg atg gat atc atc gag gcc ggt cgc att cct gtg gtc tct acg att 643
Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro Val Val Ser Thr Ile
                               170                               175                               180

gct cca ggc gaa gac ggc cag att tac aac att aac gcc gat acc gca 691
Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile Asn Ala Asp Thr Ala
                               185                               190                               195

gca ggt gct ttg gct gca gcg att ggt gca gaa cgc ctg ctg gtt ctc 739

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Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu Arg Leu Leu Val Leu  
 200 205 210

acc aat gtg gaa ggt ctg tac acc gat tgg cct gat aag agc tca ctg 787  
 Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro Asp Lys Ser Ser Leu  
 215 220 225

gtg tcc aag atc aag gcc acc gag ctg gag gcc att ctt ccg gga ctt 835  
 Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala Ile Leu Pro Gly Leu  
 230 235 240 245

gat tcc ggc atg att cca aag atg gag tct tgc ttg aac gcg gtg cgt 883  
 Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys Leu Asn Ala Val Arg  
 250 255 260

ggg gga gta agc gct gct cat gtc att gac ggc cgc atc gcg cac tcg 931  
 Gly Gly Val Ser Ala Ala His Val Ile Asp Gly Arg Ile Ala His Ser  
 265 270 275

gtg ttg ctg gag ctt ttg acc atg ggt gga att ggc acg atg gtg ctg 979  
 Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile Gly Thr Met Val Leu  
 280 285 290

ccg gat gtt ttt gat cgg gag aat tat cct gaa ggc acc gtt ttt aga  
 1027  
 Pro Asp Val Phe Asp Arg Glu Asn Tyr Pro Glu Gly Thr Val Phe Arg  
 295 300 305

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 1074  
 Lys Asp Asp Lys Asp Gly Glu Leu  
 310 315

<210> 320  
 <211> 317  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 320  
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 Val Val Lys Tyr Gly Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala  
 35 40 45  
 Ala Phe Ala Ala Asp Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro  
 50 55 60  
 Val Val Val His Gly Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg  
 65 70 75 80  
 Val Gly Leu Gln Gly Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro  
 85 90 95  
 Glu Val Met Asp Ile Val Arg Met Val Leu Phe Gly Gln Val Gly Arg  
 100 105 110



Asp Leu Val Gly Leu Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr  
115 120 125

Ser Gly Glu Asp Ala Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn  
130 135 140

Ile Asp Gly Val Pro Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn  
145 150 155 160

Val Asp Ala Ser Ser Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro  
165 170 175

Val Val Ser Thr Ile Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile  
180 185 190

Asn Ala Asp Thr Ala Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu  
195 200 205

Arg Leu Leu Val Leu Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro  
210 215 220

Asp Lys Ser Ser Leu Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala  
225 230 235 240

Ile Leu Pro Gly Leu Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys  
245 250 255

Leu Asn Ala Val Arg Gly Gly Val Ser Ala Ala His Val Ile Asp Gly  
260 265 270

Arg Ile Ala His Ser Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile  
275 280 285

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Gly Thr Val Phe Arg Lys Asp Asp Lys Asp Gly Glu Leu  
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<210> 321

<211> 903

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(880)

<223> RXN02153

<400> 321

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Met Ile Met His Asn  
1 5

gtg tat ggt gta act atg aca atc aag gtt gca atc gca gga gcc agt 163  
Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala Ile Ala Gly Ala Ser  
10 15 20

gga tat gcc ggc gga gaa atc ctt cgt ctc ctt tta ggc cat cca gct	211
Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala	
25 30 35	
tat gca tct ggt gaa cta gaa atc gga gca ctc acc gcg gca tca acc	259
Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr	
40 45 50	
gca ggc agc acg ctc ggt gaa ttg atg cca cac att ccg cag ttg gcg	307
Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala	
55 60 65	
gat cgt gtt att caa gac acc aca gct gaa act cta gcc ggt cat gat	355
Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp	
70 75 80 85	
gtc gta ttt cta gga ctt cca cac gga ttc tct gca gaa att gca ctt	403
Val Val Phe Leu Gly Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu	
90 95 100	
cag ctc gga cca gat gtc aca gtg att gac tgt gca gct gac ttt cgt	451
Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg	
105 110 115	
ctg caa aat gct gca gat tgg gag aag ttc tac ggc tca gag cac cag	499
Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln	
120 125 130	
gga aca tgg cct tat ggc att cca gaa atg cca gga cac cgc gag gct	547
Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro Gly His Arg Glu Ala	
135 140 145	
ctt cgt ggt gct aag cgt gta gca gtg cca gga tgt ttc cca acc ggt	595
Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly	
150 155 160 165	
gca acc ttg gct ctt ctt cct gcg gtt caa gcg gga ctt atc gag cca	643
Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro	
170 175 180	
gat gtt tcc gta gtg tcc atc acc ggc gta tca ggt gca ggt aag aaa	691
Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys	
185 190 195	
gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg	739
Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala	
200 205 210	
tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac	787
Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn	
215 220 225	
ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg	835
Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val	
230 235 240 245	
ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt	880
Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu Gln Pro His Leu	
250 255 260	
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<210> 322  
 <211> 260  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 322

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			20					25					30		
Leu	Gly	His	Pro	Ala	Tyr	Ala	Ser	Gly	Glu	Leu	Glu	Ile	Gly	Ala	Leu
		35					40					45			
Thr	Ala	Ala	Ser	Thr	Ala	Gly	Ser	Thr	Leu	Gly	Glu	Leu	Met	Pro	His
		50				55					60				
Ile	Pro	Gln	Leu	Ala	Asp	Arg	Val	Ile	Gln	Asp	Thr	Thr	Ala	Glu	Thr
65					70					75					80
Leu	Ala	Gly	His	Asp	Val	Val	Phe	Leu	Gly	Leu	Pro	His	Gly	Phe	Ser
				85					90					95	
Ala	Glu	Ile	Ala	Leu	Gln	Leu	Gly	Pro	Asp	Val	Thr	Val	Ile	Asp	Cys
			100					105					110		
Ala	Ala	Asp	Phe	Arg	Leu	Gln	Asn	Ala	Ala	Asp	Trp	Glu	Lys	Phe	Tyr
		115					120					125			
Gly	Ser	Glu	His	Gln	Gly	Thr	Trp	Pro	Tyr	Gly	Ile	Pro	Glu	Met	Pro
	130					135					140				
Gly	His	Arg	Glu	Ala	Leu	Arg	Gly	Ala	Lys	Arg	Val	Ala	Val	Pro	Gly
145					150					155					160
Cys	Phe	Pro	Thr	Gly	Ala	Thr	Leu	Ala	Leu	Leu	Pro	Ala	Val	Gln	Ala
				165					170					175	
Gly	Leu	Ile	Glu	Pro	Asp	Val	Ser	Val	Val	Ser	Ile	Thr	Gly	Val	Ser
			180					185					190		
Gly	Ala	Gly	Lys	Lys	Ala	Ser	Val	Ala	Leu	Leu	Gly	Ser	Glu	Thr	Met
		195				200						205			
Gly	Ser	Leu	Lys	Ala	Tyr	Asn	Thr	Ser	Gly	Lys	His	Arg	His	Thr	Pro
	210					215					220				
Glu	Ile	Ala	Gln	Asn	Leu	Gly	Glu	Val	Ser	Asp	Lys	Pro	Val	Lys	Val
225					230					235					240
Ser	Phe	Thr	Pro	Val	Leu	Ala	Pro	Leu	Pro	Arg	Glu	Phe	Ser	Pro	Leu
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Gln	Pro	His	Leu												
			260												

<210> 323

<211> 903  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(880)  
 <223> FRXA02153

<400> 323

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                                         Met Ile Met His Asn
                                         1                               5

gtg tat ggt gta act atg aca atc aag gtt gca atc gca gga gcc agt 163
Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala Ile Ala Gly Ala Ser
                        10                        15                        20

gga tat gcc ggc gga gaa atc ctt cgt ctc ctt tta ggc cat cca gct 211
Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala
                        25                        30                        35

tat gca tct ggt gaa cta gaa atc gga gca ctc acc gcg gca tca acc 259
Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr
                        40                        45                        50

gca ggc agc acg ctc ggt gaa ttg atg cca cac att ccg cag ttg gcg 307
Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala
                        55                        60                        65

gat cgt gtt att caa gac acc aca gct gaa act cta gcc ggt cat gat 355
Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp
                        70                        75                        80                        85

gtc gta ttt cta gga ctt cca cac gga ttc tct gca gaa att gca ctt 403
Val Val Phe Leu Gly Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu
                        90                        95                        100

cag ctc gga cca gat gtc aca gtg att gac tgt gca gct gac ttt cgt 451
Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg
                        105                        110                        115

ctg caa aat gct gca gat tgg gag aag ttc tac ggc tca gag cac cag 499
Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln
                        120                        125                        130

gga aca tgg cct tat ggc att cca gaa atg cca gga cac cgc gag gct 547
Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro Gly His Arg Glu Ala
                        135                        140                        145

ctt cgt ggt gct aag cgt gta gca gtg cca gga tgt ttc cca acc ggt 595
Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly
                        150                        155                        160                        165

gca acc ttg gct ctt ctt cct gcg gtt caa gcg gga ctt atc gag cca 643
Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro
                        170                        175                        180

gat gtt tcc gta gtg tcc atc acc ggc gta tca ggt gca ggt aag aaa 691

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Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys  
 185 190 195

gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg 739  
 Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala  
 200 205 210

tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac 787  
 Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn  
 215 220 225

ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg 835  
 Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val  
 230 235 240 245

ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt 880  
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 250 255 260

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<210> 324  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 324  
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 35 40 45

Thr Ala Ala Ser Thr Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His  
 50 55 60

Ile Pro Gln Leu Ala Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr  
 65 70 75 80

Leu Ala Gly His Asp Val Val Phe Leu Gly Leu Pro His Gly Phe Ser  
 85 90 95

Ala Glu Ile Ala Leu Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys  
 100 105 110

Ala Ala Asp Phe Arg Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr  
 115 120 125

Gly Ser Glu His Gln Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro  
 130 135 140

Gly His Arg Glu Ala Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly  
 145 150 155 160

Cys Phe Pro Thr Gly Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala  
 165 170 175

Gly Leu Ile Glu Pro Asp Val Ser Val Val Ser Ile Thr Gly Val Ser  
 180 185 190

Gly Ala Gly Lys Lys Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met  
 195 200 205

Gly Ser Leu Lys Ala Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro  
 210 215 220

Glu Ile Ala Gln Asn Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val  
 225 230 235 240

Ser Phe Thr Pro Val Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu  
 245 250 255

Gln Pro His Leu  
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<210> 325

<211> 414

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(391)

<223> RXA02154

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 Leu Lys Glu Gly Val  
 1 5

acc gca gaa cag gct cgc gca gta tat gaa gag ttc tat gca cag gaa 163  
 Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu  
 10 15 20

acc ttc gtg cat gtt ctt cca gaa ggt gca cag cca caa acc caa gca 211  
 Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala  
 25 30 35

gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa 259  
 Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu  
 40 45 50

gca ggc aaa gtc ctt gtt acc tcc gca atc gat aac ctc acc aag gga 307  
 Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp Asn Leu Thr Lys Gly  
 55 60 65

act gcc ggc gcc gct gtt cag tgc atg aac tta agc gtt ggt ttt gat 355  
 Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu Ser Val Gly Phe Asp  
 70 75 80 85

gag gca gca ggc ctg cca cag gtc ggc gtc gca cct taaagtagcg 401  
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 90 95

ccttaaagcg gcg 414

**<400> 326**

Pro

**<220>**

<223> RXA02157

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gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln 90 95 100			403
acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala 105 110 115			451
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cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe 150 155 160 165			595
tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn 170 175 180			643
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tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly 215 220 225			787
gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val 230 235 240 245			835
ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile 250 255 260			883
ggt gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly 265 270 275			931
aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala 280 285 290			979
aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc 1027 Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala			



295                                      300                                      305  
 cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt  
 1075  
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val  
 310                                      315                                      320                                      325  
 gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc  
 1123  
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg  
 330                                      335                                      340  
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 1171  
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile  
 345                                      350                                      355  
 ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg  
 1219  
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val  
 360                                      365                                      370  
 atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca  
 1267  
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr  
 375                                      380                                      385  
 atc gca taaaggactc aaacttatga ctt  
 1296  
 Ile Ala  
 390  
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 <211> 391  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 328  
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 Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp  
 20                                      25                                      30  
 Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn  
 35                                      40                                      45  
 Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln  
 50                                      55                                      60  
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val  
 65                                      70                                      75                                      80  
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala  
 85                                      90                                      95  
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu  
 100                                      105                                      110  
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg

115					120					125					
Ile	Leu	Ala	Ala	Val	His	Gly	Phe	His	Gly	Arg	Thr	Met	Gly	Ser	Leu
130						135					140				
Ala	Leu	Thr	Gly	Gln	Pro	Asp	Lys	Arg	Glu	Ala	Phe	Leu	Pro	Met	Pro
145					150					155					160
Ser	Gly	Val	Glu	Phe	Tyr	Pro	Tyr	Gly	Asp	Thr	Asp	Tyr	Leu	Arg	Lys
				165					170					175	
Met	Val	Glu	Thr	Asn	Pro	Thr	Asp	Val	Ala	Ala	Ile	Phe	Leu	Glu	Pro
			180					185					190		
Ile	Gln	Gly	Glu	Thr	Gly	Val	Val	Pro	Ala	Pro	Glu	Gly	Phe	Leu	Lys
	195					200						205			
Ala	Val	Arg	Glu	Leu	Cys	Asp	Glu	Tyr	Gly	Ile	Leu	Met	Ile	Thr	Asp
	210					215					220				
Glu	Val	Gln	Thr	Gly	Val	Gly	Arg	Thr	Gly	Asp	Phe	Phe	Ala	His	Gln
225				230						235					240
His	Asp	Gly	Val	Val	Pro	Asp	Val	Val	Thr	Met	Ala	Lys	Gly	Leu	Gly
				245					250					255	
Gly	Gly	Leu	Pro	Ile	Gly	Ala	Cys	Leu	Ala	Thr	Gly	Arg	Ala	Ala	Glu
			260					265					270		
Leu	Met	Thr	Pro	Gly	Lys	His	Gly	Thr	Thr	Phe	Gly	Gly	Asn	Pro	Val
	275						280					285			
Ala	Cys	Ala	Ala	Ala	Lys	Ala	Val	Leu	Ser	Val	Val	Asp	Asp	Ala	Phe
	290					295					300				
Cys	Ala	Glu	Val	Ala	Arg	Lys	Gly	Glu	Leu	Phe	Lys	Glu	Leu	Leu	Ala
305				310						315					320
Lys	Val	Asp	Gly	Val	Val	Asp	Val	Arg	Gly	Arg	Gly	Leu	Met	Leu	Gly
				325					330					335	
Val	Val	Leu	Glu	Arg	Asp	Val	Ala	Lys	Gln	Ala	Val	Leu	Asp	Gly	Phe
			340					345					350		
Lys	His	Gly	Val	Ile	Leu	Asn	Ala	Pro	Ala	Asp	Asn	Ile	Ile	Arg	Leu
	355						360					365			
Thr	Pro	Pro	Leu	Val	Ile	Thr	Asp	Glu	Glu	Ile	Ala	Asp	Ala	Val	Lys
	370					375					380				
Ala	Ile	Ala	Glu	Thr	Ile	Ala									
385				390											

&lt;210&gt; 329

&lt;211&gt; 1491

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1468)

&lt;223&gt; RXS02970

&lt;400&gt; 329

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ttatttaaag acttcataat attttgggga gtgaactggg ttg gca ttg aag ggt 115
                                   Leu Ala Leu Lys Gly
                                   1 5
tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
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aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
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cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
                40                45                50
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
                55                60                65
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
                70                75                80                85
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
                90                95                100
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
                105                110                115
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
                120                125                130
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
                135                140                145
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
                150                155                160                165
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
                170                175                180
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
                185                190                195
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag 739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys
                200                205                210

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cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg 787  
 His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala  
 215 220 225

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835  
 Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro  
 230 235 240 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883  
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile  
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931  
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys  
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979  
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile  
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc  
 1027  
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile  
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc  
 1075  
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser  
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag  
 1123  
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys  
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct  
 1171  
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala  
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa  
 1219  
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu  
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca  
 1267  
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala  
 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa  
 1315  
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
 390 395 400 405

ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac  
 1363  
 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His  
 410 415 420

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg  
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 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu  
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gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg  
 1459  
 Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly  
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 Ala Leu Phe  
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<210> 330  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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                   20                  25                  30  
 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
                   35                  40                  45  
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
   50                  55                  60  
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
   65                  70                  75                  80  
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
                   85                  90                  95  
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
                   100                  105                  110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
                   115                  120                  125  
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
   130                  135                  140  
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
   145                  150                  155                  160  
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
                   165                  170                  175  
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
                   180                  185                  190  
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
   195                  200                  205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
 210 215 220  
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240  
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
 245 250 255  
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
 260 265 270  
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
 275 280 285  
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
 290 295 300  
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
 305 310 315 320  
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
 325 330 335  
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
 340 345 350  
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
 355 360 365  
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
 370 375 380  
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala  
 385 390 395 400  
 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser  
 405 410 415  
 Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu  
 420 425 430  
 Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu  
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 Leu Thr Phe Ala Gly Ala Leu Phe  
 450 455

&lt;210&gt; 331

&lt;211&gt; 1330

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1330)

&lt;223&gt; FRXA01009

&lt;400&gt; 331

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	Leu Ala Leu Lys Gly	
	1 5	
tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca		163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala		
	10 15 20	
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc		211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe		
	25 30 35	
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His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala		
	40 45 50	
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac		307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp		
	55 60 65	
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga		355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg		
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tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac		403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn		
	90 95 100	
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg		451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val		
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tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc		499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly		
	120 125 130	
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga		547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly		
	135 140 145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga		595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly		
	150 155 160 165	
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc		643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr		
	170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc		691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser		
	185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag		739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys		
	200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg		787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala		
	215 220 225	

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835  
 Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro  
 230 235 240 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883  
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile  
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931  
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys  
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979  
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile  
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc  
 1027  
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile  
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc  
 1075  
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser  
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag  
 1123  
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys  
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct  
 1171  
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala  
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa  
 1219  
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu  
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca  
 1267  
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala  
 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa  
 1315  
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
 390 395 400 405

ttc aag gaa cgc ggc  
 1330  
 Phe Lys Glu Arg Gly  
 410

&lt;210&gt; 332

&lt;211&gt; 410

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



&lt;400&gt; 332

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 Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp  
 20 25 30  
 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
 35 40 45  
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
 50 55 60  
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
 65 70 75 80  
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
 85 90 95  
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
 100 105 110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
 115 120 125  
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
 130 135 140  
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
 145 150 155 160  
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
 165 170 175  
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
 180 185 190  
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
 195 200 205  
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
 210 215 220  
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240  
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
 245 250 255  
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
 260 265 270  
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
 275 280 285  
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
 290 295 300  
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
 305 310 315 320

Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
 325 330 335

Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
 340 345 350

Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
 355 360 365

Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
 370 375 380

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala  
 385 390 395 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly  
 405 410

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<223> RXA02158

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 Met Thr Ser Gln Pro  
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 Gln Val Arg His Phe Leu Ala Asp Asp Asp Leu Thr Pro Ala Glu Gln  
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 Ala Glu Val Leu Thr Leu Ala Ala Lys Leu Lys Ala Ala Pro Phe Ser  
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 Glu Arg Pro Leu Glu Gly Pro Lys Ser Val Ala Val Leu Phe Asp Lys  
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 Thr Ser Thr Arg Thr Arg Phe Ser Phe Asp Ala Gly Ile Ala His Leu  
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 Gly Gly His Ala Ile Val Val Asp Ser Gly Ser Ser Gln Met Gly Lys  
 70 75 80 85

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 Gly Glu Ser Leu Gln Asp Thr Ala Ala Val Leu Ser Arg Tyr Val Glu  
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 Ala Ile Val Trp Arg Thr Tyr Ala His Ser Asn Phe His Ala Met Ala  
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 Glu Thr Ser Thr Val Pro Leu Val Asn Ser Leu Ser Asp Asp Leu His  
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cca tgc cag att ctg gct gat ctg cag act atc gtg gaa aac ctc agc 547  
 Pro Cys Gln Ile Leu Ala Asp Leu Gln Thr Ile Val Glu Asn Leu Ser  
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 Pro Glu Glu Gly Pro Ala Gly Leu Lys Gly Lys Lys Ala Val Tyr Leu  
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acc gcg ggc atg gat att tcc atc atc gct cct gaa ggg ttc cag cct 691  
 Thr Ala Gly Met Asp Ile Ser Ile Ile Ala Pro Glu Gly Phe Gln Pro  
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 Arg Ala Glu Phe Val Glu Arg Ala Glu Lys Arg Gly Gln Glu Thr Gly  
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gcg aag gtt gtt gtc acc gac agc ctc gac gag gtt gcc ggc gcc gat 787  
 Ala Lys Val Val Val Thr Asp Ser Leu Asp Glu Val Ala Gly Ala Asp  
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 Ile Asp Arg Thr Thr Pro Phe Val Pro Tyr Gln Val Asn Asp Glu Val  
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atg gcg aaa gct aac gac ggc gcc atc ttc ctg cac tgc ctt cct gcc 931  
 Met Ala Lys Ala Asn Asp Gly Ala Ile Phe Leu His Cys Leu Pro Ala  
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tac cgt ggc aaa gaa gtg gca gcc tcc gtg att gat gga cca gcg tcc 979  
 Tyr Arg Gly Lys Glu Val Ala Ala Ser Val Ile Asp Gly Pro Ala Ser  
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 Val Leu Phe Asp Lys Thr Ser Thr Arg Thr Arg Phe Ser Phe Asp Ala  
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 Gly Ile Ala His Leu Gly Gly His Ala Ile Val Val Asp Ser Gly Ser  
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 Ser Gln Met Gly Lys Gly Glu Ser Leu Gln Asp Thr Ala Ala Val Leu  
                   85                  90                  95  
 Ser Arg Tyr Val Glu Ala Ile Val Trp Arg Thr Tyr Ala His Ser Asn  
                   100                  105                  110  
 Phe His Ala Met Ala Glu Thr Ser Thr Val Pro Leu Val Asn Ser Leu  
                   115                  120                  125  
 Ser Asp Asp Leu His Pro Cys Gln Ile Leu Ala Asp Leu Gln Thr Ile  
   130                  135                  140  
 Val Glu Asn Leu Ser Pro Glu Glu Gly Pro Ala Gly Leu Lys Gly Lys  
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 Lys Ala Val Tyr Leu Gly Asp Gly Asp Asn Asn Met Ala Asn Ser Tyr  
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 Met Ile Gly Phe Ala Thr Ala Gly Met Asp Ile Ser Ile Ile Ala Pro  
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 Glu Gly Phe Gln Pro Arg Ala Glu Phe Val Glu Arg Ala Glu Lys Arg  
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 Val Asn Asp Glu Val Met Ala Lys Ala Asn Asp Gly Ala Ile Phe Leu  
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 His Cys Leu Pro Ala Tyr Arg Gly Lys Glu Val Ala Ala Ser Val Ile  
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Asp Gly Pro Ala Ser Lys Val Phe Asp Glu Ala Glu Asn Arg Leu His  
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<220>

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<223> RXA02160

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 Val Leu Ala Tyr Ser Gly Gly Leu Asp Thr Thr Val Ala Ile Pro Tyr  
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 Leu Lys Lys Met Ile Asp Gly Glu Val Ile Ala Val Ser Leu Asp Leu  
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 Gly Gln Gly Gly Glu Asn Met Asp Asn Val Arg Gln Arg Ala Leu Asp  
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 Ala Gly Ala Ala Glu Ser Ile Val Val Asp Ala Lys Asp Glu Phe Ala  
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 gag gag tac tgc ctg cca acc atc aag gca aac ggc atg tac atg aag 355  
 Glu Glu Tyr Cys Leu Pro Thr Ile Lys Ala Asn Gly Met Tyr Met Lys  
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 Gln Tyr Pro Leu Val Ser Ala Ile Ser Arg Pro Leu Ile Val Lys His  
 90 95 100  
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 Leu Val Glu Ala Gly Lys Gln Phe Asn Gly Thr His Val Ala His Gly  
 105 110 115  
 tgc act ggt aag ggc aac gac cag gtt cgt ttc gag gtc ggc ttc atg 499  
 Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe Glu Val Gly Phe Met  
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 Asp Thr Asp Pro Asn Leu Glu Ile Ile Ala Pro Ala Arg Asp Phe Ala  
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Trp Thr Arg Asp Lys Ala Ile Ala Phe Ala Glu Glu Asn Asn Val Pro	
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Ile Glu Gln Ser Val Lys Ser Pro Phe Ser Ile Asp Gln Asn Val Trp	
170 175 180	
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Gly Arg Ala Ile Glu Thr Gly Tyr Leu Glu Asp Leu Trp Asn Ala Pro	
185 190 195	
acc aag gac atc tac gca tac acc gag gat cca gct ctg ggt aac gct	739
Thr Lys Asp Ile Tyr Ala Tyr Thr Glu Asp Pro Ala Leu Gly Asn Ala	
200 205 210	
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Pro Asp Glu Val Ile Ile Ser Phe Glu Gly Gly Lys Pro Val Ser Ile	
215 220 225	
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Asp Gly Arg Pro Val Ser Val Leu Gln Ala Ile Glu Glu Leu Asn Arg	
230 235 240 245	
cgt gca ggc gca cag ggc gtt ggc cgc ctt gac atg gtt gag gac cgt	883
Arg Ala Gly Ala Gln Gly Val Gly Arg Leu Asp Met Val Glu Asp Arg	
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ctc gtg ggc atc aag tcc cgc gaa atc tac gaa gca cca ggc gca atc	931
Leu Val Gly Ile Lys Ser Arg Glu Ile Tyr Glu Ala Pro Gly Ala Ile	
265 270 275	
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Ala Leu Ile Lys Ala His Glu Ala Leu Glu Asp Val Thr Ile Glu Arg	
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gaa ctg gct cgc tac aag cgc ggc gtt gac gca cgt tgg gct gag gaa	
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295 300 305	
gta tac gac ggc ctg tgg ttc gga cct ctg aag cgc tcc ctg gac gcg	
1075	
Val Tyr Asp Gly Leu Trp Phe Gly Pro Leu Lys Arg Ser Leu Asp Ala	
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1123	
Phe Ile Asp Ser Thr Gln Glu His Val Thr Gly Asp Ile Arg Met Val	
330 335 340	
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1171	
Leu His Ala Gly Ser Ile Thr Ile Asn Gly Arg Arg Ser Ser His Ser	
345 350 355	
ctg tac gac ttc aac ctg gct acc tac gac acc ggc gac acc ttc gac	
1219	
Leu Tyr Asp Phe Asn Leu Ala Thr Tyr Asp Thr Gly Asp Thr Phe Asp	
360 365 370	

cag acc ctg gct aag ggc ttt gtc cag ctg cac ggt ctg tcc tcc aag  
 1267  
 Gln Thr Leu Ala Lys Gly Phe Val Gln Leu His Gly Leu Ser Ser Lys  
 375 380 385

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 35 40 45

Gln Arg Ala Leu Asp Ala Gly Ala Ala Glu Ser Ile Val Val Asp Ala  
 50 55 60

Lys Asp Glu Phe Ala Glu Glu Tyr Cys Leu Pro Thr Ile Lys Ala Asn  
 65 70 75 80

Gly Met Tyr Met Lys Gln Tyr Pro Leu Val Ser Ala Ile Ser Arg Pro  
 85 90 95

Leu Ile Val Lys His Leu Val Glu Ala Gly Lys Gln Phe Asn Gly Thr  
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His Val Ala His Gly Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe  
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Glu Val Gly Phe Met Asp Thr Asp Pro Asn Leu Glu Ile Ile Ala Pro  
 130 135 140

Ala Arg Asp Phe Ala Trp Thr Arg Asp Lys Ala Ile Ala Phe Ala Glu  
 145 150 155 160

Glu Asn Asn Val Pro Ile Glu Gln Ser Val Lys Ser Pro Phe Ser Ile  
 165 170 175

Asp Gln Asn Val Trp Gly Arg Ala Ile Glu Thr Gly Tyr Leu Glu Asp  
 180 185 190

Leu Trp Asn Ala Pro Thr Lys Asp Ile Tyr Ala Tyr Thr Glu Asp Pro  
 195 200 205

Ala Leu Gly Asn Ala Pro Asp Glu Val Ile Ile Ser Phe Glu Gly Gly  
 210 215 220

Lys Pro Val Ser Ile Asp Gly Arg Pro Val Ser Val Leu Gln Ala Ile  
 225 230 235 240  
 Glu Glu Leu Asn Arg Arg Ala Gly Ala Gln Gly Val Gly Arg Leu Asp  
 245 250 255  
 Met Val Glu Asp Arg Leu Val Gly Ile Lys Ser Arg Glu Ile Tyr Glu  
 260 265 270  
 Ala Pro Gly Ala Ile Ala Leu Ile Lys Ala His Glu Ala Leu Glu Asp  
 275 280 285  
 Val Thr Ile Glu Arg Glu Leu Ala Arg Tyr Lys Arg Gly Val Asp Ala  
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 Arg Trp Ala Glu Glu Val Tyr Asp Gly Leu Trp Phe Gly Pro Leu Lys  
 305 310 315 320  
 Arg Ser Leu Asp Ala Phe Ile Asp Ser Thr Gln Glu His Val Thr Gly  
 325 330 335  
 Asp Ile Arg Met Val Leu His Ala Gly Ser Ile Thr Ile Asn Gly Arg  
 340 345 350  
 Arg Ser Ser His Ser Leu Tyr Asp Phe Asn Leu Ala Thr Tyr Asp Thr  
 355 360 365  
 Gly Asp Thr Phe Asp Gln Thr Leu Ala Lys Gly Phe Val Gln Leu His  
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 Met Glu Gln His Gly  
 1 5  
 acc aat gaa ggt gcg ctg tgg ggc ggc cgc ttc tcc ggt gga ccc tcc 163  
 Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe Ser Gly Gly Pro Ser  
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 Glu Ala Met Phe Ala Leu Ser Val Ser Thr His Phe Asp Trp Val Leu



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Ala	Pro	Tyr	Asp	Val	Leu	Ala	Ser	Lys	Ala	His	Ala	Lys	Val	Leu	His	
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caa	gca	gat	cta	ctt	tct	gat	gaa	gat	cta	gcc	acc	atg	ctg	gct	ggg	307
Gln	Ala	Asp	Leu	Leu	Ser	Asp	Glu	Asp	Leu	Ala	Thr	Met	Leu	Ala	Gly	
	55					60					65					
ctt	gat	cag	ctg	ggc	aag	gat	gtc	gcc	gac	gga	acc	ttc	ggt	ccg	ctg	355
Leu	Asp	Gln	Leu	Gly	Lys	Asp	Val	Ala	Asp	Gly	Thr	Phe	Gly	Pro	Leu	
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cct	tct	gat	gag	gat	gtg	cac	ggc	gcg	atg	gaa	cgc	ggt	gtg	att	gac	403
Pro	Ser	Asp	Glu	Asp	Val	His	Gly	Ala	Met	Glu	Arg	Gly	Val	Ile	Asp	
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cgc	gtt	ggt	cct	gag	gtg	ggc	ggc	cgt	ctg	cgc	gct	ggt	cgt	tcc	cgc	451
Arg	Val	Gly	Pro	Glu	Val	Gly	Gly	Arg	Leu	Arg	Ala	Gly	Arg	Ser	Arg	
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Asn	Asp	Gln	Val	Ala	Thr	Leu	Phe	Arg	Met	Trp	Val	Arg	Asp	Ala	Val	
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cgc	gac	atc	gcg	ctg	gga	aca	acc	gag	ctt	gtc	gac	gcc	ctc	agc	gcc	547
Arg	Asp	Ile	Ala	Leu	Gly	Thr	Thr	Glu	Leu	Val	Asp	Ala	Leu	Ser	Ala	
	135					140					145					
caa	gct	aag	gca	cat	gca	ggc	gcg	atc	atg	cca	ggc	aag	acc	cac	ttc	595
Gln	Ala	Lys	Ala	His	Ala	Gly	Ala	Ile	Met	Pro	Gly	Lys	Thr	His	Phe	
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Gln	Ala	Ala	Gln	Pro	Val	Leu	Leu	Ala	His	Gln	Leu	Leu	Ala	His	Ala	
				170					175					180		
cag	cct	ttg	ctg	cgc	gat	att	gat	cgt	atc	cgt	gac	ctg	gac	aag	cgt	691
Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg	Asp	Leu	Asp	Lys	Arg	
			185					190					195			
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Leu	Ala	Val	Ser	Pro	Tyr	Gly	Ser	Gly	Ala	Leu	Ala	Gly	Ser	Ser	Leu	
		200					205					210				
aag	ctc	aac	cct	gaa	gca	atc	gct	gaa	gaa	ctc	ggc	ttt	gat	tcc	gca	787
Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu	Gly	Phe	Asp	Ser	Ala	
	215					220					225					
gca	gat	aac	tcc	att	gat	gcc	acc	agc	tcc	cgc	gat	ttc	gca	tct	gaa	835
Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg	Asp	Phe	Ala	Ser	Glu	
230					235					240					245	
acc	gcc	ttc	gtg	ctg	gcg	cag	ctt	gca	gtg	gat	atg	tcc	cgc	ttg	gct	883
Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Val	Asp	Met	Ser	Arg	Leu	Ala	
			250					255						260		
gaa	gaa	atc	atc	gca	tgg	tgc	acc	cca	gaa	ttt	ggt	tac	atc	acc	ttg	931
Glu	Glu	Ile	Ile	Ala	Trp	Cys	Thr	Pro	Glu	Phe	Gly	Tyr	Ile	Thr	Leu	
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 Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met Pro Gln Lys Lys Asn  
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cct gac gtg gca gag ctg acc cgt ggc aag tct ggt cgc ttg atc ggt  
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 Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser Gly Arg Leu Ile Gly  
 295 300 305

aac ctc acc ggt ctg ctg gct acc ctg aag gca cag cct tta gcg tac  
 1075  
 Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala Gln Pro Leu Ala Tyr  
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aac cgc gac ctg cag gaa gat aag gaa cca atc gta gat tcc gtg gcg  
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 Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile Val Asp Ser Val Ala  
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cag ctc aac ctg ctg ctc cct gca atg act ggt ttg gtt tcc acc ttg  
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 Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly Leu Val Ser Thr Leu  
 345 350 355

acc ttc aac acc gag cgc atg cgt gaa ctt gca cca gca ggt ttc acc  
 1219  
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 360 365 370

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 375 380 385

cgt gag gca cac gaa gca tcc ggc gct tgc gtg cgg atc gcg gag tcc  
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 390 395 400 405

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 1363  
 Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu Glu Leu Ser Gly Val  
 410 415 420

gat gca cgt ctg acc cca gag gta cgg gaa gtg ctc acc att gat ggt  
 1411  
 Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val Leu Thr Ile Asp Gly  
 425 430 435

gca gtg gct tcc cgt gca acg cgc ggt gga acc gcg ggc gtg cgg gtt  
 1459  
 Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val  
 440 445 450

gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag  
 1507  
 Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu  
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1554

Trp Ala Arg Ala Gly Val Arg Arg  
470 475

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<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

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Phe Asp Trp Val Leu Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His  
35 40 45

Ala Lys Val Leu His Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala  
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Thr Met Leu Ala Gly Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly  
65 70 75 80

Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu  
85 90 95

Arg Gly Val Ile Asp Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg  
100 105 110

Ala Gly Arg Ser Arg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp  
115 120 125

Val Arg Asp Ala Val Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val  
130 135 140

Asp Ala Leu Ser Ala Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro  
145 150 155 160

Gly Lys Thr His Phe Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln  
165 170 175

Leu Leu Ala His Ala Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg  
180 185 190

Asp Leu Asp Lys Arg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu  
195 200 205

Ala Gly Ser Ser Leu Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu  
210 215 220

Gly Phe Asp Ser Ala Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg  
225 230 235 240

Asp Phe Ala Ser Glu Thr Ala Phe Val Leu Ala Gln Leu Ala Val Asp  
245 250 255

Met Ser Arg Leu Ala Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe

260					265					270						
Gly	Tyr	Ile	Thr	Leu	Ser	Asp	Ser	Trp	Ser	Thr	Gly	Ser	Ser	Ile	Met	
275					280					285						
Pro	Gln	Lys	Lys	Asn	Pro	Asp	Val	Ala	Glu	Leu	Thr	Arg	Gly	Lys	Ser	
290					295					300						
Gly	Arg	Leu	Ile	Gly	Asn	Leu	Thr	Gly	Leu	Leu	Ala	Thr	Leu	Lys	Ala	
305					310					315					320	
Gln	Pro	Leu	Ala	Tyr	Asn	Arg	Asp	Leu	Gln	Glu	Asp	Lys	Glu	Pro	Ile	
325					330					335						
Val	Asp	Ser	Val	Ala	Gln	Leu	Asn	Leu	Leu	Leu	Pro	Ala	Met	Thr	Gly	
340					345					350						
Leu	Val	Ser	Thr	Leu	Thr	Phe	Asn	Thr	Glu	Arg	Met	Arg	Glu	Leu	Ala	
355					360					365						
Pro	Ala	Gly	Phe	Thr	Leu	Ala	Thr	Asp	Leu	Ala	Glu	Trp	Met	Val	Arg	
370					375					380						
Gln	Gly	Val	Pro	Phe	Arg	Glu	Ala	His	Glu	Ala	Ser	Gly	Ala	Cys	Val	
385					390					395					400	
Arg	Ile	Ala	Glu	Ser	Arg	Gly	Val	Asp	Leu	Ile	Asp	Leu	Thr	Asp	Glu	
405					410					415						
Glu	Leu	Ser	Gly	Val	Asp	Ala	Arg	Leu	Thr	Pro	Glu	Val	Arg	Glu	Val	
420					425					430						
Leu	Thr	Ile	Asp	Gly	Ala	Val	Ala	Ser	Arg	Ala	Thr	Arg	Gly	Gly	Thr	
435					440					445						
Ala	Gly	Val	Arg	Val	Ala	Glu	Gln	Arg	Ala	Arg	Val	Asp	Ala	Ala	Ser	
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&lt;210&gt; 339

&lt;211&gt; 906

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(883)

&lt;223&gt; FRXA02161

&lt;400&gt; 339

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acc	aat	gaa	ggt	gcg	ctg	tgg	ggc	ggc	cgc	ttc	tcc	ggt	gga	ccc	tcc	163
Thr	Asn	Glu	Gly	Ala	Leu	Trp	Gly	Gly	Arg	Phe	Ser	Gly	Gly	Pro	Ser	

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gag	gcc	atg	ttc	gcc	ttg	agt	gtc	tcc	act	cat	ttc	gac	tgg	gtt	ttg					211
Glu	Ala	Met	Phe	Ala	Leu	Ser	Val	Ser	Thr	His	Phe	Asp	Trp	Val	Leu					
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Ala	Pro	Tyr	Asp	Val	Leu	Ala	Ser	Lys	Ala	His	Ala	Lys	Val	Leu	His					
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Gln	Ala	Asp	Leu	Leu	Ser	Asp	Glu	Asp	Leu	Ala	Thr	Met	Leu	Ala	Gly					
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ctt	gat	cag	ctg	ggc	aag	gat	gtc	gcc	gac	gga	acc	ttc	ggg	ccg	ctg					355
Leu	Asp	Gln	Leu	Gly	Lys	Asp	Val	Ala	Asp	Gly	Thr	Phe	Gly	Pro	Leu					
	70				75				80						85					
cct	tct	gat	gag	gat	gtg	cac	ggc	gcg	atg	gaa	cgc	ggg	gtg	att	gac					403
Pro	Ser	Asp	Glu	Asp	Val	His	Gly	Ala	Met	Glu	Arg	Gly	Val	Ile	Asp					
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cgc	gtt	ggg	cct	gag	gtg	ggc	ggc	cgt	ctg	cgc	gct	ggg	cgt	tcc	cgc					451
Arg	Val	Gly	Pro	Glu	Val	Gly	Gly	Arg	Leu	Arg	Ala	Gly	Arg	Ser	Arg					
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Asn	Asp	Gln	Val	Ala	Thr	Leu	Phe	Arg	Met	Trp	Val	Arg	Asp	Ala	Val					
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cgc	gac	atc	gcg	ctg	gga	aca	acc	gag	ctt	gtc	gac	gcc	ctc	agc	gcc					547
Arg	Asp	Ile	Ala	Leu	Gly	Thr	Thr	Glu	Leu	Val	Asp	Ala	Leu	Ser	Ala					
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caa	gct	aag	gca	cat	gca	ggc	gcg	atc	atg	cca	ggc	aag	acc	cac	ttc					595
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Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg	Asp	Leu	Asp	Lys	Arg					
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Leu	Ala	Val	Ser	Pro	Tyr	Gly	Ser	Gly	Ala	Leu	Ala	Gly	Ser	Ser	Leu					
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Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu	Gly	Phe	Asp	Ser	Ala					
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gca	gat	aac	tcc	att	gat	gcc	acc	agc	tcc	cgc	gat	ttc	gca	tct	gaa					835
Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg	Asp	Phe	Ala	Ser	Glu					
	230				235					240					245					
acc	gcc	ttc	gtg	ctg	gcg	cag	ctt	gca	ngt	gga	tat	gtc	ccg	ctt	ggc					883
Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Xaa	Gly	Tyr	Val	Pro	Leu	Gly					
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906

&lt;210&gt; 340

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 340

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Phe	Asp	Trp	Val	Leu	Ala	Pro	Tyr	Asp	Val	Leu	Ala	Ser	Lys	Ala	His
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Ala	Lys	Val	Leu	His	Gln	Ala	Asp	Leu	Leu	Ser	Asp	Glu	Asp	Leu	Ala
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Thr	Met	Leu	Ala	Gly	Leu	Asp	Gln	Leu	Gly	Lys	Asp	Val	Ala	Asp	Gly
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Thr	Phe	Gly	Pro	Leu	Pro	Ser	Asp	Glu	Asp	Val	His	Gly	Ala	Met	Glu
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Arg	Gly	Val	Ile	Asp	Arg	Val	Gly	Pro	Glu	Val	Gly	Gly	Arg	Leu	Arg
			100					105					110		

Ala	Gly	Arg	Ser	Arg	Asn	Asp	Gln	Val	Ala	Thr	Leu	Phe	Arg	Met	Trp
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Val	Arg	Asp	Ala	Val	Arg	Asp	Ile	Ala	Leu	Gly	Thr	Thr	Glu	Leu	Val
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Asp	Ala	Leu	Ser	Ala	Gln	Ala	Lys	Ala	His	Ala	Gly	Ala	Ile	Met	Pro
145					150					155					160

Gly	Lys	Thr	His	Phe	Gln	Ala	Ala	Gln	Pro	Val	Leu	Leu	Ala	His	Gln
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Leu	Leu	Ala	His	Ala	Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg
			180					185					190		

Asp	Leu	Asp	Lys	Arg	Leu	Ala	Val	Ser	Pro	Tyr	Gly	Ser	Gly	Ala	Leu
		195					200					205			

Ala	Gly	Ser	Ser	Leu	Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu
	210					215					220				

Gly	Phe	Asp	Ser	Ala	Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg
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Asp	Phe	Ala	Ser	Glu	Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Xaa	Gly
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Tyr	Val	Pro	Leu	Gly
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(763)  
 <223> FRXA02162

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 Met Ser Arg Leu Ala  
 1 5  
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 Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe Gly Tyr Ile Thr Leu  
 10 15 20  
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 Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met Pro Gln Lys Lys Asn  
 25 30 35  
 cct gac gtg gca gag ctg acc cgt ggc aag tct ggt cgc ttg atc ggt 259  
 Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser Gly Arg Leu Ile Gly  
 40 45 50  
 aac ctc acc ggt ctg ctg gct acc ctg aag gca cag cct tta gcg tac 307  
 Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala Gln Pro Leu Ala Tyr  
 55 60 65  
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 Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile Val Asp Ser Val Ala  
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 cag ctc aac ctg ctg ctc cct gca atg act ggt ttg gtt tcc acc ttg 403  
 Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly Leu Val Ser Thr Leu  
 90 95 100  
 acc ttc aac acc gag cgc atg cgt gaa ctt gca cca gca ggt ttc acc 451  
 Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala Pro Ala Gly Phe Thr  
 105 110 115  
 ctt gcc acc gac ttg gct gag tgg atg gtg cgc cag ggc gtt cca ttc 499  
 Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg Gln Gly Val Pro Phe  
 120 125 130  
 cgt gag gca cac gaa gca tcc ggc gct tgc gtg cgg atc gcg gag tcc 547  
 Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val Arg Ile Ala Glu Ser  
 135 140 145  
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 Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu Glu Leu Ser Gly Val  
 150 155 160 165  
 gat gca cgt ctg acc cca gag gta cgg gaa gtg ctc acc att gat ggt 643  
 Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val Leu Thr Ile Asp Gly  
 170 175 180

gca gtg gct tcc cgt gca acg cgc ggt gga acc gcg ggc gtg cgg gtt 691  
 Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val  
                   185                                  190                                  195

gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag 739  
 Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu  
                   200                                  205                                  210

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<210> 342

<211> 221

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

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                   20                                  25                                  30

Pro Gln Lys Lys Asn Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser  
                   35                                  40                                  45

Gly Arg Leu Ile Gly Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala  
   50                                  55                                  60

Gln Pro Leu Ala Tyr Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile  
   65                                  70                                  75                                  80

Val Asp Ser Val Ala Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly  
                   85                                  90                                  95

Leu Val Ser Thr Leu Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala  
                   100                                  105                                  110

Pro Ala Gly Phe Thr Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg  
                   115                                  120                                  125

Gln Gly Val Pro Phe Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val  
   130                                  135                                  140

Arg Ile Ala Glu Ser Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu  
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Glu Leu Ser Gly Val Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val  
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Leu Thr Ile Asp Gly Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr  
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Ala Gly Val Arg Val Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser  
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<210> 343
<211> 1269
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(1246)
<223> RXA02262
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<400> 343

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acc	act	gaa	acc	gcc	atc	aat	ttc	ttg	ttc	ttg	agc	gaa	ccg	gac	atg	163
Thr	Thr	Glu	Thr	Ala	Ile	Asn	Phe	Leu	Phe	Leu	Ser	Glu	Pro	Asp	Met	
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atc	gcg	gcc	gga	gtc	aaa	gac	gtc	gcg	caa	tgc	gtc	gat	gtc	atg	gag	211
Ile	Ala	Ala	Gly	Val	Lys	Asp	Val	Ala	Gln	Cys	Val	Asp	Val	Met	Glu	
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Phe	Glu	Gly	Met	Pro	Lys	Asp	Gly	Pro	Asp	Arg	Arg	Phe	Met	Ala	Met	
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Pro	Ala	Tyr	Leu	Gly	Gly	Arg	Phe	Lys	Asn	Thr	Gly	Val	Lys	Trp	Tyr	
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Tyr	Phe	Lys	Lys	Glu	Trp	Leu	Lys	Pro	Gly	Ala	Leu	Leu	Leu	Leu	Pro	
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1219																
Thr	Gln	Val	Tyr	Glu	Asn	Ala	Leu	Glu	Lys	Gly	Val	Gly	Thr	Thr	Leu	
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1269

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<213> Corynebacterium glutamicum
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**<400> 344**

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Lys	Met 50	Ala	Gly	Leu	Asn	Ser 55	Asn	Ser	His	Gly	Ala 60	Met	Ile	Thr	Phe
Pro 65	Glu	Asn	Pro	Glu	Phe 70	Glu	Gly	Met	Pro	Lys 75	Asp	Gly	Pro	Asp	Arg 80
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Gly	Val	Lys	Trp 100	Tyr	Gly	Ser	Asn 105	Ala	Glu	Asn	Lys	Ala	Ser 110	Gly	Leu
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Pro	Lys 130	Ala	Ile	Met	Ser	Ala 135	Asn	Leu	Leu	Ser	Ala 140	Tyr	Arg	Thr	Gly
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Thr	Leu	Ala	Val	Val 165	Gly	Pro	Gly	Val	Met 170	Ala	Lys	Thr	Ile	Thr 175	Glu
Ala	Cys	Ile	Ala 180	Glu	Arg	Pro	Gly	Ile 185	Thr	Thr	Ile	Lys	Ile 190	Lys	Gly
Arg	Ser	Glu 195	Arg	Gly	Ile	Asn	Ala 200	Phe	Ala	Thr	Trp	Ala 205	Leu	Glu	Lys
Phe	Pro 210	Glu	Ile	Glu	Val	Val 215	Ala	Val	Gly	Ser	Glu 220	Glu	Asp	Val	Val
Lys 225	Asp	Ala	Asp	Ile	Val 230	Ile	Ala	Ala	Thr	Thr 235	Thr	Asp	Ala	Ala	Gly 240
Ser	Ser	Ala	Phe	Pro 245	Tyr	Phe	Lys	Lys	Glu 250	Trp	Leu	Lys	Pro	Gly 255	Ala
Leu	Leu	Leu	Leu	Pro 260	Ala	Ala	Gly	Arg 265	Phe	Asp	Asp	Ala	Tyr 270	Leu	Leu

Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp  
 275 280 285  
 Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly  
 290 295 300  
 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys  
 305 310 315 320  
 Ile Ser Gln Ile Gly Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr  
 325 330 335  
 Asn Asp Glu Glu Ile Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu  
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 Val Gly Thr Thr Leu Asn Leu Trp Glu Ser Pro Ala Leu Ala  
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 <213> Corynebacterium glutamicum

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 <223> RXA00219

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 Val Ala Arg Lys Lys  
 1 5  
 aac acg tcc gat caa tcc cgc tcc caa gct gcc aac acg ccc att gct 163  
 Asn Thr Ser Asp Gln Ser Arg Ser Gln Ala Ala Asn Thr Pro Ile Ala  
 10 15 20  
 ggc acc tat gag ggt gaa tat tcc gtc atc gag ttg gag gcc gat tcc 211  
 Gly Thr Tyr Glu Gly Glu Tyr Ser Val Ile Glu Leu Glu Ala Asp Ser  
 25 30 35  
 tac acc acc gat ggc tgg ttg atc agc att aat ggc gtg ccc agc tct 259  
 Tyr Thr Thr Asp Gly Trp Leu Ile Ser Ile Asn Gly Val Pro Ser Ser  
 40 45 50  
 cat att gtc ctg ggg caa ccg cag gca ctg gaa ttt gag tac atg cgg 307  
 His Ile Val Leu Gly Gln Pro Gln Ala Leu Glu Phe Glu Tyr Met Arg  
 55 60 65  
 tgg atc gct acc ggc gct cgg gcg ttc atc gat gcg cat cag gat gca 355  
 Trp Ile Ala Thr Gly Ala Arg Ala Phe Ile Asp Ala His Gln Asp Ala  
 70 75 80 85  
 tcc aag ctg cgg att act cac ctc ggc ggc ggt gcg tgc acg atg gcc 403  
 Ser Lys Leu Arg Ile Thr His Leu Gly Gly Gly Ala Cys Thr Met Ala

90										95					100					
agg	tat	ttc	gcg	gat	gtt	tac	ccg	cag	tca	cgc	aac	act	gtc	gtg	gaa	451				
Arg	Tyr	Phe	Ala	Asp	Val	Tyr	Pro	Gln	Ser	Arg	Asn	Thr	Val	Val	Glu					
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Leu	Asp	Ala	Glu	Leu	Ala	Arg	Leu	Ser	Arg	Glu	Trp	Phe	Asp	Ile	Pro					
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cgc	gcg	cca	cgg	gta	aag	att	cgt	gtg	gat	gat	gcc	cga	atg	gtg	gca	547				
Arg	Ala	Pro	Arg	Val	Lys	Ile	Arg	Val	Asp	Asp	Ala	Arg	Met	Val	Ala					
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gaa	tct	ttc	act	ccc	gca	agc	cgc	gat	gtg	atc	atc	cgt	gac	gtt	ttt	595				
Glu	Ser	Phe	Thr	Pro	Ala	Ser	Arg	Asp	Val	Ile	Ile	Arg	Asp	Val	Phe					
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gcc	gga	gct	atc	acg	ccg	cag	aac	ttc	acc	acc	gtg	gag	ttc	ttt	gag	643				
Ala	Gly	Ala	Ile	Thr	Pro	Gln	Asn	Phe	Thr	Thr	Val	Glu	Phe	Phe	Glu					
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cac	tgt	cac	cgt	ggc	ctt	gct	ccc	ggc	gga	ttg	tac	gtt	gcc	aac	tgt	691				
His	Cys	His	Arg	Gly	Leu	Ala	Pro	Gly	Gly	Leu	Tyr	Val	Ala	Asn	Cys					
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Gly	Asp	His	Ser	Asp	Leu	Arg	Gly	Ala	Lys	Ser	Glu	Leu	Ala	Gly	Met					
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atg	gag	gtg	ttc	gag	cac	gtc	gcg	gtc	atc	gcc	gat	ccc	ccg	atg	ctt	787				
Met	Glu	Val	Phe	Glu	His	Val	Ala	Val	Ile	Ala	Asp	Pro	Pro	Met	Leu					
		215				220					225									
aaa	ggg	cgc	cgt	tac	ggc	aac	atc	att	ttg	atg	ggg	tca	gac	acc	gag	835				
Lys	Gly	Arg	Arg	Tyr	Gly	Asn	Ile	Ile	Leu	Met	Gly	Ser	Asp	Thr	Glu					
230					235					240					245					
ttc	ttt	agc	tcc	aac	agc	acg	gaa	gcg	tcc	gcg	att	acc	cgt	gag	ctt	883				
Phe	Phe	Ser	Ser	Asn	Ser	Thr	Glu	Ala	Ser	Ala	Ile	Thr	Arg	Glu	Leu					
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ctt	ggc	ggc	ggc	gtt	cca	gcg	cag	tac	aag	gat	gaa	tcc	tgg	gtg	cgg	931				
Leu	Gly	Gly	Gly	Val	Pro	Ala	Gln	Tyr	Lys	Asp	Glu	Ser	Trp	Val	Arg					
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aaa	ttc	gcc	tcg	gga	gcc	cag	gcc	cgc	cac	gat	ggg	gtc	tct	acc	ctc	979				
Lys	Phe	Ala	Ser	Gly	Ala	Gln	Ala	Arg	His	Asp	Gly	Val	Ser	Thr	Leu					
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caa	atg	ccg	agt	gat	act	cca	caa	cac	cct	gcg	gaa	acg	ccg	gag	cat					
1027																				
Gln	Met	Pro	Ser	Asp	Thr	Pro	Gln	His	Pro	Ala	Glu	Thr	Pro	Glu	His					
		295				300					305									
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Ser	Asn	Thr	Gln	Pro																
310																				

<210> 346  
 <211> 314  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 346

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Leu	Glu	Ala	Asp	Ser	Tyr	Thr	Thr	Asp	Gly	Trp	Leu	Ile	Ser	Ile	Asn		
		35					40					45					
Gly	Val	Pro	Ser	Ser	His	Ile	Val	Leu	Gly	Gln	Pro	Gln	Ala	Leu	Glu		
	50					55					60						
Phe	Glu	Tyr	Met	Arg	Trp	Ile	Ala	Thr	Gly	Ala	Arg	Ala	Phe	Ile	Asp		
65					70					75					80		
Ala	His	Gln	Asp	Ala	Ser	Lys	Leu	Arg	Ile	Thr	His	Leu	Gly	Gly	Gly		
				85					90					95			
Ala	Cys	Thr	Met	Ala	Arg	Tyr	Phe	Ala	Asp	Val	Tyr	Pro	Gln	Ser	Arg		
			100					105					110				
Asn	Thr	Val	Val	Glu	Leu	Asp	Ala	Glu	Leu	Ala	Arg	Leu	Ser	Arg	Glu		
		115					120					125					
Trp	Phe	Asp	Ile	Pro	Arg	Ala	Pro	Arg	Val	Lys	Ile	Arg	Val	Asp	Asp		
	130					135					140						
Ala	Arg	Met	Val	Ala	Glu	Ser	Phe	Thr	Pro	Ala	Ser	Arg	Asp	Val	Ile		
145					150					155					160		
Ile	Arg	Asp	Val	Phe	Ala	Gly	Ala	Ile	Thr	Pro	Gln	Asn	Phe	Thr	Thr		
				165					170					175			
Val	Glu	Phe	Phe	Glu	His	Cys	His	Arg	Gly	Leu	Ala	Pro	Gly	Gly	Leu		
			180					185					190				
Tyr	Val	Ala	Asn	Cys	Gly	Asp	His	Ser	Asp	Leu	Arg	Gly	Ala	Lys	Ser		
		195					200					205					
Glu	Leu	Ala	Gly	Met	Met	Glu	Val	Phe	Glu	His	Val	Ala	Val	Ile	Ala		
	210					215					220						
Asp	Pro	Pro	Met	Leu	Lys	Gly	Arg	Arg	Tyr	Gly	Asn	Ile	Ile	Leu	Met		
225					230					235					240		
Gly	Ser	Asp	Thr	Glu	Phe	Phe	Ser	Ser	Asn	Ser	Thr	Glu	Ala	Ser	Ala		
				245					250					255			
Ile	Thr	Arg	Glu	Leu	Leu	Gly	Gly	Gly	Val	Pro	Ala	Gln	Tyr	Lys	Asp		
			260				265						270				
Glu	Ser	Trp	Val	Arg	Lys	Phe	Ala	Ser	Gly	Ala	Gln	Ala	Arg	His	Asp		
		275					280					285					
Gly	Val	Ser	Thr	Leu	Gln	Met	Pro	Ser	Asp	Thr	Pro	Gln	His	Pro	Ala		

290	295	300
Glu Thr Pro Glu His Ser Asn Thr Gln Pro		
305	310	
<p>&lt;210&gt; 347            &lt;211&gt; 1662            &lt;212&gt; DNA            &lt;213&gt; Corynebacterium glutamicum</p> <p>&lt;220&gt;            &lt;221&gt; CDS            &lt;222&gt; (101)..(1639)            &lt;223&gt; RXA01508</p> <p>&lt;400&gt; 347</p>		
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ccgccgtcat cttgatcgtg gtgggaaccg taaacgctgc atg tct gat tta gga 115		
Met Ser Asp Leu Gly 5		
ccc atc tgg cgc tgg ctg tta tta gtt tcc gtc tcc att tgt gcg gca 163		
Pro Ile Trp Arg Trp Leu Leu Leu Val Ser Val Ser Ile Cys Ala Ala 20		
tcg ggg ctg gtc tat gag cta gcc ctg gta tcg ctt tcc acc agc ttg 211		
Ser Gly Leu Val Tyr Glu Leu Ala Leu Val Ser Leu Ser Thr Ser Leu 35		
aac ggt ggc gga att gta gaa acc tcc ctc atc gtc gca ggt tat gta 259		
Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile Val Ala Gly Tyr Val 50		
gct gcc ctt gga ctt ggt gca ctg ctg gtc aag ccg ttt ctc aac tgg 307		
Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys Pro Phe Leu Asn Trp 65		
cct gcg caa acc ttc ctc ggt gtg gaa acc ctc ctt gga ctt att ggt 355		
Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu Leu Gly Leu Ile Gly 85		
ggc tgt tcc gcg ctg gtg ctg tat ttc acc ttc gcg acc atc ggc caa 403		
Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe Ala Thr Ile Gly Gln 100		
tcc ctg tgg att ctg gtg att gcc acc gct gca att ggc atc ctg gtc 451		
Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala Ile Gly Ile Leu Val 115		
ggc gct gaa ctt cca ctg ctg atg acc atg atc cag caa ggc cgc ctc 499		
Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile Gln Gln Gly Arg Leu 130		
gcc gac gcc aaa acc aca gga tct ctg gtt gcc acc ttg aat gct gct 547		
Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala Thr Leu Asn Ala Ala 145		
gat tac ctt ggc gca ctt tta ggt ggc ctg gcc tgg cct ttt gtg ttg 595		
Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala Trp Pro Phe Val Leu		

150	155	160	165	
ctg ccg tgg ctt ggc atg atg cgc ggt gcc gca gca gcc gga atg atc				643
Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala Ala Gly Met Ile				
	170	175	180	
aac ctc gtt gca gca cta ttc gtg ggc tgt gtg ctg ctg cga cat ttg				691
Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val Leu Leu Arg His Leu				
	185	190	195	
ctt ccg cgc acc cac ttc ttc gta tcc gtg gtg gcg ctt ctt ctc gcg				739
Leu Pro Arg Thr His Phe Phe Val Ser Val Val Ala Leu Leu Leu Ala				
	200	205	210	
atc gca gcg cta gcc acc gtg ttg gtg aaa tcc gac ggg atc gtt gcc				787
Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser Asp Gly Ile Val Ala				
	215	220	225	
acc gcc cgc gca cag ctc tac cgc gac ccc gtg atc tat tca cac caa				835
Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val Ile Tyr Ser His Gln				
	230	235	240	245
tct gac tac caa gac atc gta gtg aca gaa cga ggc aaa gac cga cgc				883
Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg Gly Lys Asp Arg Arg				
	250	255	260	
ctc tac ctc aat ggc ggt ttg cag tat tcc act cgt gac cag cat aga				931
Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr Arg Asp Gln His Arg				
	265	270	275	
tat aca gaa tca ctg gtg tat cca agc ctt aat cca gag gca gaa tcg				979
Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn Pro Glu Ala Glu Ser				
	280	285	290	
gtg tta atc atc ggc ggt ggc gat ggc ctc gca gca cgg gaa ctc ctc				
1027				
Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala Ala Arg Glu Leu Leu				
	295	300	305	
cga ttc cca tca atg cag atc acc caa gtt gaa tta gac cca gaa gtc				
1075				
Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu Leu Asp Pro Glu Val				
	310	315	320	325
atc gaa gta gcc aac aca gtg ctg cgc tct gac aat ggg gga gcg atg				
1123				
Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp Asn Gly Gly Ala Met				
	330	335	340	
gaa gat ccc cgc gtc tcc atc atc gtt gac gac gct ttc acc tgg ctg				
1171				
Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp Ala Phe Thr Trp Leu				
	345	350	355	
cgc tcc ggc gga aat aat ggc gaa act tac gat tcc atc atc atc gat				
1219				
Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp Ser Ile Ile Ile Asp				
	360	365	370	
ctt ccc gac cca aac aac gac acc atg gcc agg ctg tat tca gaa gag				
1267				



Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg Leu Tyr Ser Glu Glu  
375 380 385

ttc tac acc ttg gcc cga gca cga ctg aac gaa caa ggc cgc atg gtg  
1315

Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu Gln Gly Arg Met Val  
390 395 400 405

gtg caa tcc tcc agc gcc tac acc act cca gat gtg ttc tgg cga gtt  
1363

Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp Val Phe Trp Arg Val  
410 415 420

gga gca acc ttg aaa tcg gcg ggc tgt gaa caa gtc atc cca tat cac  
1411

Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln Val Ile Pro Tyr His  
425 430 435

gtg cat gtt ccc aca ttt ggc gac tgg ggc ttc caa ctg tgt ggc cct  
1459

Val His Val Pro Thr Phe Gly Asp Trp Gly Phe Gln Leu Cys Gly Pro  
440 445 450

gcc gac atg gaa tta gag ctt cgg gaa gac acc ccg cca ctg act ttc  
1507

Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr Pro Pro Leu Thr Phe  
455 460 465

ctt aat gat gaa gtt ctg gtg gct gct ggg gtg ttt ggg ttg gat aat  
1555

Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val Phe Gly Leu Asp Asn  
470 475 480 485

cag cct cgt gaa ttg gaa cct tcc acg ctg gat cat ccc cgc gtg gtg  
1603

Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp His Pro Arg Val Val  
490 495 500

gag gat ctg cgc aag gga tac cgc gaa tca ggc gac tagctgcaac  
1649

Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly Asp  
505 510

gatgcgctgt gtg  
1662

<210> 348

<211> 513

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

Met Ser Asp Leu Gly Pro Ile Trp Arg Trp Leu Leu Leu Val Ser Val  
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Ser Ile Cys Ala Ala Ser Gly Leu Val Tyr Glu Leu Ala Leu Val Ser  
20 25 30

Leu Ser Thr Ser Leu Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile  
35 40 45

Val Ala Gly Tyr Val Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys  
 50 55 60  
 Pro Phe Leu Asn Trp Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu  
 65 70 75 80  
 Leu Gly Leu Ile Gly Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe  
 85 90 95  
 Ala Thr Ile Gly Gln Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala  
 100 105 110  
 Ile Gly Ile Leu Val Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile  
 115 120 125  
 Gln Gln Gly Arg Leu Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala  
 130 135 140  
 Thr Leu Asn Ala Ala Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala  
 145 150 155 160  
 Trp Pro Phe Val Leu Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala  
 165 170 175  
 Ala Ala Gly Met Ile Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val  
 180 185 190  
 Leu Leu Arg His Leu Leu Pro Arg Thr His Phe Phe Val Ser Val Val  
 195 200 205  
 Ala Leu Leu Leu Ala Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser  
 210 215 220  
 Asp Gly Ile Val Ala Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val  
 225 230 235 240  
 Ile Tyr Ser His Gln Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg  
 245 250 255  
 Gly Lys Asp Arg Arg Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr  
 260 265 270  
 Arg Asp Gln His Arg Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn  
 275 280 285  
 Pro Glu Ala Glu Ser Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala  
 290 295 300  
 Ala Arg Glu Leu Leu Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu  
 305 310 315 320  
 Leu Asp Pro Glu Val Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp  
 325 330 335  
 Asn Gly Gly Ala Met Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp  
 340 345 350  
 Ala Phe Thr Trp Leu Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp  
 355 360 365

Ser Ile Ile Ile Asp Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg  
 370 375 380  
 Leu Tyr Ser Glu Glu Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu  
 385 390 395 400  
 Gln Gly Arg Met Val Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp  
 405 410 415  
 Val Phe Trp Arg Val Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln  
 420 425 430  
 Val Ile Pro Tyr His Val His Val Pro Thr Phe Gly Asp Trp Gly Phe  
 435 440 445  
 Gln Leu Cys Gly Pro Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr  
 450 455 460  
 Pro Pro Leu Thr Phe Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val  
 465 470 475 480  
 Phe Gly Leu Asp Asn Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp  
 485 490 495  
 His Pro Arg Val Val Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly  
 500 505 510  
 Asp

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<220>  
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 <222> (101)..(901)  
 <223> RXA01757

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 Met Pro Thr Ala Ser  
 1 5  
 cca att tat gat gtc gtt gtc gtc gga gcc ggc att tct ggc ctc atc 163  
 Pro Ile Tyr Asp Val Val Val Val Gly Ala Gly Ile Ser Gly Leu Ile  
 10 15 20  
 gcc acg caa ctg ttg gac cgc gca ggt cta aac atc aaa tgc ttc gaa 211  
 Ala Thr Gln Leu Leu Asp Arg Ala Gly Leu Asn Ile Lys Cys Phe Glu  
 25 30 35  
 gcc tgc tca aga gtt ggc ggc cga gca gtg tct gtc caa cag tcc gat 259  
 Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser Val Gln Gln Ser Asp  
 40 45 50  
 ttg ttc ctg gac ctc ggc gca aca tgg ttc tgg ctc aac gaa cca ctt 307

Leu	Phe	Leu	Asp	Leu	Gly	Ala	Thr	Trp	Phe	Trp	Leu	Asn	Glu	Pro	Leu		
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gtg	cag	caa	ctc	gtc	aat	aat	ctc	ggc	ctc	ggc	aca	ttc	cct	cag	gcc	355	
Val	Gln	Gln	Leu	Val	Asn	Asn	Leu	Gly	Leu	Gly	Thr	Phe	Pro	Gln	Ala	85	
70					75					80							
atc	gag	ggt	gat	gcg	ctt	ttt	gag	acg	ctt	gtc	gac	gcc	ccg	agc	cgc	403	
Ile	Glu	Gly	Asp	Ala	Leu	Phe	Glu	Thr	Leu	Val	Asp	Ala	Pro	Ser	Arg	100	
				90					95								
ctg	cgg	ggt	aac	ccc	ata	gac	gct	gct	tca	ggc	agg	ttc	caa	gca	ggg	451	
Leu	Arg	Gly	Asn	Pro	Ile	Asp	Ala	Ala	Ser	Gly	Arg	Phe	Gln	Ala	Gly	115	
			105					110									
gcc	tcc	tcg	ctt	gcg	ctc	ggg	ctt	gca	gcc	cag	ctc	aag	cca	gga	gtt	499	
Ala	Ser	Ser	Leu	Ala	Leu	Gly	Leu	Ala	Ala	Gln	Leu	Lys	Pro	Gly	Val	130	
			120				125										
tta	gaa	ctc	ggg	gac	ccc	gtc	cat	tct	ctc	agt	gag	gaa	gat	ggg	gaa	547	
Leu	Glu	Leu	Gly	Asp	Pro	Val	His	Ser	Leu	Ser	Glu	Glu	Asp	Gly	Glu	145	
			135			140											
atc	gtt	gtg	aag	tct	tcc	aaa	cag	att	gtg	agg	gca	aag	cac	gtc	atc	595	
Ile	Val	Val	Lys	Ser	Ser	Lys	Gln	Ile	Val	Arg	Ala	Lys	His	Val	Ile	165	
150						155				160							
att	gcg	gtt	cca	ccg	gca	ctc	gct	gcc	gag	ttg	att	ggt	ttc	acc	cta	643	
Ile	Ala	Val	Pro	Pro	Ala	Leu	Ala	Ala	Glu	Leu	Ile	Gly	Phe	Thr	Leu	180	
				170					175								
gat	tta	cca	gct	gac	gtg	cga	aaa	gca	gcg	cat	cca	caa	cat	ata	gct	691	
Asp	Leu	Pro	Ala	Asp	Val	Arg	Lys	Ala	Ala	His	Pro	Gln	His	Ile	Ala	195	
			185					190									
gtg	atg	aat	tgg	gca	aag	gag	aaa	tac	acc	tta	ccc	aca	caa	gcc	gca	739	
Val	Met	Asn	Trp	Ala	Lys	Glu	Lys	Tyr	Thr	Leu	Pro	Thr	Gln	Ala	Ala	210	
		200					205										
tcg	gct	ggg	ggt	ttt	ggg	cat	gag	ctg	ttc	caa	caa	cca	ctc	gga	cat	787	
Ser	Ala	Gly	Gly	Phe	Gly	His	Glu	Leu	Phe	Gln	Gln	Pro	Leu	Gly	His	225	
			215			220											
ggg	cga	att	cat	tgg	gca	tca	acg	gaa	gtt	gcc	act	gag	ttt	ggt	gga	835	
Gly	Arg	Ile	His	Trp	Ala	Ser	Thr	Glu	Val	Ala	Thr	Glu	Phe	Gly	Gly	245	
230					235					240							
cac	ctt	gaa	ggc	gca	gtt	cgt	gca	gga	att	cag	gct	gcg	ctt	caa	aca	883	
His	Leu	Glu	Gly	Ala	Val	Arg	Ala	Gly	Ile	Gln	Ala	Ala	Leu	Gln	Thr	260	
				250					255								
gga	ttt	aat	cta	aaa	tct	taa	ac	ctc	gt	att	tt	cc	ctg	ata		924	
Gly	Phe	Asn	Leu	Lys	Ser											265	

&lt;210&gt; 350

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 350

Met Pro Thr Ala Ser Pro Ile Tyr Asp Val Val Val Val Gly Ala Gly  
 1 5 10 15

Ile Ser Gly Leu Ile Ala Thr Gln Leu Leu Asp Arg Ala Gly Leu Asn  
 20 25 30

Ile Lys Cys Phe Glu Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser  
 35 40 45

Val Gln Gln Ser Asp Leu Phe Leu Asp Leu Gly Ala Thr Trp Phe Trp  
 50 55 60

Leu Asn Glu Pro Leu Val Gln Gln Leu Val Asn Asn Leu Gly Leu Gly  
 65 70 75 80

Thr Phe Pro Gln Ala Ile Glu Gly Asp Ala Leu Phe Glu Thr Leu Val  
 85 90 95

Asp Ala Pro Ser Arg Leu Arg Gly Asn Pro Ile Asp Ala Ala Ser Gly  
 100 105 110

Arg Phe Gln Ala Gly Ala Ser Ser Leu Ala Leu Gly Leu Ala Ala Gln  
 115 120 125

Leu Lys Pro Gly Val Leu Glu Leu Gly Asp Pro Val His Ser Leu Ser  
 130 135 140

Glu Glu Asp Gly Glu Ile Val Val Lys Ser Ser Lys Gln Ile Val Arg  
 145 150 155 160

Ala Lys His Val Ile Ile Ala Val Pro Pro Ala Leu Ala Ala Glu Leu  
 165 170 175

Ile Gly Phe Thr Leu Asp Leu Pro Ala Asp Val Arg Lys Ala Ala His  
 180 185 190

Pro Gln His Ile Ala Val Met Asn Trp Ala Lys Glu Lys Tyr Thr Leu  
 195 200 205

Pro Thr Gln Ala Ala Ser Ala Gly Gly Phe Gly His Glu Leu Phe Gln  
 210 215 220

Gln Pro Leu Gly His Gly Arg Ile His Trp Ala Ser Thr Glu Val Ala  
 225 230 235 240

Thr Glu Phe Gly Gly His Leu Glu Gly Ala Val Arg Ala Gly Ile Gln  
 245 250 255

Ala Ala Leu Gln Thr Gly Phe Asn Leu Lys Ser  
 260 265

&lt;210&gt; 351

&lt;211&gt; 636

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(613)

&lt;223&gt; RXA02159

&lt;400&gt; 351

tgatggacca gcgtccaaag ttttcgatga agcagaaaac cgcctccacg ctcagaaagc 60

actgctgggtg tggctgctgg ccaaccagcc gaggtaagac atg tcc ctt ggc tca 115  
 Met Ser Leu Gly Ser  
 1 5

acc ccg tca aca ccg gaa aac tta aat ccc gtg act cgc act gca cgc 163  
 Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val Thr Arg Thr Ala Arg  
 10 15 20

caa gct ctc att ttg cag att ttg gac aaa caa aaa gtc acc agc cag 211  
 Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln Lys Val Thr Ser Gln  
 25 30 35

gta caa ctg tct gaa ttg ctg ctg gat gaa ggc atc gat atc acc cag 259  
 Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly Ile Asp Ile Thr Gln  
 40 45 50

gcc acc ttg tcc cga gat ctc gat gaa ctc ggt gca cgc aag gtt cgc 307  
 Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly Ala Arg Lys Val Arg  
 55 60 65

ccc gat ggg gga cgc gcc tac tac gcg gtc ggc cca gta gat agc atc 355  
 Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly Pro Val Asp Ser Ile  
 70 75 80 85

gcc cgc gaa gat ctc cgg ggt ccg tcg gag aag ctg cgc cgc atg ctt 403  
 Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys Leu Arg Arg Met Leu  
 90 95 100

gat gaa ctg ctg gtt tct aca gat cat tcc ggc aac atc gcg atg ctg 451  
 Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly Asn Ile Ala Met Leu  
 105 110 115

cgc acc ccg ccg gga gct gcc cag tac ctg gca agt ttc atc gat agg 499  
 Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala Ser Phe Ile Asp Arg  
 120 125 130

gtg ggg ctg aaa gaa gtc gtt ggc acc atc gct ggt gat gac acc gtt 547  
 Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala Gly Asp Asp Thr Val  
 135 140 145

ttc gtt ctc gcc cgt gat ccg ctc aca ggt aaa gaa cta ggt gaa tta 595  
 Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys Glu Leu Gly Glu Leu  
 150 155 160 165

ctc agc ggg cgc acc act taaagcgccc ctagttcaag gct 636  
 Leu Ser Gly Arg Thr Thr  
 170

&lt;210&gt; 352

&lt;211&gt; 171

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 352

Met Ser Leu Gly Ser Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val

1	5	10	15
Thr Arg Thr	Ala Arg Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln		
	20	25	30
Lys Val Thr	Ser Gln Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly		
	35	40	45
Ile Asp Ile Thr	Gln Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly		
	50	55	60
Ala Arg Lys Val	Arg Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly		
	65	70	75
Pro Val Asp Ser	Ile Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys		
	85	90	95
Leu Arg Arg Met	Leu Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly		
	100	105	110
Asn Ile Ala Met	Leu Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala		
	115	120	125
Ser Phe Ile Asp	Arg Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala		
	130	135	140
Gly Asp Asp Thr	Val Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys		
	145	150	155
Glu Leu Gly Glu	Leu Leu Ser Gly Arg Thr Thr		
	165	170	

<210> 353  
 <211> 414  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(391)  
 <223> RXN02154

<400> 353  
 cccagaacct cggcgaagtc agcgacaagc cagtcaaggt gagcttcacc ccagtgcttg 60  
 caccgttacc tcgcgaattc tcaccactgc aaccgcacct ttg aaa gaa ggc gtt 115  
 Leu Lys Glu Gly Val 5  
 acc gca gaa cag gct cgc gca gta tat gaa gag ttc tat gca cag gaa 163  
 Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu 20  
 acc ttc gtg cat gtt ctt cca gaa ggt gca cag cca caa acc caa gca 211  
 Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala 35  
 gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa 259  
 Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu 50

gca ggc aaa gtc ctt gtt acc tcc gca atc gat aac ctc acc aag gga 307  
Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp Asn Leu Thr Lys Gly  
55 60 65

act gcc ggc gcc gct gtt cag tgc atg aac tta agc gtt ggt ttt gat 355  
Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu Ser Val Gly Phe Asp  
70 75 80 85

gag gca gca ggc ctg cca cag gtc ggc gtc gca cct taaagtagcg 401  
Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala Pro  
90 95

ccttaaagcg gcg 414

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<210> 354
<211> 97
<212> PRT
<213> Corynebacterium glutamicum
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<400> 354
Leu Lys Glu Gly Val Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu
  1                               5                                10                    15
Phe Tyr Ala Gln Glu Thr Phe Val His Val Leu Pro Glu Gly Ala Gln
                20                              25                      30
Pro Gln Thr Gln Ala Val Leu Gly Ser Asn Met Cys His Val Gln Val
          35                                40                          45
Glu Ile Asp Glu Glu Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp
      50                             55                            60
Asn Leu Thr Lys Gly Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu
  65                               70                                 75                     80
Ser Val Gly Phe Asp Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala
                        85                                90                    95
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Pro

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<210> 355
<211> 1302
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1279)
<223> RXS00147
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<400> 355
attgcatata atgcaatgaa ttgaataaac tacattcagg gttatcaacc agccaatttc 60
ttttaaaaag gcagacacac gaaaggcgac aacagtcacc gtg agt aaa gac acc 115
                                     Val Ser Lys Asp Thr
                                     1           5

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acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg	163
Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr Leu	
10 15 20	
gtt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct atc	211
Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe Gly Phe Gly Ala Ile	
25 30 35	
ggc acc acc ctt ggt gag gca gtg ttc act acc gcc atg acc ggt tac	259
Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr Ala Met Thr Gly Tyr	
40 45 50	
caa gaa acc atg acc gat cct tcc tat cac cgc cag att gtt gtg gct	307
Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg Gln Ile Val Val Ala	
55 60 65	
acc gca cca cag atc ggc aac acc ggc tgg aac gat gag gac aac gag	355
Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn Asp Glu Asp Asn Glu	
70 75 80 85	
tcc cgc gac ggc aag att tgg gtt gca ggc ctt gtt atc cgc gac ctc	403
Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu Val Ile Arg Asp Leu	
90 95 100	
gca gca cgt gtg tcc aac tgg cgc gcc acc acc tcc ttg cag cag gaa	451
Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr Ser Leu Gln Gln Glu	
105 110 115	
atg gca ggc cag ggc atc gtc ggc atc ggc gga atc gac acc cgc gca	499
Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly Ile Asp Thr Arg Ala	
120 125 130	
ctg gtt cgc cac ctg cgc aat gaa ggt tcc att gca gcg ggc atc ttc	547
Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile Ala Ala Gly Ile Phe	
135 140 145	
tcc ggc gct gac gca cag cgc cca gtt gaa gaa ctc gta gag atc gtc	595
Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu Leu Val Glu Ile Val	
150 155 160 165	
aag aat cag cca gca atg acc ggc gca aac ctc tcc gtt gag gtc tct	643
Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu Ser Val Glu Val Ser	
170 175 180	
gct gat gaa acc tac gtc atc gaa gct gaa ggc gaa gag cgc cac acc	691
Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly Glu Glu Arg His Thr	
185 190 195	
gtc gtg gcc tac gac ctg ggc att aag caa aac acc cca cgt cgt ttc	739
Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn Thr Pro Arg Arg Phe	
200 205 210	
tct gca cgc ggt gtt cgc acc gtc atc gtg cct gct gaa acc cca ttc	787
Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro Ala Glu Thr Pro Phe	
215 220 225	
gag gat atc aag cag tac aac cca tca ggc gtg ttc atc tcc aac ggc	835
Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val Phe Ile Ser Asn Gly	
230 235 240 245	
cct ggc gat cct gca gca gca gac gtc atg gtt gat atc gtc cgc gaa	883

Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val Asp Ile Val Arg Glu  
 250 255 260

gtt ctt gaa gcc gac att cca ttc ttt ggc atc tgc ttc ggc aac cag 931  
 Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile Cys Phe Gly Asn Gln  
 265 270 275

att ctt ggc cgc gca ttc ggc atg gag acc tac aag ctg aag ttc ggc 979  
 Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr Lys Leu Lys Phe Gly  
 280 285 290

cac cgc ggc atc aac gtt cca gtg aag aac cac atc acc ggc aag atc  
 1027

His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile  
 295 300 305

gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca ggc  
 1075

Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala Gly  
 310 315 320 325

cag gaa ttc gag acc gat ttc ggc act gca att gtc acc cac acc tgc  
 1123

Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys  
 330 335 340

ctc aac gac ggc gtc gtt gaa ggt att gcg ctg aag tcc gga cgc gca  
 1171

Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu Lys Ser Gly Arg Ala  
 345 350 355

tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat gca  
 1219

Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala  
 360 365 370

agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct cag  
 1267

Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala Gln  
 375 380 385

aag aaa ggc gca taaataacat gccaaagcgt tca  
 1302

Lys Lys Gly Ala  
 390

&lt;210&gt; 356

&lt;211&gt; 393

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 356

Val Ser Lys Asp Thr Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser  
 1 5 10 15

Val Pro Ala Tyr Leu Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe  
 20 25 30

Gly Phe Gly Ala Ile Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr  
 35 40 45

Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg  
 50 55 60  
 Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn  
 65 70 75 80  
 Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu  
 85 90 95  
 Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr  
 100 105 110  
 Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly  
 115 120 125  
 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile  
 130 135 140  
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu  
 145 150 155 160  
 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu  
 165 170 175  
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly  
 180 185 190  
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn  
 195 200 205  
 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro  
 210 215 220  
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val  
 225 230 235 240  
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val  
 245 250 255  
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile  
 260 265 270  
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr  
 275 280 285  
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His  
 290 295 300  
 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu  
 305 310 315 320  
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile  
 325 330 335  
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu  
 340 345 350  
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala  
 355 360 365

Gly Pro Asn Asp Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met  
 370 375 380

Asp Ala Asp Ala Gln Lys Lys Gly Ala  
 385 390

<210> 357

<211> 924

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(901)

<223> RXS00905

<400> 357

cgctgccctt ctatgctgct cctagttacc cctgcacaaa tagcgggtttt tctcacgcat 60  
 tctgcatcga gtcgggtcga cgtatataag gtggaaaggc atg acc caa ttc gaa 115  
 Met Thr Gln Phe Glu  
 1 5  
 aac gcg caa gta ctt aaa gag aac atc gaa aac caa cgc gag cag atc 163  
 Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn Gln Arg Glu Gln Ile  
 10 15 20  
 ttt acc cag ttg aaa gaa att gtg tct ttc aac tcc gtg cac agc gat 211  
 Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn Ser Val His Ser Asp  
 25 30 35  
 cca aac cta ctg gag gac tac gcc ggc gcg aaa gaa tgg gta aaa gaa 259  
 Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys Glu Trp Val Lys Glu  
 40 45 50  
 aca ctg acc aac gca ggt ctc acc gtc agc gaa ttc gct gcc gaa gat 307  
 Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu Phe Ala Ala Glu Asp  
 55 60 65  
 gga acc acc aac ttc atc ggc acc cgc aag ggc tcc gaa ggt gca cca 355  
 Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly Ser Glu Gly Ala Pro  
 70 75 80 85  
 aag gta ctg ctg tac agc cac ttc gac gtt gtc cca tcc ggc cct ttg 403  
 Lys Val Leu Leu Tyr Ser His Phe Asp Val Val Pro Ser Gly Pro Leu  
 90 95 100  
 gat ctc tgg gac acc aat cct ttt gaa ctc acc gag cgc gac gct ggc 451  
 Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr Glu Arg Asp Ala Gly  
 105 110 115  
 cac ggc acc cgc tgg tac ggc cgc ggc gcc gct gac tgc aag ggc aac 499  
 His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala Asp Cys Lys Gly Asn  
 120 125 130  
 ctg gtc atg cac ctc gca gca ctg cgc gcc gtc gaa gcc agc ggc gac 547  
 Leu Val Met His Leu Ala Ala Leu Arg Ala Val Glu Ala Ser Gly Asp  
 135 140 145  
 acc aca ctc aac ctc acc tac gtg gtc gag ggc tcc gag gaa atg gga 595

Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly Ser Glu Glu Met Gly  
 150 155 160 165  
 ggc gga gcg ctc agc gcg ctc atc aag gac aag cct gag ctt ttc gac 643  
 Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys Pro Glu Leu Phe Asp  
 170 175 180  
 gca gat gtc atc ttg att gca gac agc gga aac gct tcc gtg ggc acc 691  
 Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn Ala Ser Val Gly Thr  
 185 190 195  
 cca acc ttg acc act acc ctg cgc ggt ggc gga cag gtc acc gtc acc 739  
 Pro Thr Leu Thr Thr Leu Arg Gly Gly Gln Val Thr Val Thr  
 200 205 210  
 gtg gac acc ctt gaa ggc gct gtt cac tcc ggc cag aac ggt ggc gct 787  
 Val Asp Thr Leu Glu Gly Ala Val His Ser Gly Gln Asn Gly Gly Ala  
 215 220 225  
 gcc cca gat gct gtt gct gct ctc gtg cgc gtt ctg gat act ttg cgc 835  
 Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val Leu Asp Thr Leu Arg  
 230 235 240 245  
 gat gaa cac gga cgc acc gtt atc gac ggc tgt caa cac cac cgc aaa 883  
 Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys Gln His His Arg Lys  
 250 255 260  
 ctg gaa ggg cga gcc tta tgatccagag actttccgca gcg 924  
 Leu Glu Gly Arg Ala Leu  
 265

&lt;210&gt; 358

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 358

Met Thr Gln Phe Glu Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn  
 1 5 10 15  
 Gln Arg Glu Gln Ile Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn  
 20 25 30  
 Ser Val His Ser Asp Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys  
 35 40 45  
 Glu Trp Val Lys Glu Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu  
 50 55 60  
 Phe Ala Ala Glu Asp Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly  
 65 70 75 80  
 Ser Glu Gly Ala Pro Lys Val Leu Leu Tyr Ser His Phe Asp Val Val  
 85 90 95  
 Pro Ser Gly Pro Leu Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr  
 100 105 110  
 Glu Arg Asp Ala Gly His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala  
 115 120 125

Asp Cys Lys Gly Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val  
 130 135 140  
 Glu Ala Ser Gly Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly  
 145 150 155 160  
 Ser Glu Glu Met Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys  
 165 170 175  
 Pro Glu Leu Phe Asp Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn  
 180 185 190  
 Ala Ser Val Gly Thr Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly  
 195 200 205  
 Gln Val Thr Val Thr Val Asp Thr Leu Glu Gly Ala Val His Ser Gly  
 210 215 220  
 Gln Asn Gly Gly Ala Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val  
 225 230 235 240  
 Leu Asp Thr Leu Arg Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys  
 245 250 255  
 Gln His His Arg Lys Leu Glu Gly Arg Ala Leu  
 260 265

<210> 359  
 <211> 627  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(604)  
 <223> RXS00906

<400> 359  
 accgtggaca cccttgaagg cgctgttcac tccggccaga acggtggcgc tgccccagat 60  
 gctgttgctg ctctcgtgcg cgttctggat actttgcgcg atg aac acg gac gca 115  
 Met Asn Thr Asp Ala  
 1 5  
 ccg tta tcg acg gct gtc aac acc acc gca aac tgg aag ggc gag cct 163  
 Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn Trp Lys Gly Glu Pro  
 10 15 20  
 tat gat cca gag act ttc cgc agc gat gcc ggc atc ctc gac ggt gta 211  
 Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly Ile Leu Asp Gly Val  
 25 30 35  
 gac atc atg ggc gac ggc gac aac cca gca agc atg ctg tgg tcc agg 259  
 Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser Met Leu Trp Ser Arg  
 40 45 50  
 cct gca atc tcc atc acc gga ttc act tcc acc cca gtg gca gaa gca 307  
 Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr Pro Val Ala Glu Ala  
 55 60 65

ctc aac gca gtg ccc gca acg gcg tcc gcc aag cta aac ctt cgc gtg 355  
 Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys Leu Asn Leu Arg Val  
 70 75 80 85

cca gca ggc ctg gaa gca aac gat gtg gcc gag aag ctg aag cag cac 403  
 Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu Lys Leu Lys Gln His  
 90 95 100

ctg atc aat cac aca cct tgg ggc gca aag atc acg gtg gag atc gat 451  
 Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile Thr Val Glu Ile Asp  
 105 110 115

gac att aac caa ccg ttc tcc acc gat att acc ggc cct gca atg tcc 499  
 Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr Gly Pro Ala Met Ser  
 120 125 130

acc ctg gcg tcc tgc ctg agc gct gcg tac gag ggc aag gat ctt gtc 547  
 Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu Gly Lys Asp Leu Val  
 135 140 145

acc gaa ggc agc ggc gga tcc att cca ctg tgt acc gaa ctg att gag 595  
 Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys Thr Glu Leu Ile Glu  
 150 155 160 165

gtc aac cca taagcagaat tggcactcta cgg 627  
 Val Asn Pro

<210> 360

<211> 168

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 360

Met Asn Thr Asp Ala Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn  
 1 5 10 15

Trp Lys Gly Glu Pro Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly  
 20 25 30

Ile Leu Asp Gly Val Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser  
 35 40 45

Met Leu Trp Ser Arg Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr  
 50 55 60

Pro Val Ala Glu Ala Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys  
 65 70 75 80

Leu Asn Leu Arg Val Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu  
 85 90 95

Lys Leu Lys Gln His Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile  
 100 105 110

Thr Val Glu Ile Asp Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr  
 115 120 125

Gly Pro Ala Met Ser Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu

130 135 140

Gly Lys Asp Leu Val Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys  
 145 150 155 160

Thr Glu Leu Ile Glu Val Asn Pro  
 165

<210> 361  
 <211> 246  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(223)  
 <223> RXS00907

<400> 361  
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actgtgtacc gaactgattg aggtcaaccc ataagcagaa ttg gca ctc tac ggt 115  
 Leu Ala Leu Tyr Gly  
 1 5

gtg gaa gaa ccc ctc acc gtt atc cac tcc gct aat gaa tct gtt gac 163  
 Val Glu Glu Pro Leu Thr Val Ile His Ser Ala Asn Glu Ser Val Asp  
 10 15 20

ccc aat gag att cgc gat atc gcc acc gca gaa gca ttg ttc ctg ctc 211  
 Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu Ala Leu Phe Leu Leu  
 25 30 35

aac tac acc aag tagacccaaa agcaggcgtt aac 246  
 Asn Tyr Thr Lys  
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<210> 362  
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<400> 362  
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Asn Glu Ser Val Asp Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu  
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Ala Leu Phe Leu Leu Asn Tyr Thr Lys  
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 <211> 1281  
 <212> DNA  
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<220>



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&lt;222&gt; (101) .. (1258)

&lt;223&gt; RXS02001

&lt;400&gt; 363

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gatagtccag catagaccgt gctttatcga aggtgaaccc atg ccc gtt atc aat 115
Met Pro Val Ile Asn
1 5

agt atc gcc agt ttt tcc gac gag atg acc cgc tgg cgg cgt cac ctg 163
Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg Trp Arg Arg His Leu
10 15 20

cat caa aac ccc gaa atc agc ttt gat tgt gtg gaa act gcg gcc ttc 211
His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val Glu Thr Ala Ala Phe
25 30 35

gtg gcc gag cag ctg cgc agc ttc ggg gtg gat gaa att cac acc ggc 259
Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp Glu Ile His Thr Gly
40 45 50

atc gcg aaa acc ggt atc atc gcc ctg att cac ggg cgc gag gct ggc 307
Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His Gly Arg Glu Ala Gly
55 60 65

ccc gtc gtc ggc ctg cgc gcc gat atg gac gcg ctg ccg ctg acc gag 355
Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala Leu Pro Leu Thr Glu
70 75 80 85

att acc ggc gtc gac tat gcc tcg acc acc ccc gga aaa atg cac gcc 403
Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro Gly Lys Met His Ala
90 95 100

tgc ggc cac gac ggc cac acg acc atg ctg ctg ggc gcc gcc aaa tat 451
Cys Gly His Asp Gly His Thr Thr Met Leu Leu Gly Ala Ala Lys Tyr
105 110 115

ctg gcc gag acg cgc aat ttc gca ggt acc gtc gcg ctg atc ttc cag 499
Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val Ala Leu Ile Phe Gln
120 125 130

cct gcg gaa gaa aac ggc ggc ggc gcg ggc gtt atg gtc gat gaa ggc 547
Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val Met Val Asp Glu Gly
135 140 145

gtc ctc gac cgc ttt gcc atc gcc gaa gtc tac gcc ctg cac aac cag 595
Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr Ala Leu His Asn Gln
150 155 160 165

ccc ggc ctg ccg ctt ggc cat ttt atg acg aca gcc ggc ccg atc atg 643
Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr Ala Gly Pro Ile Met
170 175 180

gcc gct gtc gac acg ttc gac atc aac att acc gga cgc ggc ggc cac 691
Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr Gly Arg Gly Gly His
185 190 195

ggg gcc aaa ccg cac caa acc cgc gac ccc atc gtc gca gcc gtc gga 739
Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile Val Ala Ala Val Gly

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200	205	210	
att gtc caa gcg ttt caa acg	ata gtc agc cgg aat cac aat ccg gtc		787
Ile Val Gln Ala Phe Gln Thr	Ile Val Ser Arg Asn His Asn Pro Val		
215	220	225	
gag gac ctt gtc gtg tcg gtc acg caa atc cac acc ggc agc gcc gat			835
Glu Asp Leu Val Val Ser Val Thr Gln Ile His Thr Gly Ser Ala Asp			
230	235	240	245
aat atc atc ccc gaa acc gcc tat atc aac ggc act gtc cgc acc ttc			883
Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe			
250	255	260	
aac aaa gac gtg cag gcc atg gtc atc acg cgg atg gaa gaa atc gtc			931
Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg Met Glu Glu Ile Val			
265	270	275	
gcg ggc caa gct gca gcc tat ggg gtc gag gcg acg ctg acc tac aac			979
Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn			
280	285	290	
cgc aac tat ccc gcc acc att aac gac gcc gcc aaa gcc gcc atc gct			
1027			
Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala			
295	300	305	
gcc gaa gtc gcg ggc gag gtc ggc ctc ggg gtc aac ccg aac ggc tcg			
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Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val Asn Pro Asn Gly Ser			
310	315	320	325
cgc ggg atg ggg gcc gag gat ttc tcg tat ttc ctc gaa aag cgc ccg			
1123			
Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro			
330	335	340	
ggt gcc tac ctg ttc gtc ggt aat ggc gac agc gcg ggc ctt cac aac			
1171			
Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser Ala Gly Leu His Asn			
345	350	355	
ccc gcc tat aat ttc aac gac gag gcc gcg ccc tac ggc gca tcg ttc			
1219			
Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe			
360	365	370	
ttg gcc cgc atg gca gaa cgc ccc ttg ccg tta aag ggc tgatccatgg			
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375	380	385	
cgctcgaaga tgc			
1281			
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<212> PRT			
<213> Corynebacterium glutamicum			

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 Trp Arg Arg His Leu His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val  
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 Glu Thr Ala Ala Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp  
 35 40 45  
 Glu Ile His Thr Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His  
 50 55 60  
 Gly Arg Glu Ala Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala  
 65 70 75 80  
 Leu Pro Leu Thr Glu Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro  
 85 90 95  
 Gly Lys Met His Ala Cys Gly His Asp Gly His Thr Thr Met Leu Leu  
 100 105 110  
 Gly Ala Ala Lys Tyr Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val  
 115 120 125  
 Ala Leu Ile Phe Gln Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val  
 130 135 140  
 Met Val Asp Glu Gly Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr  
 145 150 155 160  
 Ala Leu His Asn Gln Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr  
 165 170 175  
 Ala Gly Pro Ile Met Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr  
 180 185 190  
 Gly Arg Gly Gly His Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile  
 195 200 205  
 Val Ala Ala Val Gly Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg  
 210 215 220  
 Asn His Asn Pro Val Glu Asp Leu Val Val Ser Val Thr Gln Ile His  
 225 230 235 240  
 Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly  
 245 250 255  
 Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg  
 260 265 270  
 Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala  
 275 280 285  
 Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala  
 290 295 300  
 Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val  
 305 310 315 320

Asn Pro Asn Gly Ser Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe  
 325 330 335

Leu Glu Lys Arg Pro Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser  
 340 345 350

Ala Gly Leu His Asn Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro  
 355 360 365

Tyr Gly Ala Ser Phe Leu Ala Arg Met Ala Glu Arg Pro Leu Pro Leu  
 370 375 380

Lys Gly  
 385

<210> 365

<211> 1386

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1363)

<223> RXS02101

<400> 365

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agtttttagtg tcgctgcgca ggtactctac tatctaatacc atg agc cgc att tca 115  
 Met Ser Arg Ile Ser  
 1 5

gaa ctt cta aac aat cat ggt gtt gat ctg tcg tgg caa gag gcc gca 163  
 Glu Leu Leu Asn Asn His Gly Val Asp Leu Ser Trp Gln Glu Ala Ala  
 10 15 20

tat cag gat ttc cac gaa cat cct gag ctc tcc ggc ttc gaa tca gag 211  
 Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser Gly Phe Glu Ser Glu  
 25 30 35

acc gca gat cgc att cag aaa tac ctc gag cgt ttt gat tgt gag gtg 259  
 Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg Phe Asp Cys Glu Val  
 40 45 50

att cca aat gtt ggc ggt tac ggc att ctg gcc gtg ttc cga aat ggg 307  
 Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala Val Phe Arg Asn Gly  
 55 60 65

tcg aca gat cct ggt gcc cct gtt gcg tta atg cgc gca gat ttc gat 355  
 Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met Arg Ala Asp Phe Asp  
 70 75 80 85

ggc ctt ccc gtc aag gaa atc acc gga gtt ccg ttt gct tcc act cgt 403  
 Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro Phe Ala Ser Thr Arg  
 90 95 100

atg cgt ccg cat gat ggg gca aat gtc cat gtc atg cac gca tgc ggc 451  
 Met Arg Pro His Asp Gly Ala Asn Val His Val Met His Ala Cys Gly  
 105 110 115

cac gat gtc cac gtc acc gcg ctg ctt ggt gcg tgt gcc att tta gat	499
His Asp Val His Val Thr Ala Leu Leu Gly Ala Cys Ala Ile Leu Asp	
120 125 130	
gag cgt cgc gat gca tgg gaa ggc acg ttc atc gcg ttg ttc cag cca	547
Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile Ala Leu Phe Gln Pro	
135 140 145	
tcg gag gaa aac tcc caa ggc gct aac aag atg gtc gcc ggc ggt tta	595
Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met Val Ala Gly Gly Leu	
150 155 160 165	
gtt gat ctg atc cca cgc cct gat gtg tgc ttt ggc cag cat gta gtc	643
Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe Gly Gln His Val Val	
170 175 180	
ccc ggt gct gca gga acc gtg atg agc atg cct ggc ggt gct ctc gct	691
Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro Gly Gly Ala Leu Ala	
185 190 195	
gcc tgc gat tcc att gaa atc cgc att cag ggt cgc agc gcc cat ggt	739
Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly Arg Ser Ala His Gly	
200 205 210	
tcc atg cct cat aat tcc atc gat ccc act tat gtt gca gcg atg att	787
Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr Val Ala Ala Met Ile	
215 220 225	
gtc gtg cga ctc caa gga atc gtg ggc cgc gag gtt tct cca gag gat	835
Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu Val Ser Pro Glu Asp	
230 235 240 245	
ttc gcc gtt att tct gtg ggc acc ctc cag tcg ggc aac acc aac aac	883
Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser Gly Asn Thr Asn Asn	
250 255 260	
acc att cca gca agt gct cgt ttg gtg ttg aac tgc cgt ttc tac aac	931
Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn Cys Arg Phe Tyr Asn	
265 270 275	
gac aaa gtc aag cac aag gtc tac cga gcc atc gaa cgt gtt gtc cgt	979
Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile Glu Arg Val Val Arg	
280 285 290	
ggg gaa tgc ctt gct tcc ggt att gag gaa gaa cct gtc att gag tac	1027
Gly Glu Cys Leu Ala Ser Gly Ile Glu Glu Glu Pro Val Ile Glu Tyr	
295 300 305	
ttc gcc cac ggt gat ctc acc aac aac acc cct gtt gtc ttc gat act	1075
Phe Ala His Gly Asp Leu Thr Asn Asn Thr Pro Val Val Phe Asp Thr	
310 315 320 325	
gtg cgc cct gtc ttc gac gat gtt ttc ggc gag gat tct att gac gct	1123
Val Arg Pro Val Phe Asp Asp Val Phe Gly Glu Asp Ser Ile Asp Ala	
330 335 340	
tac cgg tgg act gcg tcg gag gat ttc ccc tcc att cct aag gca ttc	1171

Tyr Arg Trp Thr Ala Ser Glu Asp Phe Pro Ser Ile Pro Lys Ala Phe  
345 350 355

aac agc cct tac ctg tac tgg acg att ggt gtc acg ccg cgc gat cag  
1219

Asn Ser Pro Tyr Leu Tyr Trp Thr Ile Gly Val Thr Pro Arg Asp Gln  
360 365 370

tgg aca gaa gcc gta gaa aga gac cgc gtg gca tcg gat gtg cca gcc  
1267

Trp Thr Glu Ala Val Glu Arg Asp Arg Val Ala Ser Asp Val Pro Ala  
375 380 385

aat cac atg gga gat ttc ctc cct gat tat gcg ccg acg atg tcc gct  
1315

Asn His Met Gly Asp Phe Leu Pro Asp Tyr Ala Pro Thr Met Ser Ala  
390 395 400 405

gcc acc cgc gca gcc gca gcc gcg ctg ctg acc tac ttg gga act aac  
1363

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1386

<210> 366

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 366

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Trp Gln Glu Ala Ala Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser  
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Gly Phe Glu Ser Glu Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg  
35 40 45

Phe Asp Cys Glu Val Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala  
50 55 60

Val Phe Arg Asn Gly Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met  
65 70 75 80

Arg Ala Asp Phe Asp Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro  
85 90 95

Phe Ala Ser Thr Arg Met Arg Pro His Asp Gly Ala Asn Val His Val  
100 105 110

Met His Ala Cys Gly His Asp Val His Val Thr Ala Leu Leu Gly Ala  
115 120 125

Cys Ala Ile Leu Asp Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile  
130 135 140

Ala Leu Phe Gln Pro Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met

145		150		155		160									
Val	Ala	Gly	Gly	Leu	Val	Asp	Leu	Ile	Pro	Arg	Pro	Asp	Val	Cys	Phe
				165					170					175	
Gly	Gln	His	Val	Val	Pro	Gly	Ala	Ala	Gly	Thr	Val	Met	Ser	Met	Pro
			180					185					190		
Gly	Gly	Ala	Leu	Ala	Ala	Cys	Asp	Ser	Ile	Glu	Ile	Arg	Ile	Gln	Gly
		195					200					205			
Arg	Ser	Ala	His	Gly	Ser	Met	Pro	His	Asn	Ser	Ile	Asp	Pro	Thr	Tyr
	210					215					220				
Val	Ala	Ala	Met	Ile	Val	Val	Arg	Leu	Gln	Gly	Ile	Val	Gly	Arg	Glu
225					230					235					240
Val	Ser	Pro	Glu	Asp	Phe	Ala	Val	Ile	Ser	Val	Gly	Thr	Leu	Gln	Ser
			245						250					255	
Gly	Asn	Thr	Asn	Asn	Thr	Ile	Pro	Ala	Ser	Ala	Arg	Leu	Val	Leu	Asn
			260					265					270		
Cys	Arg	Phe	Tyr	Asn	Asp	Lys	Val	Lys	His	Lys	Val	Tyr	Arg	Ala	Ile
	275						280					285			
Glu	Arg	Val	Val	Arg	Gly	Glu	Cys	Leu	Ala	Ser	Gly	Ile	Glu	Glu	Glu
290						295					300				
Pro	Val	Ile	Glu	Tyr	Phe	Ala	His	Gly	Asp	Leu	Thr	Asn	Asn	Thr	Pro
305					310					315					320
Val	Val	Phe	Asp	Thr	Val	Arg	Pro	Val	Phe	Asp	Asp	Val	Phe	Gly	Glu
			325						330					335	
Asp	Ser	Ile	Asp	Ala	Tyr	Arg	Trp	Thr	Ala	Ser	Glu	Asp	Phe	Pro	Ser
			340					345					350		
Ile	Pro	Lys	Ala	Phe	Asn	Ser	Pro	Tyr	Leu	Tyr	Trp	Thr	Ile	Gly	Val
		355					360					365			
Thr	Pro	Arg	Asp	Gln	Trp	Thr	Glu	Ala	Val	Glu	Arg	Asp	Arg	Val	Ala
	370					375					380				
Ser	Asp	Val	Pro	Ala	Asn	His	Met	Gly	Asp	Phe	Leu	Pro	Asp	Tyr	Ala
385					390					395					400
Pro	Thr	Met	Ser	Ala	Ala	Thr	Arg	Ala	Ala	Ala	Ala	Ala	Leu	Leu	Thr
				405					410					415	
Tyr	Leu	Gly	Thr	Asn											
			420												

&lt;210&gt; 367

&lt;211&gt; 3462

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(3439)

&lt;223&gt; RXS02234

&lt;400&gt; 367

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tgatggatgc agacgctcag aagaaaggcg cataaataac atg cca aag cgt tca 115  
Met Pro Lys Arg Ser  
1 5

gat att aac cac gtc ctc gtc atc ggt tcc ggc ccc atc gtc att ggc 163  
Asp Ile Asn His Val Leu Val Ile Gly Ser Gly Pro Ile Val Ile Gly  
10 15 20

cag gca tgt gaa ttc gac tac tcc ggc acc cag gct tgc cgc gtg ctg 211  
Gln Ala Cys Glu Phe Asp Tyr Ser Gly Thr Gln Ala Cys Arg Val Leu  
25 30 35

aag gaa gag gga ctg cgc gtc acc ctc atc aac tcc aac cca gca acg 259  
Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn Ser Asn Pro Ala Thr  
40 45 50

atc atg acc gac cca gaa atg gct gac cac acc tac gtg gag cca atc 307  
Ile Met Thr Asp Pro Glu Met Ala Asp His Thr Tyr Val Glu Pro Ile  
55 60 65

gag ccg gaa tac atc gac aag att ttc gct aag gaa atc gag cag ggc 355  
Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly  
70 75 80 85

cac cca atc gac gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt 403  
His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu  
90 95 100

aac gca gct atc cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc 451  
Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly  
105 110 115

gtt gaa ctc atc ggt gca gac atc gat gcc att gag cgc ggc gaa gat 499  
Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp  
120 125 130

cgc cag aag ttc aag gat att gtc acc acc atc ggt ggc gaa tcc gcg 547  
Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala  
135 140 145

cgt tcc cgc gtc tgc cac aac atg gaa gaa gtc cac gag act gtc gca 595  
Arg Ser Arg Val Cys His Asn Met Glu Glu Val His Glu Thr Val Ala  
150 155 160 165

gaa ctc ggc ctt cca gta gtc gtg cgt cca tcc ttc act atg ggt ggc 643  
Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly  
170 175 180

ctg ggc tcc ggt ctt gca tac aac acc gaa gac ctt gag cgc atc gct 691  
Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala  
185 190 195

ggt ggc gga ctt gct gca tct cct gaa gca aac gtc ttg atc gaa gaa 739  
Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn Val Leu Ile Glu Glu  
200 205 210



tcc atc ctt ggt tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc 787  
 Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr  
 215 220 225

gca gac aac gtt gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg 835  
 Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu  
 230 235 240 245

ggc gtg cac acc ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg 883  
 Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu  
 250 255 260

act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc 931  
 Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile  
 265 270 275

cgc gag gtc ggc gtg gac acc ggt gga tgt aac atc cag ttc gcc atc 979  
 Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile  
 280 285 290

aac cca gtt gat ggc cgc atc atc acc att gag atg aac cca cgt gtg  
 1027  
 Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val  
 295 300 305

tct cgt tcc tcc gct ctg gca tcc aag gca acg ggc ttc cca att gcc  
 1075  
 Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala  
 310 315 320 325

aag atg gct gcc aag ctg gct atc gga tac acc ctg gat gag atc acc  
 1123  
 Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr  
 330 335 340

aac gac atc act ggt gaa acc cca gct gcg ttt gag ccc acc atc gac  
 1171  
 Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp  
 345 350 355

tac gtc gtg gtc aag gcc cca cgc ttt gct ttc gag aag ttt gtc ggc  
 1219  
 Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly  
 360 365 370

gct gat gac act ttg acc acc acc atg aag tcc gtc ggt gag gtc atg  
 1267  
 Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met  
 375 380 385

tcc ctg ggc cgc aac tac att gca gca ctg aac aag gca ctg cgt tcc  
 1315  
 Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser  
 390 395 400 405

ctg gaa acc aag cag cag ggt ttc tgg acc aag cct gat gag ttc ttc  
 1363  
 Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe  
 410 415 420

gca ggg gag cgc gct acc gat aag gca gct gtt ctg gaa gat ctc aag  
 1411  
 Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys  
 425 430 435

cgc cca acc gaa ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt  
 1459  
 Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu  
 440 445 450

ggc gca agc gtg gaa gaa ctc tac gaa gca tct tct att gat cct tgg  
 1507  
 Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp  
 455 460 465

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 1555  
 Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val  
 470 475 480 485

gac gca cca ttc cta aac gaa gat ctc ctg cgc gaa gca aag ttc atg  
 1603  
 Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met  
 490 495 500

ggt ctg tcc gac ctg cag atc gca gcc ctt cgc cca gag ttc gct ggc  
 1651  
 Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg Pro Glu Phe Ala Gly  
 505 510 515

gaa gac ggc gta cgc acc ttg cgt ctg tcc cta ggc atc cgc cca gta  
 1699  
 Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val  
 520 525 530

ttc aag act gtg gat acc tgt gca gca gag ttt gaa gct aag act ccg  
 1747  
 Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro  
 535 540 545

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1987

Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr Ala Asp Arg Leu Tyr  
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2035

Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu Val Tyr His Ala Glu  
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2083

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Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala Glu Asp Arg Gly Glu  
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Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val Ala Asp Glu Ile Ser  
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Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu Gly Gly Arg Gly Met  
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2371

Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp Tyr Ile Asn Arg Ala  
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Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu Ala Gly Ile His Ser  
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 Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys  
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548

Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys  
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 Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg  
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Pro	Ile	Ala	Val	Lys	Glu	Ala	Val	Leu	Pro	Phe	Asn	Arg	Phe	Arg	Arg
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Lys	Ala	Glu	Ala	Gly	Ala	Phe	Gly	Ala	Leu	Pro	Thr	Glu	Gly	Thr	Val
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			980					985						990	
Gln	Arg	Leu	Ala	Leu	Met	Gly	Tyr	Lys	Ile	Leu	Ala	Thr	Glu	Gly	Thr
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Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val  
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 Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala  
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 Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu  
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 Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu  
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 Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro  
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cag ggt atc gcc atc atc cgc gag gtc ggc gtg gac acc ggt gga tgt 720  
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 Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr  
 900 905 910

gca aag gct gaa gct ggc gcg ttt ggt gca ttg cca acc gaa ggc acc  
 2784  
 Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr  
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gtc ttc gtg acc gtg gct aac cgc gac aag cgc acc ctg atc ctg cca  
 2832  
 Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro  
 930 935 940

atc cag cgc ctg gcg ttg atg ggc tac aag atc ctc gcc acc gaa ggc  
 2880  
 Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly  
 945 950 955 960

acc gca ggc atg ctg cgc cgc aac ggc att gag tgt gaa gtt gtg ctc  
2928

Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu  
965 970 975

aag gct tcc gac atc cgc gaa ggt gta gag ggc aag tcc atc gtg gat  
2976

Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp  
980 985 990

cgt atc cgc gaa ggc gaa gtt gac ctc atc ctc aac acc cca gct ggt  
3024

Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly  
995 1000 1005

tct gct ggc gct cgc cac gat ggc tac gat atc cgc gca gca gca gtg  
3072

Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val  
1010 1015 1020

acc gtg ggt gtt ccg ctg atc acc act gtt cag ggt gtc acc gca gct  
3120

Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala  
1025 1030 1035 1040

gtc cag ggc ata gag gcc ctg cgt gag ggc gtt gtc agc gtc cgc gcg  
3168

Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala  
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ctg cag gaa ctc gac cac gca gtc aag gct taagccctat gacattcggc  
3218

Leu Gln Glu Leu Asp His Ala Val Lys Ala  
1060 1065

gag  
3221

<210> 370

<211> 1066

<212> PRT

<213> Corynebacterium glutamicum

<400> 370

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20 25 30

Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu  
35 40 45

Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly  
50 55 60

Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala  
65 70 75 80

Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr

	85	90	95
Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu	100	105	110
Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro	115	120	125
Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu	130	135	140
Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala	145	150	155
Asn Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu	165	170	175
Glu Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile	180	185	190
Glu Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val	195	200	205
Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp	210	215	220
Gln Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys	225	230	235
Asn Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile	245	250	255
Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala	260	265	270
Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr	275	280	285
Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala	290	295	300
Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala	305	310	315
Phe Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys	325	330	335
Ser Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu	340	345	350
Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr	355	360	365
Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala	370	375	380
Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val	385	390	395
Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala	405	410	415

Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln  
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 Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu  
 435 440 445  
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 450 455 460  
 Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser  
 465 470 475 480  
 Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu  
 485 490 495  
 Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro  
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 565 570 575  
 Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met  
 580 585 590  
 Glu Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile  
 595 600 605  
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 Lys Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met  
 625 630 635 640  
 Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu  
 645 650 655  
 Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr  
 660 665 670  
 Val Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val  
 675 680 685  
 Leu Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu  
 690 695 700  
 Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu  
 705 710 715 720  
 Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu  
 725 730 735



Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu  
 740 745 750  
 Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met  
 755 760 765  
 Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys  
 770 775 780  
 Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala  
 785 790 795 800  
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 Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys  
 820 825 830  
 Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp  
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 Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp  
 850 855 860  
 Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg  
 865 870 875 880  
 Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys  
 885 890 895  
 Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr  
 900 905 910  
 Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr  
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 Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro  
 930 935 940  
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 945 950 955 960  
 Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu  
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 Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp  
 980 985 990  
 Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly  
 995 1000 1005  
 Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Val  
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 Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala  
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 Leu Gln Glu Leu Asp His Ala Val Lys Ala

1060

1065

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 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1366)  
 <223> RXS02565

<400> 371

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aaccctcacc ctccttcagg aacttatccg caacgcctgc gtg aat gat cta acc 115
                                   Val Asn Asp Leu Thr
                                   1                               5

cca gat tca ggt cag gaa att aga aac gcg gaa agc cta gaa cgt ttc 163
Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu Ser Leu Glu Arg Phe
                                   10                               15                               20

ttt gaa gga acc ccc aac gtt aaa atc acc aag ctg gaa ccg cat ccg 211
Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys Leu Glu Pro His Pro
                                   25                               30                               35

ggc cgg acc tca att atc gtg act gtt cca ggc agc gat cca gat gct 259
Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly Ser Asp Pro Asp Ala
                                   40                               45                               50

gag cct tta aca ctg ctt gga cat act gat gtt gtg cct gtt gat ctg 307
Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val Val Pro Val Asp Leu
                                   55                               60                               65

cct aaa tgg act aaa gat cca ttc ggt gcg gag att tcg gat gga cag 355
Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu Ile Ser Asp Gly Gln
                                   70                               75                               80                               85

att tgg ggt aga ggg tcc gtc gat atg ctc ttt att acc gca acc caa 403
Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe Ile Thr Ala Thr Gln
                                   90                               95                               100

gcg gcc gtc acc cgt caa gta gcc cgt gaa ggc ggc ctg cgt ggc acg 451
Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly Gly Leu Arg Gly Thr
                                   105                               110                               115

ctg aca ttc gtt ggc gtt gct gat gag gaa gcc cgc ggc gga ctc gga 499
Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala Arg Gly Gly Leu Gly
                                   120                               125                               130

gcg aag tgg ctt tcc gaa gaa cac caa aac ctc ttc agc tgg aaa aac 547
Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu Phe Ser Trp Lys Asn
                                   135                               140                               145

tgc ctc tcc gaa tcc ggt gga tcg cac ctt cca gtc cac gac ggc agc 595
Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro Val His Asp Gly Ser
150                               155                               160                               165

gac gca gta gta att aac gtt gga gaa aaa ggt gca gct caa cgt cgt 643

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Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly Ala Ala Gln Arg Arg  
 170 175 180

att cac gtc aat ggc gat gct ggt cat ggt tcc att cct ttc gac cgt 691  
 Ile His Val Asn Gly Asp Ala Gly His Gly Ser Ile Pro Phe Asp Arg  
 185 190 195

gac agc gct att gtc aag atc ggt gaa gtc gcc cgc cga atc gct gcc 739  
 Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala Arg Arg Ile Ala Ala  
 200 205 210

gcc gat ctg aag gta gcc aag gac gat atc tgg caa ggc ttc gtc caa 787  
 Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp Gln Gly Phe Val Gln  
 215 220 225

gcg cac cgt ttc gac cca gaa acg gag cag gcg ctt ctt agc ggg acc 835  
 Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala Leu Leu Ser Gly Thr  
 230 235 240 245

tcc cct gag gcc tac gca gag ttc ggc gga ctc tcc cgc ttc gcc cac 883  
 Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu Ser Arg Phe Ala His  
 250 255 260

gcg gtg tct cat ctc acg atc gcc caa act gtg gtt cgt gca ggt caa 931  
 Ala Val Ser His Leu Thr Ile Ala Gln Thr Val Val Arg Ala Gly Gln  
 265 270 275

gcc atc aat gta ttg cca tcg cat gcg tac ttg gaa ctg gat atc cgt 979  
 Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu Glu Leu Asp Ile Arg  
 280 285 290

acc ctt cca ggc caa acc aat gac tat gtt gat gac acc ctg cgt gct  
 1027  
 Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp Asp Thr Leu Arg Ala  
 295 300 305

gct ctg ggc gat ctt gcc gat gaa gta gaa atc gaa cac ctc atc tct  
 1075  
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 310 315 320 325

gaa gaa gca acg gtg agc cca act gat tcc agg ttg tat aac acc ttg  
 1123  
 Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg Leu Tyr Asn Thr Leu  
 330 335 340

gaa aaa gtt ctt ggt gat ttc ttc ccc gat gcg cct gtg gtc cca att  
 1171  
 Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala Pro Val Val Pro Ile  
 345 350 355

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 Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly Arg Arg Leu Gly Gly  
 360 365 370

gtt ggt tat ggt ttt gca gtt cat gca cgt gaa cga act ttg gcg gaa  
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 Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu Arg Thr Leu Ala Glu  
 375 380 385

gca atg ggg caa ctt cac tcc cat gac gag gcg ctg tac ctg gaa gat  
1315

Ala Met Gly Gln Leu His Ser His Asp Glu Ala Leu Tyr Leu Glu Asp  
390 395 400 405

ctt gaa ctg act gtt cgg ggt tat gac tcc gtc gtg cgt gaa ttc cta  
1363

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1389

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<210> 372

<211> 422

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 372

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20 25 30

Leu Glu Pro His Pro Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly  
35 40 45

Ser Asp Pro Asp Ala Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val  
50 55 60

Val Pro Val Asp Leu Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu  
65 70 75 80

Ile Ser Asp Gly Gln Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe  
85 90 95

Ile Thr Ala Thr Gln Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly  
100 105 110

Gly Leu Arg Gly Thr Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala  
115 120 125

Arg Gly Gly Leu Gly Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu  
130 135 140

Phe Ser Trp Lys Asn Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro  
145 150 155 160

Val His Asp Gly Ser Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly  
165 170 175

Ala Ala Gln Arg Arg Ile His Val Asn Gly Asp Ala Gly His Gly Ser  
180 185 190

Ile Pro Phe Asp Arg Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala  
195 200 205

Arg Arg Ile Ala Ala Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp  
 210 215 220  
 Gln Gly Phe Val Gln Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala  
 225 230 235 240  
 Leu Leu Ser Gly Thr Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu  
 245 250 255  
 Ser Arg Phe Ala His Ala Val Ser His Leu Thr Ile Ala Gln Thr Val  
 260 265 270  
 Val Arg Ala Gly Gln Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu  
 275 280 285  
 Glu Leu Asp Ile Arg Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp  
 290 295 300  
 Asp Thr Leu Arg Ala Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile  
 305 310 315 320  
 Glu His Leu Ile Ser Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg  
 325 330 335  
 Leu Tyr Asn Thr Leu Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala  
 340 345 350  
 Pro Val Val Pro Ile Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly  
 355 360 365  
 Arg Arg Leu Gly Gly Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu  
 370 375 380  
 Arg Thr Leu Ala Glu Ala Met Gly Gln Leu His Ser His Asp Glu Ala  
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 Val Arg Glu Phe Leu Gly  
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<210> 373  
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<220>  
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 <223> RXS02937

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 Val Ile Ser Asn Gly  
 1 5  
 gaa ggt ccg gtt gtt gcg ctt cgt ggc gac att gat gcg ttg ccc atg 163

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<210> 374
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<212> PRT
<213> Corynebacterium glutamicum
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564

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Ser Ala Trp Leu Val Lys		
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	Met Leu Lys Ile Ala	1 5
gtc cca aac aaa ggc tcg ctg tcc gag cgc gcc atg gaa atc ctc gcc 163		
Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala Met Glu Ile Leu Ala	10 15 20	
gaa gca ggc tac gca ggc cgt gga gat tcc aaa tcc ctc aac gtt ttt 211		
Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys Ser Leu Asn Val Phe	25 30 35	
gat gaa gca aac aac gtt gaa ttc ttc ttc ctt cgc cct aaa gat atc 259		
Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu Arg Pro Lys Asp Ile	40 45 50	
gcc atc tac gtt gct ggt ggc cag ctc gat ttg ggt atc acc ggc cgc 307		
Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu Gly Ile Thr Gly Arg	55 60 65	
gac ctt gct cgc gat tcc cag gct gat gtc cac gaa gtt ctt tcc ctc 355		
Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His Glu Val Leu Ser Leu	70 75 80 85	
ggc ttc ggt tcc tcc act ttc cgt tac gca gca cca gct gat gaa gag 403		
Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala Pro Ala Asp Glu Glu	90 95 100	
tgg agc atc gaa aag ctc gac ggc aag cgc atc gct acc tct tac ccc 451		
Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile Ala Thr Ser Tyr Pro	105 110 115	
aac ctt gtt cgc gat gac ctc gca gca cgt ggg ctt tcc gct gag gtg 499		
Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly Leu Ser Ala Glu Val	120 125 130	
ctc cgc ctc gac ggt gca gta gag gta tcc atc aag ctt ggt gtc gca 547		
Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile Lys Leu Gly Val Ala	135 140 145	

gat gcc atc gcc gat gtt gta tcc acc ggc cgc acg ctg cgt cag caa 595  
Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg Thr Leu Arg Gln Gln  
150 155 160 165

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Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr Ser Glu Ala Val Ile  
170 175 180

gtt ggc cgc aag gat gaa aag gtc acc cca gag cag cag atc ctg ctt 691  
Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu Gln Gln Ile Leu Leu  
185 190 195

cgc cgc atc cag gga att ttg cac gcg cag aac ttc ctc atg ctg gat 739  
Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn Phe Leu Met Leu Asp  
200 205 210

tac aac gtc gac cgc gac aac ctg gac gct gcc act gca gta acc cca 787  
Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala Thr Ala Val Thr Pro  
215 220 225

ggc tta tcc ggc cca acg gta tcc cca ctg gca cgc gac aac tgg gtt 835  
Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala Arg Asp Asn Trp Val  
230 235 240 245

gct gta cgc gcc atg gtg cca cgc agg tca gct aac gcc atc atg gat 883  
Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala Asn Ala Ile Met Asp  
250 255 260

aag ctt gct gga ctc ggc gct gaa gcc atc ctg gct tct gaa atc cgc 931  
Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu Ala Ser Glu Ile Arg  
265 270 275

atc gcc cgc atc tagttttaac taccctcgaa aat 966  
Ile Ala Arg Ile  
280

&lt;210&gt; 376

&lt;211&gt; 281

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 376

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20 25 30

Ser Leu Asn Val Phe Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu  
35 40 45

Arg Pro Lys Asp Ile Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu  
50 55 60

Gly Ile Thr Gly Arg Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His  
65 70 75 80

Glu Val Leu Ser Leu Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala  
85 90 95



Pro Ala Asp Glu Glu Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile  
 100 105 110  
 Ala Thr Ser Tyr Pro Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly  
 115 120 125  
 Leu Ser Ala Glu Val Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile  
 130 135 140  
 Lys Leu Gly Val Ala Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg  
 145 150 155 160  
 Thr Leu Arg Gln Gln Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr  
 165 170 175  
 Ser Glu Ala Val Ile Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu  
 180 185 190  
 Gln Gln Ile Leu Leu Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn  
 195 200 205  
 Phe Leu Met Leu Asp Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala  
 210 215 220  
 Thr Ala Val Thr Pro Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala  
 225 230 235 240  
 Arg Asp Asn Trp Val Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala  
 245 250 255  
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 Ala Ser Glu Ile Arg Ile Ala Arg Ile  
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 <213> Corynebacterium glutamicum

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 <223> RXA02195

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 Met Tyr Arg Val Lys  
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 aca ttt gac tcg ctg tac gaa gaa ctt ctt aac cgt gct cag acc cgc 163  
 Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn Arg Ala Gln Thr Arg  
 10 15 20  
 cct gaa ggg tct gga acc gtg gcc gcc ttg gat aaa ggc atc cat cat 211  
 Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp Lys Gly Ile His His

25 30 35  
 cta ggt aag aag gtc atc gaa gaa gcc gga gag gtc tgg att gca gcc 259  
 Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu Val Trp Ile Ala Ala  
 40 45 50  
 gag tat gag acc gat gaa gag cta gcc gga gaa atc tcc cag ctc att 307  
 Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu Ile Ser Gln Leu Ile  
 55 60 65  
 tat tgg acc cag gtc atc atg gtt gct cgc ggc ctg aag cca gaa gat 355  
 Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly Leu Lys Pro Glu Asp  
 70 75 80 85  
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 Ile Tyr Lys Asn Leu  
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 <211> 90  
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 Arg Ala Gln Thr Arg Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp  
 20 25 30  
 Lys Gly Ile His His Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu  
 35 40 45  
 Val Trp Ile Ala Ala Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu  
 50 55 60  
 Ile Ser Gln Leu Ile Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly  
 65 70 75 80  
 Leu Lys Pro Glu Asp Ile Tyr Lys Asn Leu  
 85 90  
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 <223> RXA01097  
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 taaagggagc cattaaagat gcaggatttg aggtgcggaa atg agt gac aat cca 115  
 Met Ser Asp Asn Pro  
 1 5

caa gag tat gag ctg gat tgg gac gtc gaa aag cga tta aag ctt aac 163  
 Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys Arg Leu Lys Leu Asn  
                   10                  15                  20

gac gcc ggc ctg gtg ccg gca atc gtc cag gcc gac ggg acc aac gag 211  
 Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala Asp Gly Thr Asn Glu  
                   25                  30                  35

gtc ctc atg atg gcc tgg atg gat acc cac gcg cta gcc tat act ttg 259  
 Val Leu Met Met Ala Trp Met Asp Thr His Ala Leu Ala Tyr Thr Leu  
                   40                  45                  50

gcg acc cgc cgt gga acc tat ttt tct agg tcc cgc aac gag tac tgg 307  
 Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser Arg Asn Glu Tyr Trp  
                   55                  60                  65

atc aag ggc ctg acc tct gga aac gtc caa gaa gtc acc gga ctt gcc 355  
 Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu Val Thr Gly Leu Ala  
                   70                  75                  80                  85

ctc gac tgc gac ggc gac acc gtc ctt ctg acc gtg aaa caa acc ggc 403  
 Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr Val Lys Gln Thr Gly  
                   90                  95                  100

ggt gcg tgc cac act ggt gcc cac aca tgt ttc gac aat gac gtt ttg 451  
 Gly Ala Cys His Thr Gly Ala His Thr Cys Phe Asp Asn Asp Val Leu  
                   105                  110                  115

ctg taaaagcaac aacgattaag gaa 477  
 Leu

&lt;210&gt; 380

&lt;211&gt; 118

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 380

Met Ser Asp Asn Pro Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys  
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Arg Leu Lys Leu Asn Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala  
                   20                  25                  30

Asp Gly Thr Asn Glu Val Leu Met Met Ala Trp Met Asp Thr His Ala  
                   35                  40                  45

Leu Ala Tyr Thr Leu Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser  
                   50                  55                  60

Arg Asn Glu Tyr Trp Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu  
   65                  70                  75                  80

Val Thr Gly Leu Ala Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr  
                   85                  90                  95

Val Lys Gln Thr Gly Gly Ala Cys His Thr Gly Ala His Thr Cys Phe  
                   100                  105                  110

Asp Asn Asp Val Leu Leu

115

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<210> 381
<211> 861
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS  
<222> (101)..(838)  
<223> RXA01100
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**<400> 381**

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Met Thr Phe Thr Ile															
1 5															
ctt cct gca gtc gat gta gtt aac gga caa gca gtt cgc cta gat cag															163
Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala Val Arg Leu Asp Gln															
10 15 20															
ggc gag gcc ggc act gaa aag tct tat ggc acc cct ttg gaa tcc gca															211
Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr Pro Leu Glu Ser Ala															
25 30 35															
ctg aag tgg cag gag cag ggt gca aag tgg ttg cac ttt gtg gac ctg															259
Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu His Phe Val Asp Leu															
40 45 50															
gac gca gcg ttc aac cgt ggt tcc aac cat gag atg atg gcg gaa att															307
Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu Met Met Ala Glu Ile															
55 60 65															
gtc ggc aag ctc gat gtt gat gtg gag ctc act ggc ggt atc cgt gat															355
Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr Gly Gly Ile Arg Asp															
70 75 80 85															
gat gag tct ctg gag cgc gcg ctg gca acc ggt gca cgt cgt gta aac															403
Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly Ala Arg Arg Val Asn															
90 95 100															
att ggt acc gct gct ctg gag aag cca gag tgg att gct tct gcg att															451
Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp Ile Ala Ser Ala Ile															
105 110 115															
caa cgc tat ggc gag aag att gct gtc gat atc gct gtg cgt ttg gaa															499
Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile Ala Val Arg Leu Glu															
120 125 130															
gat ggt gaa tgg cgc acc cgt gga aac ggt tgg gtc tcc gat ggt ggc															547
Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp Val Ser Asp Gly Gly															
135 140 145															
gat ctg tgg gaa gtt ctc gag cgt ttg gat tcc caa ggt tgt gca cgt															595
Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser Gln Gly Cys Ala Arg															
150 155 160 165															
ttc gtg gtt acc gat gtg tcc aag gac ggc acc ttg agt ggt cca aat															643

Ph Val Val Thr Asp Val Ser Lys Asp Gly Thr Leu Ser Gly Pro Asn  
 170 175 180

gtt gag ctg ctg cgt gag gtt gct gca gct aca gac gca cct atc gtg 691  
 Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr Asp Ala Pro Ile Val  
 185 190 195

gca tct ggt gga att tct gtt ttg gaa gat gtt ttg gaa cta gcc aag 739  
 Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val Leu Glu Leu Ala Lys  
 200 205 210

tac cag gat gag ggc att gat tcc gtc atc att ggc aag gca ctt tat 787  
 Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile Gly Lys Ala Leu Tyr  
 215 220 225

gag cac aag ttc acc ctc gaa gag gct ttg gct gca gta gaa aag ctc 835  
 Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala Ala Val Glu Lys Leu  
 230 235 240 245

ggt taatacatgg atgctcgtgg gat 861  
 Gly

<210> 382  
 <211> 246  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 382  
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Val Arg Leu Asp Gln Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr  
 20 25 30

Pro Leu Glu Ser Ala Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu  
 35 40 45

His Phe Val Asp Leu Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu  
 50 55 60

Met Met Ala Glu Ile Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr  
 65 70 75 80

Gly Gly Ile Arg Asp Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly  
 85 90 95

Ala Arg Arg Val Asn Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp  
 100 105 110

Ile Ala Ser Ala Ile Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile  
 115 120 125

Ala Val Arg Leu Glu Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp  
 130 135 140

Val Ser Asp Gly Gly Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser  
 145 150 155 160

Gln Gly Cys Ala Arg Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr

	165		170		175
Leu Ser Gly	Pro Asn Val Glu Leu	Leu Arg Glu Val	Ala Ala Ala Thr		
	180	185	190		
Asp Ala Pro	Ile Val Ala Ser Gly Gly	Ile Ser Val	Leu Glu Asp Val		
	195	200	205		
Leu Glu Leu	Ala Lys Tyr Gln Asp Glu Gly	Ile Asp Ser Val	Ile Ile		
	210	215	220		
Gly Lys Ala	Leu Tyr Glu His Lys Phe Thr	Leu Glu Glu Ala	Leu Ala		
	225	230	235	240	
Ala Val Glu	Lys Leu Gly				
	245				

<210> 383  
 <211> 756  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(733)  
 <223> RXA01101

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 Met Thr Lys Thr Val  
 1 5  
 gcc ctt ctc gac tac gga tct gga aac ctt cgt tct gct caa cgc gca 163  
 Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg Ser Ala Gln Arg Ala  
 10 15 20  
 cta gag cgt gcc ggt gca gaa gtt atc gtg agc tcc gat cca gaa gtt 211  
 Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser Ser Asp Pro Glu Val  
 25 30 35  
 tgc acc aac gct gat ggc ctc cta gtt cct gga gtg ggc gca ttt gat 259  
 Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly Val Gly Ala Phe Asp  
 40 45 50  
 gcc tgc atg aag ggt ttg aaa aac gtc ttc gga cat cgc att atc gga 307  
 Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly His Arg Ile Ile Gly  
 55 60 65  
 cag cgt ctt gct ggt gga cgt cca gtg atg ggt att tgt gtg ggc atg 355  
 Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly Ile Cys Val Gly Met  
 70 75 80 85  
 cag atc ctg ttc gat gaa ggc gat gag cac ggc att aag tca gct ggt 403  
 Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly Ile Lys Ser Ala Gly  
 90 95 100  
 tgc ggc gag tgg cct ggc aaa gtg gaa cgc ctc caa gcg gag atc ctg 451  
 Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu Gln Ala Glu Ile Leu

105	110	115	
cct cac atg ggg tgg aac aca ctt gaa atg cct acc aac tca cca atg Pro His Met Gly Trp Asn Thr Leu Glu Met Pro Thr Asn Ser Pro Met 120	125	130	499
ttt gag gga att tca cct gat gag cgt ttc tac ttc gtg cac tcc tat Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr Phe Val His Ser Tyr 135	140	145	547
ggt gtg cgc aag tgg acg ttg gaa acc gac gat ctg acc acg cct cca Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp Leu Thr Thr Pro Pro 150	155	160	595
gag gtt gtg tgg gcg aag cac gaa aat gat cgt ttt gtg gca gct gtg Glu Val Val Trp Ala Lys His Glu Asn Asp Arg Phe Val Ala Ala Val 170	175	180	643
gaa aac ggc acg ctg tgg gct act caa ttc cac cca gaa aaa tca ggt Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His Pro Glu Lys Ser Gly 185	190	195	691
gac gca ggc gca cag cta ctg cga aac tgg atc aac tac atc Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile Asn Tyr Ile 200	205	210	733
taacagatag gatcaatatt cat			756
<210> 384			
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<213> Corynebacterium glutamicum			
<400> 384			
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Ser Asp Pro Glu Val Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly 35 40 45			
Val Gly Ala Phe Asp Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly 50 55 60			
His Arg Ile Ile Gly Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly 65 70 75 80			
Ile Cys Val Gly Met Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly 85 90 95			
Ile Lys Ser Ala Gly Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu 100 105 110			
Gln Ala Glu Ile Leu Pro His Met Gly Trp Asn Thr Leu Glu Met Pro 115 120 125			
Thr Asn Ser Pro Met Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr 130 135 140			

Phe Val His Ser Tyr Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp  
 145 150 155 160

Leu Thr Thr Pro Pro Glu Val Val Trp Ala Lys His Glu Asn Asp Arg  
 165 170 175

Phe Val Ala Ala Val Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His  
 180 185 190

Pro Glu Lys Ser Gly Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile  
 195 200 205

Asn Tyr Ile  
 210

<210> 385

<211> 723

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(700)

<223> RXN01657

<400> 385

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ccgacgttcc agcaccacac cgactcgccg agcgcggctg gtg atc gtt gga gtt 115  
 Val Ile Val Gly Val  
 1 5

tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163  
 Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala  
 10 15 20

ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211  
 Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly  
 25 30 35

ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259  
 Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys  
 40 45 50

ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307  
 Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg  
 55 60 65

gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355  
 Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala  
 70 75 80 85

aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403  
 Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val  
 90 95 100

gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451  
 Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe  
 105 110 115



gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499  
 Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val  
 120 125 130  
 cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547  
 Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr  
 135 140 145  
 gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595  
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg  
 150 155 160 165  
 caa ggc aac atc atc gcg ctg tct ttc cat ccc gaa gaa acc ggc gat 643  
 Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro Glu Glu Thr Gly Asp  
 170 175 180  
 tac cgc atc cac caa gcc tgg ctg gac ctg gtg aga aaa cac gct gaa 691  
 Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val Arg Lys His Ala Glu  
 185 190 195  
 ctg gcg att tgatgttttc ggtagcgctc tgt 723  
 Leu Ala Ile  
 200

<210> 386  
 <211> 200  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 386  
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 20 25 30  
 Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser  
 35 40 45  
 Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu  
 50 55 60  
 Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly  
 65 70 75 80  
 Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln  
 85 90 95  
 Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala  
 100 105 110  
 Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala  
 115 120 125  
 Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr  
 130 135 140  
 Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu  
 145 150 155 160

Val Val Gly Val Arg Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro  
 165 170 175

Glu Glu Thr Gly Asp Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val  
 180 185 190

Arg Lys His Ala Glu Leu Ala Ile  
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<210> 387

<211> 601

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> FRXA01657

<400> 387

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 Val Ile Val Gly Val  
 1 5  
 tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163  
 Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala  
 10 15 20  
 ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211  
 Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly  
 25 30 35  
 ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259  
 Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys  
 40 45 50  
 ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307  
 Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg  
 55 60 65  
 gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355  
 Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala  
 70 75 80 85  
 aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403  
 Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val  
 90 95 100  
 gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451  
 Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe  
 105 110 115  
 gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499  
 Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val  
 120 125 130  
 cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547

Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr  
 135 140 145

gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595  
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg  
 150 155 160 165

caa ggc  
 Gln Gly 601

<210> 388  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 388  
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 20 25 30  
 Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser  
 35 40 45  
 Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu  
 50 55 60  
 Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly  
 65 70 75 80  
 Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln  
 85 90 95  
 Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala  
 100 105 110  
 Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala  
 115 120 125  
 Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr  
 130 135 140  
 Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu  
 145 150 155 160  
 Val Val Gly Val Arg Gln Gly  
 165

<210> 389  
 <211> 897  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(874)  
 <223> RXA01098

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gcaggtaatg accagtcggt aaatgaggag tacaagtaaa atg ggc gtg gca att 115
                                         Met Gly Val Ala Ile
                                         1                               5

cga gtt att cct tgc ctg gac gtg gac aac ggc cgg gtt gtt aaa ggc 163
Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly Arg Val Val Lys Gly
                        10                        15                        20

gtg aac ttt gaa aac ctc cgc gat gct ggc gat cct gtg gag ttg gca 211
Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp Pro Val Glu Leu Ala
                        25                        30                        35

aag cgc tat gac gag gaa ggg gca gat gag ctg acc ttc ctg gat gtc 259
Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu Thr Phe Leu Asp Val
                        40                        45                        50

acc gcc tcg aag cat ggt cgc ggc acc atg ctg gat gtt gtt cga cgc 307
Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu Asp Val Val Arg Arg
                        55                        60                        65

acc gct gat cag gtg ttc atc cct ctg act gtc ggt ggc ggc gtg cgc 355
Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val Gly Gly Gly Val Arg
                        70                        75                        80                        85

agc gaa gaa gat gtt gat caa ttg ctg cgc gct ggc gcc gac aag gtt 403
Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala Gly Ala Asp Lys Val
                        90                        95                        100

tcg gtg aac acg tct gcg att gcc cgt cca gaa ctg ctg tca gag ctg 451
Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu Leu Leu Ser Glu Leu
                        105                        110                        115

tcc aag cgt ttt ggt gct cag tgc atc gtg ttg tct gtg gat gcc agg 499
Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu Ser Val Asp Ala Arg
                        120                        125                        130

cgc gtt cct gaa ggt gga act cct cag cca tct ggt ttt gaa gtc acc 547
Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser Gly Phe Glu Val Thr
                        135                        140                        145

acc cac ggc ggt tcc aag tcc gca gaa ctt gat gca atc gag tgg gca 595
Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp Ala Ile Glu Trp Ala
                        150                        155                        160                        165

aag cgc ggc gaa gag ctg ggc gtt ggc gaa att ctg ctc aac tcc atg 643
Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile Leu Leu Asn Ser Met
                        170                        175                        180

gac ggc gac ggc acc aaa aac ggc ttt gac cta gag ctg ctg gaa aaa 691
Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu Glu Leu Leu Glu Lys
                        185                        190                        195

gtt cgc gca gcc gta tcc att cct gta atc gcc tcc ggc ggc gct ggc 739
Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala Ser Gly Gly Ala Gly
                        200                        205                        210

aag gcg gag cat ttc cca cca gct gtt gca gct ggc gcc aac gca gtg 787

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Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala Gly Ala Asn Ala Val  
 215 220 225

ctt gcc gcg acc att ttc cac ttc cgc gaa gta acc atc gcc gaa gta 835  
 Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val Thr Ile Ala Glu Val  
 230 235 240 245

aag gga gcc att aaa gat gca gga ttt gag gtg cgg aaa tgagtgacaa 884  
 Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val Arg Lys  
 250 255

tccacaagag tat 897

<210> 390  
 <211> 258  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 390  
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Arg Val Val Lys Gly Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp  
 20 25 30

Pro Val Glu Leu Ala Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu  
 35 40 45

Thr Phe Leu Asp Val Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu  
 50 55 60

Asp Val Val Arg Arg Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val  
 65 70 75 80

Gly Gly Gly Val Arg Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala  
 85 90 95

Gly Ala Asp Lys Val Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu  
 100 105 110

Leu Leu Ser Glu Leu Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu  
 115 120 125

Ser Val Asp Ala Arg Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser  
 130 135 140

Gly Phe Glu Val Thr Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp  
 145 150 155 160

Ala Ile Glu Trp Ala Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile  
 165 170 175

Leu Leu Asn Ser Met Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu  
 180 185 190

Glu Leu Leu Glu Lys Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala  
 195 200 205

Ser Gly Gly Ala Gly Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala  
 210 215 220

Gly Ala Asn Ala Val Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val  
 225 230 235 240

Thr Ile Ala Glu Val Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val  
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Arg Lys

<210> 391

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> RXN01104

<400> 391

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 Met Thr Val Ala Pro  
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 aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163  
 Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val  
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 gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211  
 Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu  
 25 30 35  
 cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259  
 Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe  
 40 45 50  
 gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307  
 Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His  
 55 60 65  
 acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355  
 Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala  
 70 75 80 85  
 att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403  
 Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro  
 90 95 100  
 atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451  
 Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro  
 105 110 115  
 tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499  
 Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile  
 120 125 130  
 ggt gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547

Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu  
 135 140 145

gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595  
 Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg  
 150 155 160 165

gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643  
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala  
 170 175 180

ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691  
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser  
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 Thr Lys Gly Ala Leu  
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<210> 392

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<212> PRT

<213> Corynebacterium glutamicum

<400> 392

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 35 40 45

Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu  
 50 55 60

Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln  
 65 70 75 80

Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala  
 85 90 95

Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp  
 100 105 110

Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met  
 115 120 125

Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His  
 130 135 140

Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile  
 145 150 155 160

Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys  
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Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu  
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Met Thr Val Ala Pro  
1 5

aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163  
Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val  
10 15 20

gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211  
Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu  
25 30 35

cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259  
Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe  
40 45 50

gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307  
Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His  
55 60 65

acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355  
Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala  
70 75 80 85

att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403  
Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro  
90 95 100

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Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro  
105 110 115

tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499  
Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile  
120 125 130

ggt gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547  
Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu  
135 140 145

gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595  
Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg  
150 155 160 165



gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643  
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala  
                   170                  175                  180

ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691  
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser  
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<210> 394

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 394

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Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly  
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Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu  
                   50                  55                  60

Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln  
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Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala  
                   85                  90                  95

Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp  
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Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met  
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Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His  
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Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile  
                   145                  150                  155                  160

Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys  
                   165                  170                  175

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 <223> RXN00446

<400> 395

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                                         1           5

ctc cgt gag gct ctt gca gag cat tta gag gtt gag ttt gac cag gtc 163
Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val Glu Phe Asp Gln Val
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Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln Gln Leu Val Gln Ala
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acg tgc gct cag ggc gat gag gtc att ttt cca tgg cgc agc ttt gag 259
Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro Trp Arg Ser Phe Glu
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Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala Thr Pro Val Ala Ile
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ccg ctg act gct gat cag aat cat gat ctt gat gcg atg gca gcc gcg 355
Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp Ala Met Ala Ala Ala
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atc act gat aag acc cgc ctc att ttc atc tgc aac ccc aac aat cct 403
Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys Asn Pro Asn Asn Pro
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tcg ggc acc acc atc acc cag gcg cag ttt gat aat ttc atg gaa aag 451
Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp Asn Phe Met Glu Lys
                        105                110                115

gtt cca aac gat gtc gtt gtt ggg ctg gat gag gct tat ttt gag ttc 499
Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr Phe Glu Phe
                        120                125                130

aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc cac cgc cac 547
Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile His Arg His
                        135                140                145

gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat ggc ctg gcg 595
Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr Gly Leu Ala
                        150                155                160                165

ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc atc gca gcg 643
Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile Ile Ala Ala
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atg aat aag gtg gct att cct ttc gcg gtg aat tca gca gct cag gcg 691

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Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala Ala Gln Ala  
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 Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met Glu Arg Val  
 200 205 210

gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg ctt ggt gct 787  
 Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala Leu Gly Ala  
 215 220 225

gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag ggc gcc gct 835  
 Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu Gly Ala Ala  
 230 235 240 245

gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883  
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe  
 250 255 260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931  
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys  
 265 270 275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtctttgg cgttttgcgg 984  
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tgc 987

<210> 396  
 <211> 288  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 396  
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Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro  
 35 40 45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala  
 50 55 60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp  
 65 70 75 80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys  
 85 90 95

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp  
 100 105 110

Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu  
 115 120 125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu

6

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Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
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 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
 85 90 95  
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 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
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 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
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 145 150 155 160  
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 50 55 60  
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
 65 70 75 80  
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
 85 90 95  
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
 100 105 110  
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
 115 120 125  
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile

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 <223> RXA01105

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 ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163  
 Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr  
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 ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211  
 Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn  
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 Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val  
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 Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile Leu Ala Lys Gly Thr  
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Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp Val Thr Ser Leu Asp	
170 175 180	
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Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp	
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Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala	
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Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala	
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Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala	
280 285 290	
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Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe	
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1171	
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<210> 400

<211> 366

<212> PRT

<213> Corynebacterium glutamicum

<400> 400

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35 40 45

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65 70 75 80

Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn  
85 90 95

Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro  
100 105 110

Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile  
115 120 125

Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala  
130 135 140

Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys  
145 150 155 160

Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp  
165 170 175

Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly  
180 185 190

Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser  
195 200 205

Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg  
210 215 220

Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe  
225 230 235 240

Val Ala Asn Pro Ala Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro  
245 250 255

Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg  
260 265 270



His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg  
 275 280 285  
 Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro  
 290 295 300  
 Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala  
 305 310 315 320  
 Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly  
 325 330 335  
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 340 345 350  
 Ala Phe Leu Asp Ala Ala Ala Glu Ile Ile Lys Leu Asn Leu  
 355 360 365

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 <212> DNA  
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 <223> RXA01106

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 Met Leu Asn Val Thr  
 1 5  
 gac ctg cga ggt caa aca cca tcc aag agc gac atc cga cgt gct ttg 163  
 Asp Leu Arg Gly Gln Thr Pro Ser Lys Ser Asp Ile Arg Arg Ala Leu  
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 cca cgt ggt ggc act gac gtg tgg tct gtg ctt ccc ata gtg cag cct 211  
 Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu Pro Ile Val Gln Pro  
 25 30 35  
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 Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu Ala Ala Leu Asp Tyr  
 40 45 50  
 ggc gag aag ttc gac cat att cgc ccc gcc tcg gtg cgg gtg cca gct 307  
 Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser Val Arg Val Pro Ala  
 55 60 65  
 gag gtt att gct gca gca gaa aac acc tta gat ccg ttg gtg cgt gaa 355  
 Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp Pro Leu Val Arg Glu  
 70 75 80 85  
 tcg att gaa gag tcg att cgt cgc gtc cgc aag gtt cac gct gag caa 403  
 Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys Val His Ala Glu Gln  
 90 95 100

aag cca tcc gag cac acc act gaa ctt tca cca ggt ggc acc gtc act	451
Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro Gly Gly Thr Val Thr	
105 110 115	
gag cgt ttc atg ccg att gat cgc gtg gga ctg tac gtt cca ggc ggc	499
Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu Tyr Val Pro Gly Gly	
120 125 130	
aat gcg gtg tac cca tca agc gtg att atg aat act gtc cca gct caa	547
Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn Thr Val Pro Ala Gln	
135 140 145	
gag gct ggt gtg aac tcc ctt gtg gtt gcg tcg cct cct cag gct gag	595
Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser Pro Pro Gln Ala Glu	
150 155 160 165	
cac ggt ggc tgg cct cac ccc acc att ttg gcg gcg tgt tcc atc ttg	643
His Gly Gly Trp Pro His Pro Thr Ile Leu Ala Ala Cys Ser Ile Leu	
170 175 180	
ggt gtt gat gag gtg tgg gct gtc ggc ggc ggt cag gcc gtg gcg ttg	691
Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly Gln Ala Val Ala Leu	
185 190 195	
ctg gct tat ggt gat gac gct gca ggt ctc gag cct gtg gat atg atc	739
Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu Pro Val Asp Met Ile	
200 205 210	
act gga cct ggc aat atc ttt gtc acc gct gcg aag cgc ctg gtc agg	787
Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala Lys Arg Leu Val Arg	
215 220 225	
gga gtg gta ggt act gat tct gag gct ggc cct aca gaa atc gct gtg	835
Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro Thr Glu Ile Ala Val	
230 235 240 245	
ctt gct gat gcc tct gcc aac gcc gtc aac gtt gcc tac gat ctg atc	883
Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val Ala Tyr Asp Leu Ile	
250 255 260	
agc caa gca gaa cac gat gtc atg gct gcg tcc gtg ctc atc act gac	931
Ser Gln Ala Glu His Asp Val Met Ala Ala Ser Val Leu Ile Thr Asp	
265 270 275	
tcc gag cag ctt gcc aag gac gta aac agg gaa atc gag gcg cgt tac	979
Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu Ile Glu Ala Arg Tyr	
280 285 290	
tca atc acg cgc aac gcc gag cgc gtc gca gaa gct ttg cgc ggg gcc	
1027	
Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu Ala Leu Arg Gly Ala	
295 300 305	
cag agt ggc atc gtg ctt gtc gac gac att tcc gtg ggt atc caa gta	
1075	
Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser Val Gly Ile Gln Val	
310 315 320 325	
gcc gat caa tac gca gcg gaa cac ctg gaa atc cac act gag aac gcg	
1123	
Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile His Thr Glu Asn Ala	

330 335 340  
 cgc gcc gta gca gag cag atc acc aac gcg ggt gcg atc ttc gtg ggc  
 1171  
 Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly Ala Ile Phe Val Gly  
 345 350 355  
 gat ttc tca cca gta cca ctg ggt gat tac tcc gca gga tcc aac cac  
 1219  
 Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser Ala Gly Ser Asn His  
 360 365 370  
 gtg ctg cca acc tct gga tcc gct cgt ttc tcc gca ggt cta tcc acg  
 1267  
 Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser Ala Gly Leu Ser Thr  
 375 380 385  
 cac acg ttc ctt cgc cca gtc aac ctc att gaa tac gat gag gct gct  
 1315  
 His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu Tyr Asp Glu Ala Ala  
 390 395 400 405  
 ctg aag gac gtc tcg cag gtt gtc atc aac ttt gcc aac gcc gaa gat  
 1363  
 Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe Ala Asn Ala Glu Asp  
 410 415 420  
 ctt cca gcg cac ggc gaa gca atc cgt gca cgc ttt gaa aac ctc ccc  
 1411  
 Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg Phe Glu Asn Leu Pro  
 425 430 435  
 acc acc gac gag gcc taagaaaaat gaccaaaatt act  
 1449  
 Thr Thr Asp Glu Ala  
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<210> 402  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 402  
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 Ile Arg Arg Ala Leu Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu  
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 Pro Ile Val Gln Pro Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu  
 35 40 45  
 Ala Ala Leu Asp Tyr Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser  
 50 55 60  
 Val Arg Val Pro Ala Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp  
 65 70 75 80  
 Pro Leu Val Arg Glu Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys  
 85 90 95

Val	His	Ala	Glu	Gln	Lys	Pro	Ser	Glu	His	Thr	Thr	Glu	Leu	Ser	Pro	100	105	110	
Gly	Gly	Thr	Val	Thr	Glu	Arg	Phe	Met	Pro	Ile	Asp	Arg	Val	Gly	Leu	115	120	125	
Tyr	Val	Pro	Gly	Gly	Asn	Ala	Val	Tyr	Pro	Ser	Ser	Val	Ile	Met	Asn	130	135	140	
Thr	Val	Pro	Ala	Gln	Glu	Ala	Gly	Val	Asn	Ser	Leu	Val	Val	Ala	Ser	145	150	155	160
Pro	Pro	Gln	Ala	Glu	His	Gly	Gly	Trp	Pro	His	Pro	Thr	Ile	Leu	Ala	165	170	175	
Ala	Cys	Ser	Ile	Leu	Gly	Val	Asp	Glu	Val	Trp	Ala	Val	Gly	Gly	Gly	180	185	190	
Gln	Ala	Val	Ala	Leu	Leu	Ala	Tyr	Gly	Asp	Asp	Ala	Ala	Gly	Leu	Glu	195	200	205	
Pro	Val	Asp	Met	Ile	Thr	Gly	Pro	Gly	Asn	Ile	Phe	Val	Thr	Ala	Ala	210	215	220	
Lys	Arg	Leu	Val	Arg	Gly	Val	Val	Gly	Thr	Asp	Ser	Glu	Ala	Gly	Pro	225	230	235	240
Thr	Glu	Ile	Ala	Val	Leu	Ala	Asp	Ala	Ser	Ala	Asn	Ala	Val	Asn	Val	245	250	255	
Ala	Tyr	Asp	Leu	Ile	Ser	Gln	Ala	Glu	His	Asp	Val	Met	Ala	Ala	Ser	260	265	270	
Val	Leu	Ile	Thr	Asp	Ser	Glu	Gln	Leu	Ala	Lys	Asp	Val	Asn	Arg	Glu	275	280	285	
Ile	Glu	Ala	Arg	Tyr	Ser	Ile	Thr	Arg	Asn	Ala	Glu	Arg	Val	Ala	Glu	290	295	300	
Ala	Leu	Arg	Gly	Ala	Gln	Ser	Gly	Ile	Val	Leu	Val	Asp	Asp	Ile	Ser	305	310	315	320
Val	Gly	Ile	Gln	Val	Ala	Asp	Gln	Tyr	Ala	Ala	Glu	His	Leu	Glu	Ile	325	330	335	
His	Thr	Glu	Asn	Ala	Arg	Ala	Val	Ala	Glu	Gln	Ile	Thr	Asn	Ala	Gly	340	345	350	
Ala	Ile	Phe	Val	Gly	Asp	Phe	Ser	Pro	Val	Pro	Leu	Gly	Asp	Tyr	Ser	355	360	365	
Ala	Gly	Ser	Asn	His	Val	Leu	Pro	Thr	Ser	Gly	Ser	Ala	Arg	Phe	Ser	370	375	380	
Ala	Gly	Leu	Ser	Thr	His	Thr	Phe	Leu	Arg	Pro	Val	Asn	Leu	Ile	Glu	385	390	395	400
Tyr	Asp	Glu	Ala	Ala	Leu	Lys	Asp	Val	Ser	Gln	Val	Val	Ile	Asn	Phe	405	410	415	

Ala Asn Ala Glu Asp Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg  
 420 425 430

Phe Glu Asn Leu Pro Thr Thr Asp Glu Ala  
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<210> 403

<211> 876

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(853)

<223> RXC00930

<400> 403

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ttccggtgga tgatggaagc tagacgacga aagggagcat atg tct ggc cac tca 115  
 Met Ser Gly His Ser  
 1 5

aaa tgg gcg act acc aag cac aag aag gct gct aac gac gcc aag cga 163  
 Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala Asn Asp Ala Lys Arg  
 10 15 20

ggc aag gaa ttt gcc aag ctg atc aag aac atc gaa gtt gcg gca cgt 211  
 Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile Glu Val Ala Ala Arg  
 25 30 35

aca ggc ggt gga gat ccg tct gcg aac cca acg ctt gat gac atg atc 259  
 Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr Leu Asp Asp Met Ile  
 40 45 50

aag aaa gcc aag aag gct tct gtg ccg aac gat aac atc gaa cgt gca 307  
 Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp Asn Ile Glu Arg Ala  
 55 60 65

cgc aag cgt ggc tcc ggc gaa gaa gct ggt ggc gct gac tgg atg aac 355  
 Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly Ala Asp Trp Met Asn  
 70 75 80 85

atc atg tac gag gga tac ggc ccc aac ggc gtt gcc atg ctt atc gag 403  
 Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val Ala Met Leu Ile Glu  
 90 95 100

tgt ctg acc gac aac cgt aac cgc gca gct acc gaa gtt cgc acc gca 451  
 Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr Glu Val Arg Thr Ala  
 105 110 115

atg acc aaa aac ggt ggc aac ttg ggc gag tcc ggt tcc gtg tcc tac 499  
 Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser Gly Ser Val Ser Tyr  
 120 125 130

atg ttc acc cgc acc ggt gtc gtc acc gta caa aag ggc gat ctt agt 547  
 Met Phe Thr Arg Thr Gly Val Val Thr Val Gln Lys Gly Asp Leu Ser  
 135 140 145

gaa gat gac gtg ctc atg gct gtt ctt gaa gct ggt gct gaa gaa gtc 595

Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala Gly Ala Glu Glu Val  
 150 155 160 165  
 aac gac aac ggc gat ctg ttc gag gtt acc tgc gca cca act gac att 643  
 Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys Ala Pro Thr Asp Ile  
 170 175 180  
 cag gct gtt cgc gac gca ctc gtg gaa gct ggc att gaa gta gaa gat 691  
 Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly Ile Glu Val Glu Asp  
 185 190 195  
 tct gaa tca gac ttc cgg gca tct gtt cag gtc ccc ctg gac gct gac 739  
 Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val Pro Leu Asp Ala Asp  
 200 205 210  
 ggt gca cgc aag atc ttc aag ctt gtg gac gcg ttg gaa gat tcc gac 787  
 Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala Leu Glu Asp Ser Asp  
 215 220 225  
 gat gtg caa aac gtc tac acc aac atc gac ttg agc gat gag gtt ttg 835  
 Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu Ser Asp Glu Val Leu  
 230 235 240 245  
 aca gag ctg gaa aac gac tagttcgtat tttccgcact ccg 876  
 Thr Glu Leu Glu Asn Asp  
 250

<210> 404  
 <211> 251  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 404  
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 Asn Asp Ala Lys Arg Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile  
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 Glu Val Ala Ala Arg Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr  
 35 40 45  
 Leu Asp Asp Met Ile Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp  
 50 55 60  
 Asn Ile Glu Arg Ala Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly  
 65 70 75 80  
 Ala Asp Trp Met Asn Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val  
 85 90 95  
 Ala Met Leu Ile Glu Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr  
 100 105 110  
 Glu Val Arg Thr Ala Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser  
 115 120 125  
 Gly Ser Val Ser Tyr Met Phe Thr Arg Thr Gly Val Val Thr Val Gln  
 130 135 140

Lys Gly Asp Leu Ser Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala  
145 150 155 160

Gly Ala Glu Glu Val Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys  
165 170 175

Ala Pro Thr Asp Ile Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly  
180 185 190

Ile Glu Val Glu Asp Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val  
195 200 205

Pro Leu Asp Ala Asp Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala  
210 215 220

Leu Glu Asp Ser Asp Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu  
225 230 235 240

Ser Asp Glu Val Leu Thr Glu Leu Glu Asn Asp  
245 250

<210> 405

<211> 547

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(547)

<223> RXC01096

<400> 405

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gttttgctgt aaaagcaaca acgattaagg aagaaatctt atg aag cca cgc gtg 115  
Met Lys Pro Arg Val  
1 5

ctg tca gca tta ggc att gga gct ggc gcc ctg gtt gtc tgg atc agc 163  
Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu Val Val Trp Ile Ser  
10 15 20

tca cgc atg aac tgg gta acc atc gag gct ttc gac gat aaa tca ggt 211  
Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe Asp Asp Lys Ser Gly  
25 30 35

agt gtc acc caa tct att gtg ggt gca acc tgg tct aca gaa atc atg 259  
Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp Ser Thr Glu Ile Met  
40 45 50

gcg ctt gca ctt gct ttg ctc gct gcc ttc gcc gcc gcg ttg gtg ctc 307  
Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala Ala Ala Leu Val Leu  
55 60 65

aag cgc atg ggt cgg cgc atc att ggt ggt att tcg gcg ctg atc gcg 355  
Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile Ser Ala Leu Ile Ala  
70 75 80 85

gtg ggt gcc agc ctg tct cca ctc gcg ctt ctc acc caa gac cca gac 403  
Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu Thr Gln Asp Pro Asp

	90	95	100	
gca gaa cgg gcc cga acc ctg ctg acc tcc ggt gtg gcc tca cag aag				451
Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly Val Ala Ser Gln Lys				
	105	110	115	
gct aat tcc gga acc ctg ctg tct gat tgg gcg gag atc atc aat acc				499
Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala Glu Ile Ile Asn Thr				
	120	125	130	
acc acc cat cca ctg gcg gca gtg gta gcc atg att ggc tgc gcg cta				547
Thr Thr His Pro Leu Ala Ala Val Val Ala Met Ile Gly Cys Ala Leu				
	135	140	145	

<210> 406  
 <211> 149  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 406  
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 Val Val Trp Ile Ser Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe  
 20 25 30  
 Asp Asp Lys Ser Gly Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp  
 35 40 45  
 Ser Thr Glu Ile Met Ala Leu Ala Leu Ala Leu Ala Ala Phe Ala  
 50 55 60  
 Ala Ala Leu Val Leu Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile  
 65 70 75 80  
 Ser Ala Leu Ile Ala Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu  
 85 90 95  
 Thr Gln Asp Pro Asp Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly  
 100 105 110  
 Val Ala Ser Gln Lys Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala  
 115 120 125  
 Glu Ile Ile Asn Thr Thr Thr His Pro Leu Ala Ala Val Val Ala Met  
 130 135 140  
 Ile Gly Cys Ala Leu  
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<210> 407  
 <211> 1020  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101) .. (997)  
 <223> RXC01656



&lt;400&gt; 407

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atctaccgct agtccacttt gtggcggttg atcatctgtc atg acc gaa act caa 115  
 Met Thr Glu Thr Gln  
 1 5

gaa act tac caa gca acc act cgt gtg aag cgc ggc ctt gcc gac atg 163  
 Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg Gly Leu Ala Asp Met  
 10 15 20

ctc aag ggt ggt gtg atc atg gat gtg gtc acc cct gaa caa gcg cgc 211  
 Leu Lys Gly Gly Val Ile Met Asp Val Val Thr Pro Glu Gln Ala Arg  
 25 30 35

atc gcc gaa gat gca ggt gcc agc gca gtt atg gca ctc gag cgc gtt 259  
 Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met Ala Leu Glu Arg Val  
 40 45 50

ccc gcc gat atc cgt tct cag ggc ggc gtt gct cgc atg agt gat cct 307  
 Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala Arg Met Ser Asp Pro  
 55 60 65

gac ctg atc gaa gga atc gtc aat gcg gtc tcc atc ccg gtc atg gcg 355  
 Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser Ile Pro Val Met Ala  
 70 75 80 85

aaa gct cgc atc ggt cac ttc gtg gaa gct cag gtt ctg gaa gct ctc 403  
 Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln Val Leu Glu Ala Leu  
 90 95 100

ggc gtt gat ttc atc gac gag tcc gaa gtt ctc agc cct gcc gac tac 451  
 Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu Ser Pro Ala Asp Tyr  
 105 110 115

acg cac cac atc aac aag tgg aag ttc gac gtt cct ttc gtc tgt ggc 499  
 Thr His His Ile Asn Lys Trp Lys Phe Asp Val Pro Phe Val Cys Gly  
 120 125 130

gcg acc aac ctc ggc gaa gct ttg cga cgc atc acc gaa ggc gct gca 547  
 Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile Thr Glu Gly Ala Ala  
 135 140 145

atg atc cgt tcc aag ggc gaa gcc ggc acc ggc gat gtc tct gaa gct 595  
 Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly Asp Val Ser Glu Ala  
 150 155 160 165

gtc cgt cac ctg cgc acc atc cgc ggc gac atc aat cgc ctg cgc tcc 643  
 Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile Asn Arg Leu Arg Ser  
 170 175 180

ctg gat gag gat gaa ctc ttc gtc gcc gcc aag gaa ttc cag gca cca 691  
 Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys Glu Phe Gln Ala Pro  
 185 190 195

tac gac ctg gtc cgc gaa gtc gcc tcc acc ggc aag ctc cct gtg gtc 739  
 Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly Lys Leu Pro Val Val  
 200 205 210

acc ttc gtt gca ggt ggc gtc gca acc cca gcc gac gct gca ctc gtg 787

Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala Asp Ala Ala Leu Val  
 215 220 225  
 cgc caa atg ggc gcc gaa ggc gtc ttt gtc ggc tcc ggc atc ttc aaa 835  
 Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly Ser Gly Ile Phe Lys  
 230 235 240 245  
 tcc ggc aat cca gcc gcc cgc gcc gca gcg atc gtc aag gct gca acg 883  
 Ser Gly Asn Pro Ala Ala Arg Ala Ala Ile Val Lys Ala Ala Thr  
 250 255 260  
 ctt ttc gac gac ccc tcc gtc att gcc gac gta tcc cgc ggc ctg ggt 931  
 Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val Ser Arg Gly Leu Gly  
 265 270 275  
 gaa gcc atg gtg ggc atc aac gta tcc gac gtt cca gca cca cac cga 979  
 Glu Ala Met Val Gly Ile Asn Val Ser Asp Val Pro Ala Pro His Arg  
 280 285 290  
 ctc gcc gag cgc ggc tgg tgatcggttg agtttttagct ctc  
 1020  
 Leu Ala Glu Arg Gly Trp  
 295

&lt;210&gt; 408

&lt;211&gt; 299

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 408

Met Thr Glu Thr Gln Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg  
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 Gly Leu Ala Asp Met Leu Lys Gly Gly Val Ile Met Asp Val Val Thr  
 20 25 30  
 Pro Glu Gln Ala Arg Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met  
 35 40 45  
 Ala Leu Glu Arg Val Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala  
 50 55 60  
 Arg Met Ser Asp Pro Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser  
 65 70 75 80  
 Ile Pro Val Met Ala Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln  
 85 90 95  
 Val Leu Glu Ala Leu Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu  
 100 105 110  
 Ser Pro Ala Asp Tyr Thr His His Ile Asn Lys Trp Lys Phe Asp Val  
 115 120 125  
 Pro Phe Val Cys Gly Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile  
 130 135 140  
 Thr Glu Gly Ala Ala Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly  
 145 150 155 160

Asp Val Ser Glu Ala Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile  
 165 170 175  
 Asn Arg Leu Arg Ser Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys  
 180 185 190  
 Glu Phe Gln Ala Pro Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly  
 195 200 205  
 Lys Leu Pro Val Val Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala  
 210 215 220  
 Asp Ala Ala Leu Val Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly  
 225 230 235 240  
 Ser Gly Ile Phe Lys Ser Gly Asn Pro Ala Ala Arg Ala Ala Ala Ile  
 245 250 255  
 Val Lys Ala Ala Thr Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val  
 260 265 270  
 Ser Arg Gly Leu Gly Glu Ala Met Val Gly Ile Asn Val Ser Asp Val  
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 Pro Ala Pro His Arg Leu Ala Glu Arg Gly Trp  
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<210> 409  
 <211> 1065  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1042)  
 <223> RXC01158

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 Met Ser Ile Val Glu  
 1 5  
 cac atc aaa gag ttt cga cgc cga ctt ctt atc gct ctg gcg ggc atc 163  
 His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile Ala Leu Ala Gly Ile  
 10 15 20  
 ctc gtg ggc acc att atc ggc ttt att tgg tac gat ttc tca ttt tgg 211  
 Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr Asp Phe Ser Phe Trp  
 25 30 35  
 cag atc ccc act ttg ggc gag ctg ctg agg gat ccg tac tgt tct ctg 259  
 Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp Pro Tyr Cys Ser Leu  
 40 45 50  
 cct gct gaa tcc cgc tgg gcc atg agc gac tca gag gaa tgt cga ctg 307  
 Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser Glu Glu Cys Arg Leu  
 55 60 65

ctc gca acc ggc ccg ttt gat cca ttc atg ctt cgc ctt aaa gta gcg	355
Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu Arg Leu Lys Val Ala	
70 75 80 85	
gcg ttg gtg ggt atg gtt ctt ggc tca ccc gtg tgg ctg agc cag ctg	403
Ala Leu Val Gly Met Val Leu Gly Ser Pro Val Trp Leu Ser Gln Leu	
90 95 100	
tgg ggc ttt atc acc cca ggt ttg atg aag aat gag cgc cgt tac acc	451
Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn Glu Arg Arg Tyr Thr	
105 110 115	
gca atc ttc gtc acg att gct gtt gtg ctg ttt gtc ggc ggt gct gtt	499
Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe Val Gly Gly Ala Val	
120 125 130	
ctt gcg tac ttc gtc gtt gca tat ggt ttg gag ttc ctc ctt acc att	547
Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu Phe Leu Leu Thr Ile	
135 140 145	
ggt gga gac acc cag gca gcg gcc ctg act ggt gat aag tac ttc gga	595
Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly Asp Lys Tyr Phe Gly	
150 155 160 165	
ttc ttg ctc gcg ttg ttg gcg att ttc ggc gtg agc ttc gaa gtt cca	643
Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val Ser Phe Glu Val Pro	
170 175 180	
ctg gtg atc ggc atg ctc aac att gtg ggt atc ttg cct tac gat gcc	691
Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile Leu Pro Tyr Asp Ala	
185 190 195	
att aaa gat aag cga gcg atg atc atc atg att ttg ttc gtg ttc gct	739
Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile Leu Phe Val Phe Ala	
200 205 210	
gct ttc atg aca ccc ggc cag gat cct ttc acc atg ttg gtg ttg gcg	787
Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr Met Leu Val Leu Ala	
215 220 225	
ctt tca ctc acc gtt ctg gta gag ctt gcc ctg cag ttc tgt cgc ttc	835
Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu Gln Phe Cys Arg Phe	
230 235 240 245	
aac gac aaa cgc cgg gac aag aag cgc cca gaa tgg ctt gat ggc gat	883
Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu Trp Leu Asp Gly Asp	
250 255 260	
gac ctc tct gca tca cca ctg gat act tct gct ggt gga gaa gat gct	931
Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala Gly Gly Glu Asp Ala	
265 270 275	
cca agc cca gtc gaa acc cca gag gcg gtg gag cct tcg cgg atg ctg	979
Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu Pro Ser Arg Met Leu	
280 285 290	
aac cca agt ggg gag gcg tcg ata agc tat aaa ccc ggg cgc gcc gac	
1027	
Asn Pro Ser Gly Glu Ala Ser Il Ser Tyr Lys Pro Gly Arg Ala Asp	
295 300 305	

ttc ggt gac gtg ctc tagggcctag ccaggtaccc tta  
 1065  
 Phe Gly Asp Val Leu  
 310

<210> 410  
 <211> 314  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 410  
 Met Ser Ile Val Glu His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile  
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 Ala Leu Ala Gly Ile Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr  
                   20                  25                  30  
 Asp Phe Ser Phe Trp Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp  
           35                  40                  45  
 Pro Tyr Cys Ser Leu Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser  
       50                  55                  60  
 Glu Glu Cys Arg Leu Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu  
   65                  70                  75                  80  
 Arg Leu Lys Val Ala Ala Leu Val Gly Met Val Leu Gly Ser Pro Val  
                   85                  90                  95  
 Trp Leu Ser Gln Leu Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn  
           100                  105                  110  
 Glu Arg Arg Tyr Thr Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe  
           115                  120                  125  
 Val Gly Gly Ala Val Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu  
   130                  135                  140  
 Phe Leu Leu Thr Ile Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly  
  145                  150                  155                  160  
 Asp Lys Tyr Phe Gly Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val  
                   165                  170                  175  
 Ser Phe Glu Val Pro Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile  
           180                  185                  190  
 Leu Pro Tyr Asp Ala Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile  
       195                  200                  205  
 Leu Phe Val Phe Ala Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr  
   210                  215                  220  
 Met Leu Val Leu Ala Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu  
  225                  230                  235                  240  
 Gln Phe Cys Arg Phe Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu  
           245                  250                  255  
 Trp Leu Asp Gly Asp Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala

260	265	270
Gly Gly Glu Asp Ala Pro Ser	Pro Val Glu Thr Pro	Glu Ala Val Glu
275	280	285
Pro Ser Arg Met Leu Asn	Pro Ser Gly Glu Ala	Ser Ile Ser Tyr Lys
290	295	300
Pro Gly Arg Ala Asp Phe	Gly Asp Val Leu	
305	310	

<210> 411  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1390)  
 <223> RXA02458

<400> 411  
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 ggtggtgaac aaaacaaatc ttccacacat aacatctatt atg gtc ttt gtg tct 115  
 Met Val Phe Val Ser  
 1 5  
 gat tcg tct atc tct ttg ccc att tgg gat gct ccg cgc gct cgc ggc 163  
 Asp Ser Ser Ile Ser Leu Pro Ile Trp Asp Ala Pro Arg Ala Arg Gly  
 10 15 20  
 ccc ata gtc tcg gac ctg gct atc cct ggt tcc aag tcg atc acc aac 211  
 Pro Ile Val Ser Asp Leu Ala Ile Pro Gly Ser Lys Ser Ile Thr Asn  
 25 30 35  
 cgc gcc ctc atc ttg gct gcg ctc gca tca act cca tcc acc atc att 259  
 Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr Pro Ser Thr Ile Ile  
 40 45 50  
 gat gtc ctt cgt agt cgt gat acc gat ctc atg act gat ggt cta cgc 307  
 Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met Thr Asp Gly Leu Arg  
 55 60 65  
 agc ctc gga atc acc att act gaa gag gca gtc gat cgc tac cgc gtt 355  
 Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val Asp Arg Tyr Arg Val  
 70 75 80 85  
 gag ccc gga cag ttg tct gct ggc tcc gtt gag tgt ggt ctt gct ggt 403  
 Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu Cys Gly Leu Ala Gly  
 90 95 100  
 acg gtc atg cgc ttt ttg cct cct gtt gct gct ttc gct gat ggt cct 451  
 Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala Phe Ala Asp Gly Pro  
 105 110 115  
 gtt cat ttt gat ggc gat cct caa gct cgt gtt cgt ccg atg acc agc 499  
 Val His Phe Asp Gly Asp Pro Gln Ala Arg Val Arg Pro Met Thr Ser  
 120 125 130

att ttg gat gcg ctg cgt tcg ctt ggt gtg gag gta gac aac aac aat	547
Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu Val Asp Asn Asn Asn	
135 140 145	
ctg cct ttc act gtt aat gct ggt gag gtc cct gag ggt ggc gtg gtt	595
Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro Glu Gly Gly Val Val	
150 155 160 165	
gag att gat gct tcc ggc tca tct cag ttt gtt tct ggt ctt ttg ctt	643
Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val Ser Gly Leu Leu Leu	
170 175 180	
tca gcg cct cgt ttt aaa aat ggc gtc acc gtt aag cac gtc ggt ggt	691
Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val Lys His Val Gly Gly	
185 190 195	
cgt ctg ccg agc atg ccg cat att gag atg acc gtc gat atg ctt cgt	739
Arg Leu Pro Ser Met Pro His Ile Glu Met Thr Val Asp Met Leu Arg	
200 205 210	
tcc gca ggc att gag atc gaa gag tca gaa aat cag tgg gtt gtt cat	787
Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn Gln Trp Val Val His	
215 220 225	
cct ggt gag atc ttg ggt cgg acc tgg cgc att gag ccg gat ctt tct	835
Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile Glu Pro Asp Leu Ser	
230 235 240 245	
aat gcg act ccg ttc cta gct gcc gct gcg gtc act ggt gga acc atc	883
Asn Ala Thr Pro Phe Leu Ala Ala Ala Val Thr Gly Gly Thr Ile	
250 255 260	
aag att aac cac tgg cca atc aaa act act cag cct ggc gat gct att	931
Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln Pro Gly Asp Ala Ile	
265 270 275	
cgt tcg att ctt gag cgc atg ggc tgc gaa gtt gag ctg gtt gct cag	979
Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val Glu Leu Val Ala Gln	
280 285 290	
ggg gaa ggt tac gat ctg tcg gtg act ggt ccg gtt gct ctc aag ggc	
1027	
Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro Val Ala Leu Lys Gly	
295 300 305	
att gag atc gat atg tcc gat atc ggt gag ttg acc cct acc gtg gcg	
1075	
Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu Thr Pro Thr Val Ala	
310 315 320 325	
gcg ttg gct gcg ttg gcg tcg aca gag tct cgt ttg acc ggt att gct	
1123	
Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg Leu Thr Gly Ile Ala	
330 335 340	
cat ctt cgt ggc cat gag acg gat cgt ttg gct gcg ttg act gcg gag	
1171	
His Leu Arg Gly His Glu Thr Asp Arg Leu Ala Ala Leu Thr Ala Glu	
345 350 355	

atc aac aaa ctt ggt gga aag tgc act gag ctt aag gat ggt ctg ttg  
1219

Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu Lys Asp Gly Leu Leu  
360 365 370

att gag cct gcg tcg ctg cac ggt ggt gtg tgg cat tca tat gct gat  
1267

Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp His Ser Tyr Ala Asp  
375 380 385

cac cgt atg gct act gct ggt gcg atc att ggc ctc gcg gtt gat ggc  
1315

His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly Leu Ala Val Asp Gly  
390 395 400 405

gtt cag gtt gaa gac att aag acc act tcc aaa act ttc cct ggt ttt  
1363

Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys Thr Phe Pro Gly Phe  
410 415 420

gaa aat gtt tgg gag gag atg gtt ggc tagacgcagc tatgacgaat  
1410

Glu Asn Val Trp Glu Glu Met Val Gly  
425 430

ccg  
1413

<210> 412

<211> 430

<212> PRT

<213> Corynebacterium glutamicum

<400> 412

Met Val Phe Val Ser Asp Ser Ser Ile Ser Leu Pro Ile Trp Asp Ala  
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Pro Arg Ala Arg Gly Pro Ile Val Ser Asp Leu Ala Ile Pro Gly Ser  
20 25 30

Lys Ser Ile Thr Asn Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr  
35 40 45

Pro Ser Thr Ile Ile Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met  
50 55 60

Thr Asp Gly Leu Arg Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val  
65 70 75 80

Asp Arg Tyr Arg Val Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu  
85 90 95

Cys Gly Leu Ala Gly Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala  
100 105 110

Phe Ala Asp Gly Pro Val His Phe Asp Gly Asp Pro Gln Ala Arg Val  
115 120 125

Arg Pro Met Thr Ser Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu  
130 135 140



Val Asp Asn Asn Asn Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro  
 145 150 155 160  
 Glu Gly Gly Val Val Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val  
 165 170 175  
 Ser Gly Leu Leu Leu Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val  
 180 185 190  
 Lys His Val Gly Gly Arg Leu Pro Ser Met Pro His Ile Glu Met Thr  
 195 200 205  
 Val Asp Met Leu Arg Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn  
 210 215 220  
 Gln Trp Val Val His Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile  
 225 230 235 240  
 Glu Pro Asp Leu Ser Asn Ala Thr Pro Phe Leu Ala Ala Ala Val  
 245 250 255  
 Thr Gly Gly Thr Ile Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln  
 260 265 270  
 Pro Gly Asp Ala Ile Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val  
 275 280 285  
 Glu Leu Val Ala Gln Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro  
 290 295 300  
 Val Ala Leu Lys Gly Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu  
 305 310 315 320  
 Thr Pro Thr Val Ala Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg  
 325 330 335  
 Leu Thr Gly Ile Ala His Leu Arg Gly His Glu Thr Asp Arg Leu Ala  
 340 345 350  
 Ala Leu Thr Ala Glu Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu  
 355 360 365  
 Lys Asp Gly Leu Leu Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp  
 370 375 380  
 His Ser Tyr Ala Asp His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly  
 385 390 395 400  
 Leu Ala Val Asp Gly Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys  
 405 410 415  
 Thr Phe Pro Gly Phe Glu Asn Val Trp Glu Glu Met Val Gly  
 420 425 430

&lt;210&gt; 413

&lt;211&gt; 1266

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1243)

&lt;223&gt; RXA02790

&lt;400&gt; 413

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agggaattt cccaggatga accaaatccg aaaccgccgg atg gag ccc gtc tac 115  
 Met Glu Pro Val Tyr  
 1 5

gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163  
 Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile  
 10 15 20

ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211  
 Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg  
 25 30 35

acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259  
 Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val  
 40 45 50

gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa 307  
 Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu  
 55 60 65

gaa cga gat atc gtg gcc acc aac tca gcg ttc caa aca gcg gcc agc 355  
 Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser  
 70 75 80 85

aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag 403  
 Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln  
 90 95 100

gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac 451  
 Glu Gln Met Asn Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp  
 105 110 115

aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac 499  
 Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp  
 120 125 130

gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc 547  
 Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile  
 135 140 145

gca gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag 595  
 Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu  
 150 155 160 165

gat ttg cag cag gtt gcc tcc acc gtg tcg cct gca gaa ttg ggt gtc 643  
 Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val  
 170 175 180

cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag 691  
 Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys  
 185 190 195

cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc 739

Arg	Leu	Glu	Gly	Leu	Ile	Met	Pro	Gly	Gln	Tyr	Val	Val	Asp	Pro	Ser		
		200					205					210					
aac	gac	gcc	cag	gga	atc	ctc	acc	gat	ctg	atc	acg	cga	tca	gca	aac	787	
Asn	Asp	Ala	Gln	Gly	Ile	Leu	Thr	Asp	Leu	Ile	Thr	Arg	Ser	Ala	Asn		
	215					220				225							
cat	ttc	caa	gaa	acc	gac	atc	acg	ggc	cgt	gca	gat	gcc	atc	gga	ctt	835	
His	Phe	Gln	Glu	Thr	Asp	Ile	Thr	Gly	Arg	Ala	Asp	Ala	Ile	Gly	Leu		
230					235					240					245		
act	cca	tat	gag	ctg	gtc	acc	gca	gca	tct	tta	atc	gag	cgc	gaa	gca	883	
Thr	Pro	Tyr	Glu	Leu	Val	Thr	Ala	Ala	Ser	Leu	Ile	Glu	Arg	Glu	Ala		
				250					255					260			
cca	gca	gga	gat	ttt	gat	aag	gtc	gcc	cgc	gtc	atc	ttg	aac	cgt	ctc	931	
Pro	Ala	Gly	Asp	Phe	Asp	Lys	Val	Ala	Arg	Val	Ile	Leu	Asn	Arg	Leu		
			265					270					275				
gcc	gag	cca	atg	cag	ctg	caa	ttc	gac	tcc	acc	gtc	aac	tac	ggc	ctg	979	
Ala	Glu	Pro	Met	Gln	Leu	Gln	Phe	Asp	Ser	Thr	Val	Asn	Tyr	Gly	Leu		
		280					285					290					
tct	gaa	caa	gaa	gta	gca	acc	acc	gac	gaa	gac	cgt	cag	acc	gtc	acc		
1027																	
Ser	Glu	Gln	Glu	Val	Ala	Thr	Thr	Asp	Glu	Asp	Arg	Gln	Thr	Val	Thr		
	295					300					305						
cca	tgg	aac	act	tac	gcc	atg	gac	ggc	ctg	cca	caa	acc	ccc	atc	gcc		
1075																	
Pro	Trp	Asn	Thr	Tyr	Ala	Met	Asp	Gly	Leu	Pro	Gln	Thr	Pro	Ile	Ala		
310					315					320					325		
gca	gta	tcc	acc	gaa	gca	ctc	caa	gcc	atg	gaa	aac	cct	gca	gaa	gga		
1123																	
Ala	Val	Ser	Thr	Glu	Ala	Leu	Gln	Ala	Met	Glu	Asn	Pro	Ala	Glu	Gly		
				330					335					340			
aac	tgg	ctg	tac	ttt	gtc	acc	atc	gac	acc	gat	gga	acc	acc	gtg	ttc		
1171																	
Asn	Trp	Leu	Tyr	Phe	Val	Thr	Ile	Asp	Thr	Asp	Gly	Thr	Thr	Val	Phe		
			345					350					355				
aac	gac	acc	ttc	gaa	gag	cac	gaa	gcc	gac	att	gag	caa	gct	ttg	aac		
1219																	
Asn	Asp	Thr	Phe	Glu	Glu	His	Glu	Ala	Asp	Ile	Glu	Gln	Ala	Leu	Asn		
		360					365					370					
agt	ggc	gtt	cta	gac	agc	aac	cga	taaggatcag	cgaataaaaat	tgg							
1266																	
Ser	Gly	Val	Leu	Asp	Ser	Asn	Arg										
	375					380											

<210> 414  
 <211> 381  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
  
 <400> 414  
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Ile Ala Ser Leu 20	Ile Leu Ile Ile	Gly Ala Ile Ile 25	Tyr Ile Gly Val 30
Ala Thr Ser Asn 35	Arg Thr Pro His 40	Asp Tyr Glu Gly 45	Ser Gly Asn Gly
Val Val Gln Leu 50	Val Glu Ile Pro 55	Glu Gly Ser Ser 60	Ile Ser Glu Leu
Gly Pro Glu Leu 65	Glu Glu Arg Asp 70	Ile Val Ala Thr 75	Asn Ser Ala Phe 80
Gln Thr Ala Ala 85	Ser Asn Asn Pro 90	Asn Ala Gly Ser 95	Val Gln Pro Gly
Phe Tyr Arg Leu 100	Gln Glu Gln Met 105	Asn Ala Ala Ala 110	Val Ser Ala
Leu Leu Asp Pro 115	Asp Asn Gln Val 120	Asp Leu Leu Asp 125	Ile His Gly Gly
Ala Thr Leu Met 130	Asp Val Thr Val 135	Val Gly Gly Asn 140	Thr Arg Ala Gly
Ile Tyr Ser Gln 145	Ile Ala Ala Val 150	Thr Cys Thr Glu 155	Gly Ser Ala Asn 160
Cys Ile Thr Ala 165	Glu Asp Leu Gln 170	Gln Val Ala Ser 175	Thr Val Ser Pro
Ala Glu Leu Gly 180	Val Pro Asp Trp 185	Ala Ile Ala Ala 190	Val Glu Ala Arg
Gly Thr Asp Pro 195	Lys Arg Leu Glu 200	Gly Leu Ile Met 205	Pro Gly Gln Tyr
Val Val Asp Pro 210	Ser Asn Asp Ala 215	Gln Gly Ile Leu 220	Thr Asp Leu Ile
Thr Arg Ser Ala 225	Asn His Phe Gln 230	Glu Thr Asp Ile 235	Thr Gly Arg Ala 240
Asp Ala Ile Gly 245	Leu Thr Pro Tyr 250	Glu Leu Val Thr 255	Ala Ala Ser Leu
Ile Glu Arg Glu 260	Ala Pro Ala Gly 265	Asp Phe Asp Lys 270	Val Ala Arg Val
Ile Leu Asn Arg 275	Leu Ala Glu Pro 280	Met Gln Leu Gln 285	Phe Asp Ser Thr
Val Asn Tyr Gly 290	Leu Ser Glu Gln 295	Glu Val Ala Thr 300	Thr Asp Glu Asp
Arg Gln Thr Val 305	Thr Pro Trp Asn 310	Thr Tyr Ala Met 315	Asp Gly Leu Pro 320
Gln Thr Pro Ile 325	Ala Ala Val Ser 330	Thr Glu Ala Leu 335	Gln Ala Met Glu

Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp  
 340 345 350

Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile  
 355 360 365

Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg  
 370 375 380

<210> 415

<211> 644

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(621)

<223> RXN00954

<400> 415

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 Ala Val Lys Trp Phe Glu Ala Ser Asn Phe Thr Phe Leu Phe Ala Pro  
 1 5 10 15

gcg tac aac cct gcg att gcg cat gtg cag ccg gtt cgc cag gcg ctg 96  
 Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro Val Arg Gln Ala Leu  
 20 25 30

aaa ttc ccc acc atc ttc aac acg ctt gga cca ttg ctg tcc ccg gcg 144  
 Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala  
 35 40 45

cgc ccg gag cgt cag atc atg ggc gtg gcc aat gcc aat cat gga cag 192  
 Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln  
 50 55 60

ctc atc gcc gag gtc ttc cgc gag ttg ggc cgt aca cgc gcg ctt gtt 240  
 Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val  
 65 70 75 80

gtg cat ggc gca ggc acc gat gag atc gca gtc cac ggc acc acc ttg 288  
 Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu  
 85 90 95

gtg tgg gag ctt aaa gaa gac ggc acc atc gag cat tac acc atc gag 336  
 Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu  
 100 105 110

cct gag gac ctt ggc ctt ggc cgc tac acc ctt gag gat ctc gta ggt 384  
 Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly  
 115 120 125

ggc ctc ggc act gag aac gcc gaa gct atg cgc gct act ttc gcg ggc 432  
 Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly  
 130 135 140

acc ggc cct gat gca cac cgt gat gcg ttg gct gcg tcc gca ggt gcg 480  
 Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala  
 145 150 155 160

atg ttc tac ctc aac ggc gat gtc gac tcc ttg aaa gat ggt gca caa 528  
 Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln  
                   165                                  170                                  175

aag gcg ctt tcc ttg ctt gcc gac ggc acc acc cag gca tgg ttg gcc 576  
 Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala  
                   180                                  185                                  190

aag cac gaa gag atc gat tac tca gaa aag gag tct tcc aat gac 621  
 Lys His Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp  
                   195                                  200                                  205

tagtaataat ctgcccacag tgt 644

<210> 416

<211> 207

<212> PRT

<213> Corynebacterium glutamicum

<400> 416

Ala Val Lys Trp Phe Glu Ala Ser Asn Phe Thr Phe Leu Phe Ala Pro  
   1                                  5                                  10                                  15

Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro Val Arg Gln Ala Leu  
                   20                                  25                                  30

Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala  
                   35                                  40                                  45

Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln  
                   50                                  55                                  60

Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val  
   65                                  70                                  75                                  80

Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu  
                   85                                  90                                  95

Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu  
                   100                                  105                                  110

Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly  
                   115                                  120                                  125

Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly  
                   130                                  135                                  140

Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala  
   145                                  150                                  155                                  160

Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln  
                   165                                  170                                  175

Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala  
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Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp  
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 Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro  
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 Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn  
 35 40 45  
 gcc aat cat gga cag ctc atc gcc gag gtc ttc cgc gag ttg ggc cgt 192  
 Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg  
 50 55 60  
 aca cgc gcg ctt gtt gtg cat ggc gca ggc acc gat gag atc gca gtc 240  
 Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val  
 65 70 75 80  
 cac ggc acc acc ttg gtg tgg gag ctt aaa gaa gac ggc acc atc gag 288  
 His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu  
 85 90 95  
 cat tac acc atc gag cct gag gac ctt ggc ctt ggc cgc tac acc ctt 336  
 His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu  
 100 105 110  
 gag gat ctc gta ggt ggc ctc ggc act gag aac gcc gaa gct atg cgc 384  
 Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg  
 115 120 125  
 gct act ttc gcg ggc acc ggc cct gat gca cac cgt gat gcg ttg gct 432  
 Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala  
 130 135 140  
 gcg tcc gca ggt gcg atg ttc tac ctc aac ggc gat gtc gac tcc ttg 480  
 Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu  
 145 150 155 160  
 aaa gat ggt gca caa aag gcg ctt tcc ttg ctt gcc gac ggc acc acc 528  
 Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr  
 165 170 175  
 cag gca tgg ttg gcc aag cac gaa gag atc gat tac tca gaa aag gag 576  
 Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu  
 180 185 190  
 tct tcc aat gac tagtaataat ctgcccacag tgt 611

Ser Ser Asn Asp  
195

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<211> 196  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 418  
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Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro  
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Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn  
35 40 45  
Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg  
50 55 60  
Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val  
65 70 75 80  
His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu  
85 90 95  
His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu  
100 105 110  
Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg  
115 120 125  
Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala  
130 135 140  
Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu  
145 150 155 160  
Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr  
165 170 175  
Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu  
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Ser Ser Asn Asp  
195

<210> 419  
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<212> DNA  
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<220>  
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<223> RXN00957

<400> 419



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Met Ser Thr Asn Pro  
1 5  
cat gtt ttc tcc cta gat gtc cgc tat cac gag gat gct tct gca ttg 163  
His Val Phe Ser Leu Asp Val Arg Tyr His Glu Asp Ala Ser Ala Leu  
10 15 20  
ttt gcc cac ttg ggt ggc aca acc gca gat gat gca gcc ctg ttg gaa 211  
Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp Ala Ala Leu Leu Glu  
25 30 35  
agc gct gat atc acc acc aag aat ggt att tct tcc ctc gcg gtg ttg 259  
Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser Ser Leu Ala Val Leu  
40 45 50  
aag agt tcg gtg cgc att acg tgc acg ggc aac acg gtg gta acg cag 307  
Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn Thr Val Val Thr Gln  
55 60 65  
ccg ctg acg gac tcg ggt agg gca gtg gtt gcg cgc cta acg cag cag 355  
Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala Arg Leu Thr Gln Gln  
70 75 80 85  
ctt ggc cag tac aac acc gca gag aac acc ttt agc ttc ccc gcc tca 403  
Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe Ser Phe Pro Ala Ser  
90 95 100  
gat gcg gtt gat gag cgc gag cgc ctc acc gca cca agc acc atc gaa 451  
Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala Pro Ser Thr Ile Glu  
105 110 115  
gtg ctg cgc aag ttg cag ttc gag tcc ggt tac agc gac gcg tcc ctg 499  
Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr Ser Asp Ala Ser Leu  
120 125 130  
cca ctg ctc atg ggc ggt ttc gcg ttt gat ttc tta gaa acc ttt gaa 547  
Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe Leu Glu Thr Phe Glu  
135 140 145  
acg ctc ccc gct gtc gag gag agc gtc aac act tac ccc gat tac cag 595  
Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr Tyr Pro Asp Tyr Gln  
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ttc gtc ctc gcg gaa atc gtc ctg gac atc aat cac cag gac cag acc 643  
Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn His Gln Asp Gln Thr  
170 175 180  
gcc aaa ctc gcc ggc gtc tcc aac gcc cca ggc gag ctc gag gcc gag 691  
Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly Glu Leu Glu Ala Glu  
185 190 195  
ctc aac aag ctt tca ttg ctt atc gac gcc gcc ctc ccc gca acc gaa 739  
Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala Leu Pro Ala Thr Glu  
200 205 210  
cac gcc tac caa acc acc cct cac gac ggc gac act ctt cgc gtt gtg 787  
His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp Thr Leu Arg Val Val  
215 220 225

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Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln Ile Asn Glu Leu Lys	
230 235 240 245	
gaa aac att tac aac ggt gac atc tac caa gtt gtc ccg gcg cgc act	883
Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val Val Pro Ala Arg Thr	
250 255 260	
ttc acc gca cca tgt cct gat gca ttc gct gct tat ctg cag ctg cgt	931
Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala Tyr Leu Gln Leu Arg	
265 270 275	
gcc acc aac ccg tcg ccg tac atg ttc tat atc cgt ggc ctc aac gaa	979
Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile Arg Gly Leu Asn Glu	
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ggc cgc tcc tat gaa ctt ttt ggc gca tcc cct gag tcc aac ctc aag	
1027 Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro Glu Ser Asn Leu Lys	
295 300 305	
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1075 Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr Pro Ile Ala Gly Thr	
310 315 320 325	
cgc ccc cgt gga ctc aac cca gat ggc tcc atc aac gat gag cta gat	
1123 Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile Asn Asp Glu Leu Asp	
330 335 340	
atc cgc aat gag ttg gat atg cgc act gat gcc aaa gag atc gcg gag	
1171 Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala Lys Glu Ile Ala Glu	
345 350 355	
cac acc atg ctt gtc gat ctc gcc cgc aac gac ctg gcc cgc gtc tcg	
1219 His Thr Met Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Val Ser	
360 365 370	
gtc cca gcg tcg cgc cgg gtt gcg gat ctt ttg cag gtg gat cgc tat	
1267 Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu Gln Val Asp Arg Tyr	
375 380 385	
tcc cgc gtg atg cac ttg gtg tcc cgt gtg acg gcg acg ttg gac cca	
1315 Ser Arg Val Met His Leu Val Ser Arg Val Thr Ala Thr Leu Asp Pro	
390 395 400 405	
gag ctt gat gct ttg gac gcc tat cgg gcg tgc atg aat atg ggc acg	
1363 Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys Met Asn Met Gly Thr	
410 415 420	
ttg acc ggc gct ccg aag ttg cgc gct atg gag ctg ttg cgc ggc gtc	
1411 Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu Leu Leu Arg Gly Val	
425 430 435	

gaa aag cgc agg cgt ggt tct tat ggt ggg gca gtg ggg tac ctg cgc  
1459

Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala Val Gly Tyr Leu Arg  
440 445 450

ggc aat ggc gat atg gat aat tgc att gtt att cgt tcg gcg ttt gtc  
1507

Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile Arg Ser Ala Phe Val  
455 460 465

cag gat ggt gtg gct gct gtg cag gct ggt gct ggt gtg gtc cgc gat  
1555

Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala Gly Val Val Arg Asp  
470 475 480 485

tct aat cct caa tct gaa gcc gat gag acg ttg cac aag gcg tat gcc  
1603

Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu His Lys Ala Tyr Ala  
490 495 500

gtg ttg aat gcc att gcg ctt gct gct ggt tcc act ttg gag gtc atc  
1651

Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser Thr Leu Glu Val Ile  
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1677

Arg

<210> 420

<211> 518

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

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Asp Ala Ser Ala Leu Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp  
20 25 30

Ala Ala Leu Leu Glu Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser  
35 40 45

Ser Leu Ala Val Leu Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn  
50 55 60

Thr Val Val Thr Gln Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala  
65 70 75 80

Arg Leu Thr Gln Gln Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe  
85 90 95

Ser Phe Pro Ala Ser Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala  
100 105 110

Pro Ser Thr Ile Glu Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr  
115 120 125

Ser Asp Ala Ser Leu Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe  
 130 135 140  
 Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr  
 145 150 155 160  
 Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn  
 165 170 175  
 His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly  
 180 185 190  
 Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala  
 195 200 205  
 Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp  
 210 215 220  
 Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln  
 225 230 235 240  
 Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val  
 245 250 255  
 Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala  
 260 265 270  
 Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile  
 275 280 285  
 Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro  
 290 295 300  
 Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr  
 305 310 315 320  
 Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile  
 325 330 335  
 Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala  
 340 345 350  
 Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg Asn Asp  
 355 360 365  
 Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu  
 370 375 380  
 Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg Val Thr  
 385 390 395 400  
 Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys  
 405 410 415  
 Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu  
 420 425 430  
 Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala  
 435 440 445

Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile  
 450 455 460

Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala  
 465 470 475 480

Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu  
 485 490 495

His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser  
 500 505 510

Thr Leu Glu Val Ile Arg  
 515

<210> 421  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(1128)  
 <223> FRXA00957

<400> 421

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aac act tac ccc gat tac cag ttc gtc ctc gcg gaa atc gtc ctg gac	96
Asn Thr Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp	
20 25 30	
atc aat cac cag gac cag acc gcc aaa ctc gcc ggc gtc tcc aac gcc	144
Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala	
35 40 45	
cca ggc gag ctc gag gcc gag ctc aac aag ctt tca ttg ctt atc gac	192
Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp	
50 55 60	
gcc gcc ctc ccc gca acc gaa cac gcc tac caa acc acc cct cac gac	240
Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp	
65 70 75 80	
ggc gac act ctt cgc gtt gtg gct gat att ccc gat gct cag ttc cgc	288
Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg	
85 90 95	
acc cag atc aat gag ctg aaa gaa aac att tac aac ggt gac atc tac	336
Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr	
100 105 110	
caa gtt gtc ccg gcg cgc act ttc acc gca cca tgt cct gat gca ttc	384
Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe	
115 120 125	
gct gct tat ctg cag ctg cgt gcc acc aac ccg tcg ccg tac atg ttc	432
Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe	

130	135	140	
tat atc cgt ggc ctc aac gaa ggc cgc tcc tat gaa ctt ttt ggc gca Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala 145 150 155 160			480
tcc cct gag tcc aac ctc aag ttc acc gct gct aac cgt gag ctg cag Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln 165 170 175			528
ctg tac cca atc gca ggt acc cgc ccc cgt gga ctc aac cca gat ggc Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly 180 185 190			576
tcc atc aac gat gag cta gat atc cgc aat gag ttg gat atg cgc act Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr 195 200 205			624
gat gcc aaa gag atc gcg gag cac acc atg ctt gtc gat ctc gcc cgc Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg 210 215 220			672
aac gac ctg gcc cgc gtc tcg gtc cca gcg tcg cgc cgg gtt gcg gat Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp 225 230 235 240			720
ctt ttg cag gtg gat cgc tat tcc cgc gtg atg cac ttg gtg tcc cgt Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg 245 250 255			768
gtg acg gcg acg ttg gac cca gag ctt gat gct ttg gac gcc tat cgg Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg 260 265 270			816
gcg tgc atg aat atg ggc acg ttg acc ggc gct ccg aag ttg cgc gct Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala 275 280 285			864
atg gag ctg ttg cgc ggc gtc gaa aag cgc agg cgt ggt tct tat ggt Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly 290 295 300			912
ggg gca gtg ggg tac ctg cgc ggc aat ggc gat atg gat aat tgc att Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile 305 310 315 320			960
gtt att cgt tcg gcg ttt gtc cag gat ggt gtg gct gct gtg cag gct 1008 Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala 325 330 335			
ggt gct ggt gtg gtc cgc gat tct aat cct caa tct gaa gcc gat gag 1056 Gly Ala Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu 340 345 350			
acg ttg cac aag gcg tat gcc gtg ttg aat gcc att gcg ctt gct gct 1104 Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala 355 360 365			

ggt tcc act ttg gag gtc atc cga tgacacacgt tggttctcatt gat  
1151

Gly Ser Thr Leu Glu Val Ile Arg  
370 375

<210> 422

<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 422

Asp Phe Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val  
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Asn Thr Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp  
20 25 30

Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala  
35 40 45

Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp  
50 55 60

Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp  
65 70 75 80

Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg  
85 90 95

Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr  
100 105 110

Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe  
115 120 125

Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe  
130 135 140

Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala  
145 150 155 160

Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln  
165 170 175

Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly  
180 185 190

Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr  
195 200 205

Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg  
210 215 220

Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp  
225 230 235 240

Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg  
245 250 255

Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg

260					265					270						
Ala	Cys	Met	Asn	Met	Gly	Thr	Leu	Thr	Gly	Ala	Pro	Lys	Leu	Arg	Ala	
275					280					285						
Met	Glu	Leu	Leu	Arg	Gly	Val	Glu	Lys	Arg	Arg	Arg	Gly	Ser	Tyr	Gly	
290					295					300						
Gly	Ala	Val	Gly	Tyr	Leu	Arg	Gly	Asn	Gly	Asp	Met	Asp	Asn	Cys	Ile	
305					310					315					320	
Val	Ile	Arg	Ser	Ala	Phe	Val	Gln	Asp	Gly	Val	Ala	Ala	Val	Gln	Ala	
325					330					335						
Gly	Ala	Gly	Val	Val	Arg	Asp	Ser	Asn	Pro	Gln	Ser	Glu	Ala	Asp	Glu	
340					345					350						
Thr	Leu	His	Lys	Ala	Tyr	Ala	Val	Leu	Asn	Ala	Ile	Ala	Leu	Ala	Ala	
355					360					365						
Gly	Ser	Thr	Leu	Glu	Val	Ile	Arg									
370					375											

&lt;210&gt; 423

&lt;211&gt; 1068

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1045)

&lt;223&gt; RXA02687

&lt;400&gt; 423

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tggacacca	ccttagttcg	gcgggttaag	ctgtgtaacc	atg	agc	gac	gca	cca	115
				Met	Ser	Asp	Ala	Pro	
				1				5	

act	gtt	gtg	gcc	tat	ttg	ggg	cct	gcc	gga	acc	ttc	acc	gaa	gaa	gcc	163
Thr	Val	Val	Ala	Tyr	Leu	Gly	Pro	Ala	Gly	Thr	Phe	Thr	Glu	Glu	Ala	
			10						15					20		

ctc	tac	aaa	ttt	gcc	gac	gcc	ggc	gta	ttc	ggc	gac	ggg	gag	atc	gag	211
Leu	Tyr	Lys	Phe	Ala	Asp	Ala	Gly	Val	Phe	Gly	Asp	Gly	Glu	Ile	Glu	
			25					30					35			

cag	cta	cca	gcc	aaa	tcg	cca	caa	gaa	gct	gtc	gac	gcc	gtc	cgc	cac	259
Gln	Leu	Pro	Ala	Lys	Ser	Pro	Gln	Glu	Ala	Val	Asp	Ala	Val	Arg	His	
		40					45					50				

ggc	acc	gcc	cag	ttc	gcg	gtg	gtc	gcc	atc	gaa	aac	ttc	gtc	gac	ggc	307
Gly	Thr	Ala	Gln	Phe	Ala	Val	Val	Ala	Ile	Glu	Asn	Phe	Val	Asp	Gly	
	55					60					65					

ccc	gtc	acc	ccc	acc	ttc	gac	gcc	ctt	gac	cag	ggc	tcc	aac	gtg	caa	355
Pro	Val	Thr	Pro	Thr	Phe	Asp	Ala	Leu	Asp	Gln	Gly	Ser	Asn	Val	Gln	
	70				75					80					85	



atc atc gcc gaa gaa gaa ctc gac atc gcc ttt tcc atc atg gtc cgg	403
Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe Ser Ile Met Val Arg	
90 95 100	
cca ggg act tcg ctt gcc gac gtc aaa acc ctc gcc acc cac ccg gtt	451
Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu Ala Thr His Pro Val	
105 110 115	
ggg tac caa caa gtg aaa aac tgg atg gca acc acc att ccg gac gcc	499
Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr Thr Ile Pro Asp Ala	
120 125 130	
atg tat ctt tca gca agc tcc aac ggc gcc ggc gca caa atg gtt gcc	547
Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly Ala Gln Met Val Ala	
135 140 145	
gaa gga acc gcc gac gca gcc gca gcg ccc tcc cgc gca gcc gaa ctc	595
Glu Gly Thr Ala Asp Ala Ala Ala Pro Ser Arg Ala Ala Glu Leu	
150 155 160 165	
ttc gga ctg gaa cgc ctt gtt gat gat gtc gcc gac gtc cgt ggc gcc	643
Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala Asp Val Arg Gly Ala	
170 175 180	
cgc acc cgc ttc gtt gct gtc caa gcc caa gca gcc gtt tcc gaa ccg	691
Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala Ala Val Ser Glu Pro	
185 190 195	
acc ggc cac gac cgc acc tcc gtc att ttc tcc cta ccg aat gtg cca	739
Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser Leu Pro Asn Val Pro	
200 205 210	
ggc agc ctc gtg cgc gcc ctc aac gaa ttc gcc atc cgc ggc gtt gac	787
Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala Ile Arg Gly Val Asp	
215 220 225	
ctc acc cgc atc gaa tcc cgc ccc acc cgc aaa gtc ttc gga acc tac	835
Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys Val Phe Gly Thr Tyr	
230 235 240 245	
cgc ttc cac ctg gac ata tcc gga cat atc cgc gat atc ccc gtc gcc	883
Arg Phe His Leu Asp Ile Ser Gly His Ile Arg Asp Ile Pro Val Ala	
250 255 260	
gaa gcc ctc cgc gca ctc cac ctc caa gcc gaa gaa ctc gtc ttc gtc	931
Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu Glu Leu Val Phe Val	
265 270 275	
ggc tcc tgg ccc tcc aac cgt gcg gaa gac agc acg ccc caa acc gac	979
Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser Thr Pro Gln Thr Asp	
280 285 290	
caa cta gct aag cta cac aag gcg gac gaa tgg gtt cgc gca gca agc	
1027	
Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp Val Arg Ala Ala Ser	
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Glu Gly Arg Lys Leu Asn	
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 424

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Asp	Gly	Glu	Ile	Glu	Gln	Leu	Pro	Ala	Lys	Ser	Pro	Gln	Glu	Ala	Val
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Asp	Ala	Val	Arg	His	Gly	Thr	Ala	Gln	Phe	Ala	Val	Val	Ala	Ile	Glu
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Asn	Phe	Val	Asp	Gly	Pro	Val	Thr	Pro	Thr	Phe	Asp	Ala	Leu	Asp	Gln
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Gly	Ser	Asn	Val	Gln	Ile	Ile	Ala	Glu	Glu	Glu	Leu	Asp	Ile	Ala	Phe
				85					90					95	
Ser	Ile	Met	Val	Arg	Pro	Gly	Thr	Ser	Leu	Ala	Asp	Val	Lys	Thr	Leu
			100					105					110		
Ala	Thr	His	Pro	Val	Gly	Tyr	Gln	Gln	Val	Lys	Asn	Trp	Met	Ala	Thr
		115					120					125			
Thr	Ile	Pro	Asp	Ala	Met	Tyr	Leu	Ser	Ala	Ser	Ser	Asn	Gly	Ala	Gly
	130					135						140			
Ala	Gln	Met	Val	Ala	Glu	Gly	Thr	Ala	Asp	Ala	Ala	Ala	Ala	Pro	Ser
145					150				155					160	
Arg	Ala	Ala	Glu	Leu	Phe	Gly	Leu	Glu	Arg	Leu	Val	Asp	Asp	Val	Ala
				165					170					175	
Asp	Val	Arg	Gly	Ala	Arg	Thr	Arg	Phe	Val	Ala	Val	Gln	Ala	Gln	Ala
			180					185					190		
Ala	Val	Ser	Glu	Pro	Thr	Gly	His	Asp	Arg	Thr	Ser	Val	Ile	Phe	Ser
		195					200					205			
Leu	Pro	Asn	Val	Pro	Gly	Ser	Leu	Val	Arg	Ala	Leu	Asn	Glu	Phe	Ala
	210					215					220				
Ile	Arg	Gly	Val	Asp	Leu	Thr	Arg	Ile	Glu	Ser	Arg	Pro	Thr	Arg	Lys
225					230					235					240
Val	Phe	Gly	Thr	Tyr	Arg	Phe	His	Leu	Asp	Ile	Ser	Gly	His	Ile	Arg
				245					250					255	
Asp	Ile	Pro	Val	Ala	Glu	Ala	Leu	Arg	Ala	Leu	His	Leu	Gln	Ala	Glu
			260				265						270		
Glu	Leu	Val	Phe	Val	Gly	Ser	Trp	Pro	Ser	Asn	Arg	Ala	Glu	Asp	Ser
		275					280					285			

Thr Pro Gln Thr Asp Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp  
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Val Arg Ala Ala Ser Glu Gly Arg Lys Leu Asn  
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<210> 425

<211> 1353

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1330)

<223> RXN01698

<400> 425

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gggtgggctg gatacgtctt ctgcggcctt tcgtgcgata atg cta ggc atg ctt 115  
 Met Leu Gly Met Leu  
 1 5

cga tgg act aca gca ggt gaa tcc cac ggc cag gcg ctt atc gcc acg 163  
 Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln Ala Leu Ile Ala Thr  
 10 15 20

gtt gaa cac atg cca gca ggc gtg ccc gtg act aaa gat gag gtc tcg 211  
 Val Glu His Met Pro Ala Gly Val Pro Val Thr Lys Asp Glu Val Ser  
 25 30 35

tat caa ttg gcg cgc cga cgc ctt gga tat ggt cgc ggc gct cgc atg 259  
 Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly Arg Gly Ala Arg Met  
 40 45 50

aag ttt gag caa gac gcg ttg acc ttc ctc acc ggc atc cgc cac ggc 307  
 Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr Gly Ile Arg His Gly  
 55 60 65

ctc act ttg ggt agc ccc atc tca atc atg atc ggc aac act gag tgg 355  
 Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile Gly Asn Thr Glu Trp  
 70 75 80 85

gat aag tgg acc acc atc atg tcc tct gac gct ttg gac atg gaa gac 403  
 Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala Leu Asp Met Glu Asp  
 90 95 100

cca gat aac gtt gcg gcg atg tct tcg ggt cgg ggc gca aaa ctg act 451  
 Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg Gly Ala Lys Leu Thr  
 105 110 115

cgt ccg cgt cca ggc cac gct gat tac gca ggc atg ctc aag tac gga 499  
 Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly Met Leu Lys Tyr Gly  
 120 125 130

ttc gat gat gcc cgc aac gtg ctg gag cgt tct tca gcc cgt gag acg 547  
 Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser Ser Ala Arg Glu Thr  
 135 140 145

gca gca cgc gtg gca gca gca acc gtt gcg cgt tcc ttc ctg cgt gaa	595
Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg Ser Phe Leu Arg Glu	
150 155 160 165	
acc ttg ggc gtg gaa gtg ctt tcc cac gta att tcc att ggt gcg tcc	643
Thr Leu Gly Val Glu Val Leu Ser His Val Ile Ser Ile Gly Ala Ser	
170 175 180	
gag cct tac act ggc gcg gag cca acc ttt gca gat att caa gca atc	691
Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala Asp Ile Gln Ala Ile	
185 190 195	
gat gat tcc cca gtt cgt gca ttc ggt aaa gac gct gaa gaa tcc atg	739
Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp Ala Glu Glu Ser Met	
200 205 210	
atc gcg gaa atc gag gcc gca aag aaa gcc ggc gat acc ctc ggt ggc	787
Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly Asp Thr Leu Gly Gly	
215 220 225	
atc gtg gaa gtg att gtt gaa ggc ctg ccc atc ggt ttg ggc tca cac	835
Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile Gly Leu Gly Ser His	
230 235 240 245	
att tct ggc gaa gat cgc ctc gat gcg cag atc gca gct gca ctc atg	883
Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile Ala Ala Ala Leu Met	
250 255 260	
ggc att cag gcc atc aag ggc gtg gaa atc ggt gac ggt ttc gaa gaa	931
Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly Asp Gly Phe Glu Glu	
265 270 275	
gct cgt cga cgt ggc tcc gaa gcc cac gat gaa gtg ttc ctg gat gac	979
Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu Val Phe Leu Asp Asp	
280 285 290	
aac ggc gta tac cgc aac acc aac cgt gca ggt ggc ctc gaa ggc ggc	
1027	
Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly Gly Leu Glu Gly Gly	
295 300 305	
atg acc aac ggt gaa acc ctg cgc gtt cgt gct ggc atg aag cca att	
1075	
Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala Gly Met Lys Pro Ile	
310 315 320 325	
tct act gtg cct cgc gcc ctg aaa acc att gat atg gaa aac ggc aag	
1123	
Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp Met Glu Asn Gly Lys	
330 335 340	
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1171	
Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val Cys Ala Val Pro Ala	
345 350 355	
gcc ggt gtc gtt gca gaa gca atg gtc acc ctg gtt ctc gcc cgc gca	
1219	
Ala Gly Val Val Ala Glu Ala Met Val Thr Leu Val Leu Ala Arg Ala	
360 365 370	

gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc gaa acc aag agc aac  
1267

Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser Glu Thr Lys Ser Asn  
375 380 385

att gac acc tac ctc aaa aac att gag gaa cga atg aaa ttc gaa ggt  
1315

Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg Met Lys Phe Glu Gly  
390 395 400 405

tta gag gat gga gcg taatgaagtg aatgatcaaa ttc  
1353

Leu Glu Asp Gly Ala  
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<210> 426

<211> 410

<212> PRT

<213> Corynebacterium glutamicum

<400> 426

Met Leu Gly Met Leu Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln  
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20 25 30

Lys Asp Glu Val Ser Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly  
35 40 45

Arg Gly Ala Arg Met Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr  
50 55 60

Gly Ile Arg His Gly Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile  
65 70 75 80

Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala  
85 90 95

Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg  
100 105 110

Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly  
115 120 125

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser  
130 135 140

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg  
145 150 155 160

Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile  
165 170 175

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala  
180 185 190

Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp  
195 200 205

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly  
 210 215 220

Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile  
 225 230 235 240

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile  
 245 250 255

Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly  
 260 265 270

Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu  
 275 280 285

Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly  
 290 295 300

Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala  
 305 310 315 320

Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp  
 325 330 335

Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val  
 340 345 350

Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu  
 355 360 365

Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser  
 370 375 380

Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg  
 385 390 395 400

Met Lys Phe Glu Gly Leu Glu Asp Gly Ala  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(990)  
 <223> FRXA01698

<400> 427

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Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala	
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ttg gac atg gaa gac cca gat aac gtt gcg gcg atg tct tcg ggt cgg	96
Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg	
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ggc gca aaa ctg act cgt ccg cgt cca ggc cac gct gat tac gca ggc	144
Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly	

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atg	ctc	aag	tac	gga	ttc	gat	gat	gcc	cgc	aac	gtg	ctg	gag	cgt	tct	192
Met	Leu	Lys	Tyr	Gly	Phe	Asp	Asp	Ala	Arg	Asn	Val	Leu	Glu	Arg	Ser	
	50					55					60					
tca	gcc	cgt	gag	acg	gca	gca	cgc	gtg	gca	gca	gca	acc	gtt	gcg	cgt	240
Ser	Ala	Arg	Glu	Thr	Ala	Ala	Arg	Val	Ala	Ala	Ala	Thr	Val	Ala	Arg	
	65				70					75					80	
tcc	ttc	ctg	cgt	gaa	acc	ttg	ggc	gtg	gaa	gtg	ctt	tcc	cac	gta	att	288
Ser	Phe	Leu	Arg	Glu	Thr	Leu	Gly	Val	Glu	Val	Leu	Ser	His	Val	Ile	
				85					90					95		
tcc	att	ggc	gcg	tcc	gag	cct	tac	act	ggc	gcg	gag	cca	acc	ttt	gca	336
Ser	Ile	Gly	Ala	Ser	Glu	Pro	Tyr	Thr	Gly	Ala	Glu	Pro	Thr	Phe	Ala	
			100					105					110			
gat	att	caa	gca	atc	gat	gat	tcc	cca	gtt	cgt	gca	ttc	ggc	aaa	gac	384
Asp	Ile	Gln	Ala	Ile	Asp	Asp	Ser	Pro	Val	Arg	Ala	Phe	Gly	Lys	Asp	
		115					120					125				
gct	gaa	gaa	tcc	atg	atc	gcg	gaa	atc	gag	gcc	gca	aag	aaa	gcc	ggc	432
Ala	Glu	Glu	Ser	Met	Ile	Ala	Glu	Ile	Glu	Ala	Ala	Lys	Lys	Ala	Gly	
	130					135					140					
gat	acc	ctc	ggc	ggc	atc	gtg	gaa	gtg	att	gtt	gaa	ggc	ctg	ccc	atc	480
Asp	Thr	Leu	Gly	Gly	Ile	Val	Glu	Val	Ile	Val	Glu	Gly	Leu	Pro	Ile	
	145				150					155					160	
ggc	ttg	ggc	tca	cac	att	tct	ggc	gaa	gat	cgc	ctc	gat	gcg	cag	atc	528
Gly	Leu	Gly	Ser	His	Ile	Ser	Gly	Glu	Asp	Arg	Leu	Asp	Ala	Gln	Ile	
				165					170					175		
gca	gct	gca	ctc	atg	ggc	att	cag	gcc	atc	aag	ggc	gtg	gaa	atc	ggc	576
Ala	Ala	Ala	Leu	Met	Gly	Ile	Gln	Ala	Ile	Lys	Gly	Val	Glu	Ile	Gly	
			180					185					190			
gac	ggc	ttc	gaa	gaa	gct	cgt	cga	cgt	ggc	tcc	gaa	gcc	cac	gat	gaa	624
Asp	Gly	Phe	Glu	Glu	Ala	Arg	Arg	Arg	Gly	Ser	Glu	Ala	His	Asp	Glu	
		195					200					205				
gtg	ttc	ctg	gat	gac	aac	ggc	gta	tac	cgc	aac	acc	aac	cgt	gca	ggc	672
Val	Phe	Leu	Asp	Asp	Asn	Gly	Val	Tyr	Arg	Asn	Thr	Asn	Arg	Ala	Gly	
	210					215					220					
ggc	ctc	gaa	ggc	ggc	atg	acc	aac	ggc	gaa	acc	ctg	cgc	gtt	cgt	gct	720
Gly	Leu	Glu	Gly	Gly	Met	Thr	Asn	Gly	Glu	Thr	Leu	Arg	Val	Arg	Ala	
	225				230					235					240	
ggc	atg	aag	cca	att	tct	act	gtg	cct	cgc	gcc	ctg	aaa	acc	att	gat	768
Gly	Met	Lys	Pro	Ile	Ser	Thr	Val	Pro	Arg	Ala	Leu	Lys	Thr	Ile	Asp	
				245					250					255		
atg	gaa	aac	ggc	aag	gca	gca	acc	gga	atc	cac	cag	cgt	tcc	gac	gtg	816
Met	Glu	Asn	Gly	Lys	Ala	Ala	Thr	Gly	Ile	His	Gln	Arg	Ser	Asp	Val	
			260					265					270			
tgc	gct	gtt	cca	gcc	gcc	ggc	gtc	gtt	gca	gaa	gca	atg	gtc	acc	ctg	864
Cys	Ala	Val	Pro	Ala	Ala	Gly	Val	Val	Ala	Glu	Ala	Met	Val	Thr	Leu	
		275					280					285				

gtt ctc gcc cgc gca gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc 912  
 Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser  
 290 295 300

gaa acc aag agc aac att gac acc tac ctc aaa aac att gag gaa cga 960  
 Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg  
 305 310 315 320

atg aaa ttc gaa ggt tta gag gat gga gcg taatgaagtg aatgatcaaa  
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 Met Lys Phe Glu Gly Leu Glu Asp Gly Ala  
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ttc  
 1013

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 <211> 330  
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 <213> Corynebacterium glutamicum

<400> 428  
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 35 40 45

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser  
 50 55 60

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg  
 65 70 75 80

Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile  
 85 90 95

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala  
 100 105 110

Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp  
 115 120 125

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly  
 130 135 140

Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile  
 145 150 155 160

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile  
 165 170 175

Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly  
 180 185 190

Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu



195	200	205
Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly 210 215 220		
Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala 225 230 235 240		
Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp 245 250 255		
Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val 260 265 270		
Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu 275 280 285		
Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser 290 295 300		
Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg 305 310 315 320		
Met Lys Phe Glu Gly Leu Glu Asp Gly Ala 325 330		

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 <212> DNA  
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<220>  
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 <222> (101)..(883)  
 <223> RXA01095

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 Met Val Ala Thr Glu  
 1 5  
 aac cgc atg ttg atg gaa atc gct gcg gaa ata tcg gct cgg gaa gca 163  
 Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile Ser Ala Arg Glu Ala  
 10 15 20  
 acg ctt ggt ttt caa gaa gtc aaa act aaa tct cga tca gca ggt ctc 211  
 Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser Arg Ser Ala Gly Leu  
 25 30 35  
 acg gcg gct ttc gat att gct tca gtc ttt ttt tcg tct gga tgt aat 259  
 Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe Ser Ser Gly Cys Asn  
 40 45 50  
 gtc gta gtc gcc ttt gat cgt ttt gca tcc aat tgg tct gat cat tcg 307  
 Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn Trp Ser Asp His Ser  
 55 60 65  
 gat cat gtg gac tac gct gca cag gtt gcg ggt ttt ggc gca tca atg 355

Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly Phe Gly Ala Ser Met  
 70 75 80 85  
 ctt gca tat acg gtg cgc agg gga cag ttt gat acc gca gta cgc gat 403  
 Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp Thr Ala Val Arg Asp  
 90 95 100  
 atc agg gac atc aaa tct gaa gta gac att ccc att ctg ctt cat gat 451  
 Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro Ile Leu Leu His Asp  
 105 110 115  
 ccc atc atc gat ccg tat caa atc cac gaa gcc cgc gtc atg ggc atc 499  
 Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala Arg Val Met Gly Ile  
 120 125 130  
 gac gct ctt caa ttc ccc gta tgg gcg atg gaa caa gct cga ctg gaa 547  
 Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu Gln Ala Arg Leu Glu  
 135 140 145  
 tct ttg gtg gac cgc acc gaa tca ttg ggc atg aca gcc atc gtg tct 595  
 Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met Thr Ala Ile Val Ser  
 150 155 160 165  
 gtg cga aac cac gaa gaa gcg cat cgt gca gtg gac gca gga gcg aca 643  
 Val Arg Asn His Glu Glu Ala His Arg Ala Val Asp Ala Gly Ala Thr  
 170 175 180  
 gtg gta gca att gat att act ggt tat acc ggc tca ctc act ttg cct 691  
 Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly Ser Leu Thr Leu Pro  
 185 190 195  
 gaa gcg ttt tcg ggt atc acc caa ttc atg ccc aaa gag gta gcc cgc 739  
 Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro Lys Glu Val Ala Arg  
 200 205 210  
 att gtg ctc gga ggt tgc agc agc cct aaa gaa ctc atg cgg ttt gca 787  
 Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu Leu Met Arg Phe Ala  
 215 220 225  
 cga cat tct gca gac gcc atc ttt gtt cca cat gca gac ctc gcc acc 835  
 Arg His Ser Ala Asp Ala Ile Phe Val Pro His Ala Asp Leu Ala Thr  
 230 235 240 245  
 aca aaa tct ctt gtg aca gca ggt atg cat cca gcg tgc cca tcg cgt 883  
 Thr Lys Ser Leu Val Thr Ala Gly Met His Pro Ala Cys Pro Ser Arg  
 250 255 260  
 tgaagaggtg ctctgtggtc agc 906

&lt;210&gt; 430

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 430

Met Val Ala Thr Glu Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile  
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Ser Ala Arg Glu Ala Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser  
 20 25 30

Arg Ser Ala Gly Leu Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe  
 35 40 45  
 Ser Ser Gly Cys Asn Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn  
 50 55 60  
 Trp Ser Asp His Ser Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly  
 65 70 75 80  
 Phe Gly Ala Ser Met Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp  
 85 90 95  
 Thr Ala Val Arg Asp Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro  
 100 105 110  
 Ile Leu Leu His Asp Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala  
 115 120 125  
 Arg Val Met Gly Ile Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu  
 130 135 140  
 Gln Ala Arg Leu Glu Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met  
 145 150 155 160  
 Thr Ala Ile Val Ser Val Arg Asn His Glu Glu Ala His Arg Ala Val  
 165 170 175  
 Asp Ala Gly Ala Thr Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly  
 180 185 190  
 Ser Leu Thr Leu Pro Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro  
 195 200 205  
 Lys Glu Val Ala Arg Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu  
 210 215 220  
 Leu Met Arg Phe Ala Arg His Ser Ala Asp Ala Ile Phe Val Pro His  
 225 230 235 240  
 Ala Asp Leu Ala Thr Thr Lys Ser Leu Val Thr Ala Gly Met His Pro  
 245 250 255  
 Ala Cys Pro Ser Arg  
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<210> 431  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1522)  
 <223> RXA00955

<400> 431  
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																Met Thr Ser Asn Asn	
																1	5
ctg	ccc	aca	gtg	ttg	gaa	agc	atc	gtc	gag	ggg	cgt	cgc	gga	cac	ctg	163	
Leu	Pro	Thr	Val	Leu	Glu	Ser	Ile	Val	Glu	Gly	Arg	Arg	Gly	His	Leu		
				10							15					20	
gag	gaa	att	cgc	gct	cgc	atc	gct	cac	gtg	gat	gtg	gat	gcg	ctt	cca	211	
Glu	Glu	Ile	Arg	Ala	Arg	Ile	Ala	His	Val	Asp	Val	Asp	Ala	Leu	Pro		
				25							30					35	
aaa	tcc	acc	cgt	tct	ctg	ttt	gat	tcc	ctc	aac	cag	ggg	agg	gga	ggg	259	
Lys	Ser	Thr	Arg	Ser	Leu	Phe	Asp	Ser	Leu	Asn	Gln	Gly	Arg	Gly	Gly		
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gcg	cgt	ttc	atc	atg	gag	tgc	aag	tcc	gca	tcg	cct	tct	ttg	gga	atg	307	
Ala	Arg	Phe	Ile	Met	Glu	Cys	Lys	Ser	Ala	Ser	Pro	Ser	Leu	Gly	Met		
				55							60					65	
att	cgt	gag	cac	tac	cag	ccg	ggg	gaa	atc	gct	cgc	gtg	tac	tct	cgc	355	
Ile	Arg	Glu	His	Tyr	Gln	Pro	Gly	Glu	Ile	Ala	Arg	Val	Tyr	Ser	Arg		
				70							75					80	85
tac	gcc	agc	ggc	att	tcc	gtg	ctg	tgc	gag	ccg	gat	cgt	ttt	ggg	ggc	403	
Tyr	Ala	Ser	Gly	Ile	Ser	Val	Leu	Cys	Glu	Pro	Asp	Arg	Phe	Gly	Gly		
				90							95					100	
gat	tac	gat	cac	ctc	gct	acc	gtt	gcc	gct	acc	tct	cat	ctt	ccg	gtg	451	
Asp	Tyr	Asp	His	Leu	Ala	Thr	Val	Ala	Ala	Thr	Ser	His	Leu	Pro	Val		
				105							110					115	
ctg	tgc	aaa	gac	ttc	atc	att	gat	cct	gtc	cag	gta	cac	gcg	gcg	cgt	499	
Leu	Cys	Lys	Asp	Phe	Ile	Ile	Asp	Pro	Val	Gln	Val	His	Ala	Ala	Arg		
				120							125					130	
tac	ttt	ggg	gct	gat	gcc	atc	ctg	ctc	atg	ctc	tct	gtg	ctt	gat	gat	547	
Tyr	Phe	Gly	Ala	Asp	Ala	Ile	Leu	Leu	Met	Leu	Ser	Val	Leu	Asp	Asp		
				135							140					145	
gaa	gag	tac	gca	gca	ctc	gct	gcc	gag	gct	gcg	cgt	ttt	gat	ctg	gat	595	
Glu	Glu	Tyr	Ala	Ala	Leu	Ala	Ala	Glu	Ala	Ala	Arg	Phe	Asp	Leu	Asp		
				150							155					160	165
atc	ctc	acc	gag	gtt	att	gat	gag	gag	gaa	gtc	gcc	cgc	gcc	atc	aag	643	
Ile	Leu	Thr	Glu	Val	Ile	Asp	Glu	Glu	Glu	Val	Ala	Arg	Ala	Ile	Lys		
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ctg	ggg	gcg	aag	atc	ttt	ggc	gtc	aac	cac	cgc	aac	ctg	cat	gat	ctg	691	
Leu	Gly	Ala	Lys	Ile	Phe	Gly	Val	Asn	His	Arg	Asn	Leu	His	Asp	Leu		
				185							190					195	
tcc	att	gat	ttg	gat	cgt	tca	cgt	cgc	ctg	tcc	aag	ctc	att	cca	gca	739	
Ser	Ile	Asp	Leu	Asp	Arg	Ser	Arg	Arg	Leu	Ser	Lys	Leu	Ile	Pro	Ala		
				200							205					210	
gat	gcc	gtg	ctc	gtg	tct	gag	tct	ggc	gtg	cgc	gat	acc	gaa	acc	gtc	787	
Asp	Ala	Val	Leu	Val	Ser	Glu	Ser	Gly	Val	Arg	Asp	Thr	Glu	Thr	Val		
				215							220					225	
cgc	cag	cta	ggg	ggg	cac	tcc	aat	gca	ttc	ctc	gtt	ggc	tcc	cag	ctg	835	
Arg	Gln	Leu	Gly	Gly	His	Ser	Asn	Ala	Phe	Leu	Val	Gly	Ser	Gln	Leu		

230	235	240	245	
acc agc cag gaa aac gtc gat ctg gca gcc cgc gaa tta gtc tac ggc				883
Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg Glu Leu Val Tyr Gly	250	255	260	
ccc aac aaa gtc tgc gga ctc acc tca cca agt gca gca caa acc gct				931
Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser Ala Ala Gln Thr Ala	265	270	275	
cgc gca gcg ggt gcg gtc tac ggc ggg ctc atc ttc gaa gag gca tcg				979
Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile Phe Glu Glu Ala Ser	280	285	290	
cca cgc aat gtt tca cgt gaa aca ttg caa aaa atc atc gcc gca gag				
1027				
Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys Ile Ile Ala Ala Glu	295	300	305	
ccc aac ctg cgc tac gtc gcg gtc agc cgt cgc acc tcc ggg tac aag				
1075				
Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg Thr Ser Gly Tyr Lys	310	315	320	325
gat ttg ctt gtc gac ggc atc ttc gcc gta caa atc cac gcc cca ctg				
1123				
Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln Ile His Ala Pro Leu	330	335	340	
cag gac agc gtc gaa gca gaa aag gca ttg atc gcc gcc gtt cgt gaa				
1171				
Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile Ala Ala Val Arg Glu	345	350	355	
gag gtt gga ccg cag gtc cag gtc tgg cgc gcg atc tcg atg tcc agc				
1219				
Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala Ile Ser Met Ser Ser	360	365	370	
ccc ttg ggg gct gaa gtg gca gct gcg gtg gag ggt gac gtc gat aag				
1267				
Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu Gly Asp Val Asp Lys	375	380	385	
cta att ctt gat gcc cat gaa ggt ggc agc ggg gaa gta ttc gac tgg				
1315				
Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly Glu Val Phe Asp Trp	390	395	400	405
gct acg gtg ccg gcc gct gtg aag gca aag tct ttg ctc gcg gga ggc				
1363				
Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser Leu Leu Ala Gly Gly	410	415	420	
atc tct ccg gac aac gct gcg cag gca ctc gct gtg ggc tgc gca ggt				
1411				
Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala Val Gly Cys Ala Gly	425	430	435	
ttg gac atc aac tct ggc gtg gaa tac ccc gcc ggt gca ggc acg tgg				
1459				

Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala Gly Ala Gly Thr Trp  
 440 445 450

gct ggg gcg aaa gac gcc ggc gcg ctg ctg aaa att tta gcg acc atc  
 1507

Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys Ile Leu Ala Thr Ile  
 455 460 465

tcc aca ttc cat tac taaaggttta aataggatca tga  
 1545

Ser Thr Phe His Tyr  
 470

<210> 432

<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Met Thr Ser Asn Asn Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly  
 1 5 10 15

Arg Arg Gly His Leu Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp  
 20 25 30

Val Asp Ala Leu Pro Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn  
 35 40 45

Gln Gly Arg Gly Gly Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser  
 50 55 60

Pro Ser Leu Gly Met Ile Arg Glu His Tyr Gln Pro Gly Glu Ile Ala  
 65 70 75 80

Arg Val Tyr Ser Arg Tyr Ala Ser Gly Ile Ser Val Leu Cys Glu Pro  
 85 90 95

Asp Arg Phe Gly Gly Asp Tyr Asp His Leu Ala Thr Val Ala Ala Thr  
 100 105 110

Ser His Leu Pro Val Leu Cys Lys Asp Phe Ile Ile Asp Pro Val Gln  
 115 120 125

Val His Ala Ala Arg Tyr Phe Gly Ala Asp Ala Ile Leu Leu Met Leu  
 130 135 140

Ser Val Leu Asp Asp Glu Glu Tyr Ala Ala Leu Ala Ala Glu Ala Ala  
 145 150 155 160

Arg Phe Asp Leu Asp Ile Leu Thr Glu Val Ile Asp Glu Glu Glu Val  
 165 170 175

Ala Arg Ala Ile Lys Leu Gly Ala Lys Ile Phe Gly Val Asn His Arg  
 180 185 190

Asn Leu His Asp Leu Ser Ile Asp Leu Asp Arg Ser Arg Arg Leu Ser  
 195 200 205

Lys Leu Ile Pro Ala Asp Ala Val Leu Val Ser Glu Ser Gly Val Arg  
 210 215 220

Asp Thr Glu Thr Val Arg Gln Leu Gly Gly His Ser Asn Ala Phe Leu  
 225 230 235 240  
 Val Gly Ser Gln Leu Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg  
 245 250 255  
 Glu Leu Val Tyr Gly Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser  
 260 265 270  
 Ala Ala Gln Thr Ala Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile  
 275 280 285  
 Phe Glu Glu Ala Ser Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys  
 290 295 300  
 Ile Ile Ala Ala Glu Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg  
 305 310 315 320  
 Thr Ser Gly Tyr Lys Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln  
 325 330 335  
 Ile His Ala Pro Leu Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile  
 340 345 350  
 Ala Ala Val Arg Glu Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala  
 355 360 365  
 Ile Ser Met Ser Ser Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu  
 370 375 380  
 Gly Asp Val Asp Lys Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly  
 385 390 395 400  
 Glu Val Phe Asp Trp Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser  
 405 410 415  
 Leu Leu Ala Gly Gly Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala  
 420 425 430  
 Val Gly Cys Ala Gly Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala  
 435 440 445  
 Gly Ala Gly Thr Trp Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys  
 450 455 460  
 Ile Leu Ala Thr Ile Ser Thr Phe His Tyr  
 465 470

<210> 433  
 <211> 494  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(471)  
 <223> RXA02814

<400> 433

gcc aaa aac cta gaa gaa cac tcc tac gtg gtc aac cac ctg cgc acc 48  
 Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr  
 1 5 10 15  
 atc ctg gaa cca ctg tgc tca caa ttc gac gcc cca aca gtt cct gaa 96  
 Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu  
 20 25 30  
 ctg acc aaa acc aac gaa atg tgg cac ctc gca aca ccc atc gtt ggc 144  
 Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly  
 35 40 45  
 acc ctc aag tac cca cac atc acc gca cta gaa cta gcc ata cga aca 192  
 Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr  
 50 55 60  
 cac ccc acc ccc gcg atc tgt ggc acc ccc acc gac gcc gcc gaa gcc 240  
 His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala  
 65 70 75 80  
 ctc atc atc gaa gcg gaa tcc ccc cga aac ttc tac gcc gga gca gcc 288  
 Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala  
 85 90 95  
 ggc tgg tgt gac tcc acc gga gac ggc gaa tac atg gta gcc atc cgc 336  
 Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg  
 100 105 110  
 tgc gcc gaa gta tcc gaa gac gga acc tgg gcc aga gca tgg gca ggc 384  
 Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly  
 115 120 125  
 gga ggc atc gtc gcc gaa tca gac gcc caa gaa gag ttt gat gaa acc 432  
 Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr  
 130 135 140  
 acc gcg aag ctc caa acc atc atg cgc tcg ctt ggt ttg tgagatgtgg 481  
 Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu  
 145 150 155  
 tcttaaaaca ccg 494

&lt;210&gt; 434

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 434

Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr  
 1 5 10 15  
 Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu  
 20 25 30  
 Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly  
 35 40 45  
 Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr  
 50 55 60



His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala  
 65 70 75 80  
 Leu Il Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala  
 85 90 95  
 Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg  
 100 105 110  
 Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly  
 115 120 125  
 Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr  
 130 135 140  
 Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu  
 145 150 155

<210> 435  
 <211> 803  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(780)  
 <223> RXA00229

<400> 435  
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 Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile  
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 gac acg ctt ggg tcg cgt gct tcc ggg caa gat tta aat acg ctt ctc 96  
 Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu  
 20 25 30  
 gac gcc gcc ctc tac ctt ggc ttc agc ggc ctg aac atc act cac ccg 144  
 Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro  
 35 40 45  
 tac aag caa gca gta tta ccc ctg ctt ggc gaa gtc tcc gaa caa gcc 192  
 Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala  
 50 55 60  
 acc caa ctc ggc gca gtg aat act gtc gtt atg gac gcc acc ggc cac 240  
 Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His  
 65 70 75 80  
 acc acc ggc cac aac acc gac gtc tcc gga ttt ggc cgc gga atg gaa 288  
 Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu  
 85 90 95  
 gaa ggc ctc ccc aac gcc aag ctc gat tcc gtc gtg cag gtc ggc gcc 336  
 Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala  
 100 105 110  
 ggc ggc gta gaa aac gca gtg gca tac gcc ctg gtc acc cac ggt gtg 384  
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val  
 115 120 125

cag aaa ctt cag gtc gct gac ctc gac act tcc cgc gcg cag gca ctg 432  
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu  
 130 135 140  
  
 gca gat gtc atc aac aac gca gtc ggc cgt gaa gcc gtc gtg gga gta 480  
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val  
 145 150 155 160  
  
 gac gcc cgc ggc atc gaa gac gtc atc gcc gcc gcc gac gga gta gtc 528  
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val  
 165 170 175  
  
 aac gca acc ccc atg gga atg cca gca cac ccc ggc acc gcc ttt gat 576  
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp  
 180 185 190  
  
 gtc agc tgc ctc acc aag gat cac tgg gtt ggc gac gtc gtg tac atg 624  
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met  
 195 200 205  
  
 ccc atc gaa act gaa ctt ctc aaa gcc gcc cgt gcc ctc ggc tgc gaa 672  
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu  
 210 215 220  
  
 acc ctc gac gga acc cgc atg gca atc cac caa gcc gtc gat gcc ttc 720  
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe  
 225 230 235 240  
  
 cga ctg ttc acc ggc ctc gaa ccc gac gtc tcc cgc atg cgg gaa act 768  
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr  
 245 250 255  
  
 ttc ctg tcc ctc taaaagagtc agtaaaacct cga 803  
 Phe Leu Ser Leu  
 260

&lt;210&gt; 436

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 436

Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile  
 1 5 10 15  
  
 Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu  
 20 25 30  
  
 Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro  
 35 40 45  
  
 Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala  
 50 55 60  
  
 Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His  
 65 70 75 80  
  
 Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu  
 85 90 95

Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala  
 100 105 110  
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val  
 115 120 125  
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu  
 130 135 140  
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val  
 145 150 155 160  
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Asp Gly Val Val  
 165 170 175  
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp  
 180 185 190  
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met  
 195 200 205  
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu  
 210 215 220  
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe  
 225 230 235 240  
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr  
 245 250 255  
 Phe Leu Ser Leu  
 260

<210> 437  
 <211> 927  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(904)  
 <223> RXA02093

<400> 437  
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 Met Val Asn Tyr Val  
 1 5  
 gac agg gaa aca acc ctg tgc atc tct ctc gct gct cgt cca tcc aac 163  
 Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala Ala Arg Pro Ser Asn  
 10 15 20  
 cat ggt gtt cgt ttc cac aac tgg ctt tac gct gaa ctt gga ttg aac 211  
 His Gly Val Arg Phe His Asn Trp Leu Tyr Ala Glu Leu Gly Leu Asn  
 25 30 35  
 tac ctg tac aag gct gtt gcc cca gca gat atc acc gct gca gtc gca 259

Tyr	Leu	Tyr	Lys	Ala	Val	Ala	Pro	Ala	Asp	Ile	Thr	Ala	Ala	Val	Ala		
		40					45					50					
ggt	atc	cgt	ggt	ctg	aac	att	cgc	ggc	gca	ggt	gtc	tcc	atg	cca	tac		307
Gly	Ile	Arg	Gly	Leu	Asn	Ile	Arg	Gly	Ala	Gly	Val	Ser	Met	Pro	Tyr		
		55				60					65						
aag	agc	gat	gtc	atc	cca	ctc	atc	gat	gag	ttg	cat	cct	tcc	gca	gag		355
Lys	Ser	Asp	Val	Ile	Pro	Leu	Ile	Asp	Glu	Leu	His	Pro	Ser	Ala	Glu		
		70			75					80					85		
cgc	ata	cgt	tct	gtt	aac	acc	atc	gtc	aac	aat	gac	gga	cac	ctt	gtc		403
Arg	Ile	Arg	Ser	Val	Asn	Thr	Ile	Val	Asn	Asn	Asp	Gly	His	Leu	Val		
				90					95					100			
gga	tac	aac	acc	gac	tac	act	gcg	gtg	tac	cac	ctc	ctt	gaa	gaa	cac		451
Gly	Tyr	Asn	Thr	Asp	Tyr	Thr	Ala	Val	Tyr	His	Leu	Leu	Glu	Glu	His		
			105					110					115				
cgc	gtg	aac	ccc	aat	gca	cga	gta	gct	atc	aag	gga	tcc	ggc	ggc	atg		499
Arg	Val	Asn	Pro	Asn	Ala	Arg	Val	Ala	Ile	Lys	Gly	Ser	Gly	Gly	Met		
		120					125					130					
gcc	aat	gct	gtt	gtt	gca	gct	ctt	gct	gag	tat	ggt	ctg	agt	ggc	acc		547
Ala	Asn	Ala	Val	Val	Ala	Ala	Leu	Ala	Glu	Tyr	Gly	Leu	Ser	Gly	Thr		
		135				140					145						
gtc	gtt	gcc	cgc	aac	cac	acc	acc	ggt	tct	gcg	cta	gct	tcc	cgt	tac		595
Val	Val	Ala	Arg	Asn	His	Thr	Thr	Gly	Ser	Ala	Leu	Ala	Ser	Arg	Tyr		
					155					160					165		
ggt	tgg	gaa	tac	tcc	gca	act	gtt	ccg	gaa	gac	gca	aaa	att	ttg	gtt		643
Gly	Trp	Glu	Tyr	Ser	Ala	Thr	Val	Pro	Glu	Asp	Ala	Lys	Ile	Leu	Val		
				170					175					180			
aat	gta	acc	cca	atg	gga	atg	aat	gga	cct	gac	caa	gac	gtt	gta	tct		691
Asn	Val	Thr	Pro	Met	Gly	Met	Asn	Gly	Pro	Asp	Gln	Asp	Val	Val	Ser		
			185					190					195				
ttt	ggt	gag	gat	gaa	gta	gac	cga	gcc	gac	gta	atc	ttt	gac	tgc	gta		739
Phe	Gly	Glu	Asp	Glu	Val	Asp	Arg	Ala	Asp	Val	Ile	Phe	Asp	Cys	Val		
		200					205					210					
gca	ttc	ccc	gtc	gag	acc	cca	ctg	att	aag	ttg	gcc	aag	gaa	aag	ggt		787
Ala	Phe	Pro	Val	Glu	Thr	Pro	Leu	Ile	Lys	Leu	Ala	Lys	Glu	Lys	Gly		
		215				220					225						
aag	caa	acc	atc	gac	ggc	gga	gaa	gtt	gcc	gct	ctt	cag	gca	gca	gag		835
Lys	Gln	Thr	Ile	Asp	Gly	Gly	Glu	Val	Ala	Ala	Leu	Gln	Ala	Ala	Glu		
		230			235				240						245		
cag	ttc	cac	ctc	tac	acc	gga	gtt	ctt	cca	acc	aac	gac	cag	atc	att		883
Gln	Phe	His	Leu	Tyr	Thr	Gly	Val	Leu	Pro	Thr	Asn	Asp	Gln	Ile	Ile		
				250				255						260			
gct	gcg	gag	gag	ttc	tcc	aag	taaatttctc	tcccctattt	tta								927
Ala	Ala	Glu	Glu	Phe	Ser	Lys											
				265													

&lt;210&gt; 438

&lt;211&gt; 268

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 438

Met Val Asn Tyr Val Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala  
 1 5 10 15

Ala Arg Pro Ser Asn His Gly Val Arg Phe His Asn Trp Leu Tyr Ala  
 20 25 30

Glu Leu Gly Leu Asn Tyr Leu Tyr Lys Ala Val Ala Pro Ala Asp Ile  
 35 40 45

Thr Ala Ala Val Ala Gly Ile Arg Gly Leu Asn Ile Arg Gly Ala Gly  
 50 55 60

Val Ser Met Pro Tyr Lys Ser Asp Val Ile Pro Leu Ile Asp Glu Leu  
 65 70 75 80

His Pro Ser Ala Glu Arg Ile Arg Ser Val Asn Thr Ile Val Asn Asn  
 85 90 95

Asp Gly His Leu Val Gly Tyr Asn Thr Asp Tyr Thr Ala Val Tyr His  
 100 105 110

Leu Leu Glu Glu His Arg Val Asn Pro Asn Ala Arg Val Ala Ile Lys  
 115 120 125

Gly Ser Gly Gly Met Ala Asn Ala Val Val Ala Ala Leu Ala Glu Tyr  
 130 135 140

Gly Leu Ser Gly Thr Val Val Ala Arg Asn His Thr Thr Gly Ser Ala  
 145 150 155 160

Leu Ala Ser Arg Tyr Gly Trp Glu Tyr Ser Ala Thr Val Pro Glu Asp  
 165 170 175

Ala Lys Ile Leu Val Asn Val Thr Pro Met Gly Met Asn Gly Pro Asp  
 180 185 190

Gln Asp Val Val Ser Phe Gly Glu Asp Glu Val Asp Arg Ala Asp Val  
 195 200 205

Ile Phe Asp Cys Val Ala Phe Pro Val Glu Thr Pro Leu Ile Lys Leu  
 210 215 220

Ala Lys Glu Lys Gly Lys Gln Thr Ile Asp Gly Gly Glu Val Ala Ala  
 225 230 235 240

Leu Gln Ala Ala Glu Gln Phe His Leu Tyr Thr Gly Val Leu Pro Thr  
 245 250 255

Asn Asp Gln Ile Ile Ala Ala Glu Glu Phe Ser Lys  
 260 265

&lt;210&gt; 439

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(928)

&lt;223&gt; RXA02791

&lt;400&gt; 439

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accgtgttca acgacacctt cgaagagcac gaagccgaca ttgagcaagc tttgaacagt 60

ggcgttctag acagcaaccg ataaggatca gcgaataaaa ttg ggt tct cac atc 115
                                   Leu Gly Ser His Ile
                                   1                               5

act cac cgg gcg gcc gta ctc ggc tca ccc atc gag cat tcc aaa tcc 163
Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile Glu His Ser Lys Ser
                                   10                               15                               20

cca gtc ctc cac aac acc ggc tat aaa gcc ctc gga ctg gac caa tgg 211
Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu Gly Leu Asp Gln Trp
                                   25                               30                               35

gaa tac gac cgc ttt gag tgc acc ggc gac atg ctc ccc ggc atc gtc 259
Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met Leu Pro Gly Ile Val
                                   40                               45                               50

tcc ggc gct gat gaa acc tac tgc gga ttc tcc gtc acc atg ccg tct 307
Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser Val Thr Met Pro Ser
                                   55                               60                               65

aaa ttc gca gct ctt gaa ttc gcc gac gaa gta acc gaa cgc gcc tgc 355
Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val Thr Glu Arg Ala Cys
                                   70                               75                               80                               85

gcc atc ggc tcc gca aac acc ttg ctg cgc acg gcc acc gga tgg cgc 403
Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr Ala Thr Gly Trp Arg
                                   90                               95                               100

gcc gac aac acc gac gtc gac ggc atc agg gga gct ctc ggt gaa ctc 451
Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly Ala Leu Gly Glu Leu
                                   105                               110                               115

ctc ggc ggc gca tca ctg gcc ggc aaa cac gcc atc gtc atc ggc tcc 499
Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala Ile Val Ile Gly Ser
                                   120                               125                               130

ggc ggc acc gca cgc ccc gcc atc tgg gca ctc atc gaa gcc ggg gtc 547
Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu Ile Glu Ala Gly Val
                                   135                               140                               145

gcc cgg atc acg gtg ctc aac cgc tcc gat cgc acc gcc gaa ctg caa 595
Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg Thr Ala Glu Leu Gln
                                   150                               155                               160                               165

acg ctt ttc gac gaa acc ccc acc acc ttg gcc tac gcc ccg ctc gag 643
Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala Tyr Ala Pro Leu Glu
                                   170                               175                               180

cat ctc cac atc gaa gcc gac gtc gta gtc tct aca gtg ccc tcc gca 691
His Leu His Ile Glu Ala Asp Val Val Val Ser Thr Val Pro Ser Ala
                                   185                               190                               195

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gca atc gca ggc ctc gaa gac acc ctt gcg atc gcc cca gtc ctc gac 739  
 Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile Ala Pro Val Leu Asp  
           200                          205                          210

gtc atc tac gac ccc tgg cca aca cca ctc gta gaa gtc aca cga gcc 787  
 Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val Glu Val Thr Arg Ala  
           215                          220                          225

aaa ggc ctc aaa gct gtc gga ggc cac gtc atg ctg gca cac cag tcc 835  
 Lys Gly Leu Lys Ala Val Gly Gly His Val Met Leu Ala His Gln Ser  
           230                          235                          240                          245

tac gga cag ttt gaa caa ttc acc gga atg gat gca ccc cgc gat gcc 883  
 Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp Ala Pro Arg Asp Ala  
                           250                          255                          260

atg cgt gag gct ttg gaa gag tct tta ggc atc tca gaa gaa cac 928  
 Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile Ser Glu Glu His  
                           265                          270                          275

taagtcctccg ccacctcctc aac 951

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 440  
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Glu His Ser Lys Ser Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu  
           20                          25                          30

Gly Leu Asp Gln Trp Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met  
           35                          40                          45

Leu Pro Gly Ile Val Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser  
           50                          55                          60

Val Thr Met Pro Ser Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val  
   65                          70                          75                          80

Thr Glu Arg Ala Cys Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr  
           85                          90                          95

Ala Thr Gly Trp Arg Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly  
           100                          105                          110

Ala Leu Gly Glu Leu Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala  
           115                          120                          125

Ile Val Ile Gly Ser Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu  
           130                          135                          140

Ile Glu Ala Gly Val Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg  
   145                          150                          155                          160

Thr Ala Glu Leu Gln Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala  
           165                          170                          175

Tyr Ala Pro Leu Glu His Leu His Ile Glu Ala Asp Val Val Val Ser  
 180 185 190  
 Thr Val Pro Ser Ala Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile  
 195 200 205  
 Ala Pro Val Leu Asp Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val  
 210 215 220  
 Glu Val Thr Arg Ala Lys Gly Leu Lys Ala Val Gly Gly His Val Met  
 225 230 235 240  
 Leu Ala His Gln Ser Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp  
 245 250 255  
 Ala Pro Arg Asp Ala Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile  
 260 265 270  
 Ser Glu Glu His  
 275

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 <211> 693  
 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(670)  
 <223> RXA01699

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 aaaaacattg aggaacgaat gaaattcgaa ggttttagagg atg gag cgt aat gaa 115  
 Met Glu Arg Asn Glu 5  
 1  
 gtg aat gat caa att cac tta gat cat caa tca gat gac acc tct gaa 163  
 Val Asn Asp Gln Ile His Leu Asp His Gln Ser Asp Asp Thr Ser Glu 20  
 10 15  
 tgc tcc tgc ccg atc gtg gtt ctt gtg ggt ttg cca gga gct gga aaa 211  
 Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu Pro Gly Ala Gly Lys 35  
 25 30  
 tcc acc att gga cgt cga tta gcg cgc gcc tta aac act gaa ctc gtc 259  
 Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu Asn Thr Glu Leu Val 50  
 40 45  
 gac tcc gac gaa ctg att gag cgc gcc acc gga aaa gcc tgt ggc gcc 307  
 Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly Lys Ala Cys Gly Ala 65  
 55 60  
 gtg ttc agc gag ctc ggc gag cca gcc ttc cgc gag ctc gag gcc atc 355  
 Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg Glu Leu Glu Ala Ile 85  
 70 75 80  
 cac gtg gcc gaa gca ctg aaa tcc tcc gga gtg gtg agc ttg gga ggc 403



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<400> 442
Met Glu Arg Asn Glu Val Asn Asp Gln Ile His Leu Asp His Gln Ser
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Asp Asp Thr Ser Glu Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu
          20          25          30

Pro Gly Ala Gly Lys Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu
          35          40          45

Asn Thr Glu Leu Val Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly
 50          55          60

Lys Ala Cys Gly Ala Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg
 65          70          75          80

Glu Leu Glu Ala Ile His Val Ala Glu Ala Leu Lys Ser Ser Gly Val
          85          90          95

Val Ser Leu Gly Gly Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu
          100          105          110

Leu Lys Gly Gln Asp Val Val Trp Ile Asp Val Pro Val Glu Glu Gly
          115          120          125

Ile Arg Arg Thr Ala Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala

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130	135	140	
Asp Pro Ala Glu His Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu			
145	150	155	160
Tyr Glu Glu Val Ala Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro			
	165	170	175
Gln Gln Val Val Ala Ala Val Leu His His Leu Glu Ile Asp			
	180	185	190

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (97)..(936)  
 <223> RXA00952

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 Met Ser Arg Tyr Asp Asp  
 1 5

ctt ttt gca cgc ctc gac acg gca ggg gag ggc gcc ttt gtt ccc ttc 162  
 Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu Gly Ala Phe Val Pro Phe  
 10 15 20

atc atg ctg agc gac cct tca cca gag gag gct ttc cag atc atc tcc 210  
 Ile Met Leu Ser Asp Pro Ser Pro Glu Glu Ala Phe Gln Ile Ile Ser  
 25 30 35

aca gca atc gaa gct ggc gca gat gca ctg gaa ctt ggc gta cct ttc 258  
 Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu Glu Leu Gly Val Pro Phe  
 40 45 50

tcc gac cca gtt gcc gat ggc ccc acc gtc gcg gaa tcc cac ctc cgc 306  
 Ser Asp Pro Val Ala Asp Gly Pro Thr Val Ala Glu Ser His Leu Arg  
 55 60 65 70

gca ctc gac ggc ggc gcc acc gta gac agc gca ctc gag cag atc aag 354  
 Ala Leu Asp Gly Gly Ala Thr Val Asp Ser Ala Leu Glu Gln Ile Lys  
 75 80 85

cgc gtg cgc gca gcc tac cca gag gtt ccc atc gga atg ctc atc tac 402  
 Arg Val Arg Ala Ala Tyr Pro Glu Val Pro Ile Gly Met Leu Ile Tyr  
 90 95 100

ggc aac gtt cct ttc acc cgt ggc ttg gat cgc ttc tac caa gag ttc 450  
 Gly Asn Val Pro Phe Thr Arg Gly Leu Asp Arg Phe Tyr Gln Glu Phe  
 105 110 115

gct gaa gct ggc gca gac tcc atc ctc ctg cca gac gtc cca gtc cga 498  
 Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu Pro Asp Val Pro Val Arg  
 120 125 130

gaa ggc gca ccg ttt tct gca gca gct gca gca gcc gga att gat ccc 546  
 Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala Ala Ala Gly Ile Asp Pro  
 135 140 145 150  
  
 att tac atc gct ccg gcc aac gcc agc gag aaa acc ctc gag ggt gtc 594  
 Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu Lys Thr Leu Glu Gly Val  
 155 160 165  
  
 tcc gcc gca tca aag ggc tac atc tac gcc atc tcc cgc gac ggc gtc 642  
 Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala Ile Ser Arg Asp Gly Val  
 170 175 180  
  
 acc ggc acc gaa cgt gaa tca tcc acc gac ggc ctg tcc gca gtg gtg 690  
 Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp Gly Leu Ser Ala Val Val  
 185 190 195  
  
 gac aac atc aag aaa ttt gat ggc gca ccc atc ctc ttg ggc ttc ggc 738  
 Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro Ile Leu Leu Gly Phe Gly  
 200 205 210  
  
 atc tca tcc cct cag cac gtg gca gac gcg att gca gcg ggt gct tcc 786  
 Ile Ser Ser Pro Gln His Val Ala Asp Ala Ile Ala Ala Gly Ala Ser  
 215 220 225 230  
  
 ggt gcg atc acg ggt tcc gcg atc acc aag atc att gct tcc cac tgc 834  
 Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys Ile Ile Ala Ser His Cys  
 235 240 245  
  
 gaa ggt gag cac ccg aac ccg tcc acc att cga gat atg gac ggt ttg 882  
 Glu Gly Glu His Pro Asn Pro Ser Thr Ile Arg Asp Met Asp Gly Leu  
 250 255 260  
  
 aag aag gat ctc act gag ttc atc tct gcg atg aag gca gcg acc aag 930  
 Lys Lys Asp Leu Thr Glu Phe Ile Ser Ala Met Lys Ala Ala Thr Lys  
 265 270 275  
  
 aag gtt taggccttta aatgtggcaa tgt 959  
 Lys Val  
 280

&lt;210&gt; 444

&lt;211&gt; 280

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 444

Met Ser Arg Tyr Asp Asp Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu  
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Gly Ala Phe Val Pro Phe Ile Met Leu Ser Asp Pro Ser Pro Glu Glu  
 20 25 30

Ala Phe Gln Ile Ile Ser Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu  
 35 40 45

Glu Leu Gly Val Pro Phe Ser Asp Pro Val Ala Asp Gly Pro Thr Val  
 50 55 60

Ala Glu Ser His Leu Arg Ala Leu Asp Gly Gly Ala Thr Val Asp Ser  
 65 70 75 80

Ala Leu Glu Gln Ile Lys Arg Val Arg Ala Ala Tyr Pro Glu Val Pro  
85 90 95

Ile Gly Met Leu Ile Tyr Gly Asn Val Pro Phe Thr Arg Gly Leu Asp  
100 105 110

Arg Phe Tyr Gln Glu Phe Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu  
115 120 125

Pro Asp Val Pro Val Arg Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala  
130 135 140

Ala Ala Gly Ile Asp Pro Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu  
145 150 155 160

Lys Thr Leu Glu Gly Val Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala  
165 170 175

Ile Ser Arg Asp Gly Val Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp  
180 185 190

Gly Leu Ser Ala Val Val Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro  
195 200 205

Ile Leu Leu Gly Phe Gly Ile Ser Ser Pro Gln His Val Ala Asp Ala  
210 215 220

Ile Ala Ala Gly Ala Ser Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys  
225 230 235 240

Ile Ile Ala Ser His Cys Glu Gly Glu His Pro Asn Pro Ser Thr Ile  
245 250 255

Arg Asp Met Asp Gly Leu Lys Lys Asp Leu Thr Glu Phe Ile Ser Ala  
260 265 270

Met Lys Ala Ala Thr Lys Lys Val  
275 280

<210> 445  
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<223> RXN00956

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accatctcca cattccatta ctaaagggttt aaataggatc atg act gaa aaa gaa 115  
Met Thr Glu Lys Glu  
1 5  
aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163  
Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly  
10 15 20

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag	211
Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu	
25 30 35	
aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc	259
Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu	
40 45 50	
ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa	307
Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu	
55 60 65	
tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc	355
Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile	
70 75 80 85	
ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac	403
Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn	
90 95 100	
cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc	451
Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg	
105 110 115	
atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc	499
Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu	
120 125 130	
gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag	547
Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys	
135 140 145	
gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc	595
Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly	
150 155 160 165	
gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc	643
Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala	
170 175 180	
gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac	691
Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His	
185 190 195	
tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg	739
Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val	
200 205 210	
cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta	787
Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu	
215 220 225	
gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt	835
Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly	
230 235 240 245	
ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt	883
Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly	
250 255 260	

gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc ggc 931  
 Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly  
                   265                  270                  275

aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc 979  
 Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly  
                   280                  285                  290

acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc  
 1027  
 Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser  
                   295                  300                  305

tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac  
 1075  
 Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His  
 310                  315                  320                  325

gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac  
 1123  
 Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp  
                   330                  335                  340

gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc  
 1171  
 Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile  
                   345                  350                  355

atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc  
 1219  
 Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg  
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gcc aag acc gcc gaa gta  
 1237  
 Ala Lys Thr Ala Glu Val  
                   375

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 <211> 379  
 <212> PRT  
 <213> Corynebacterium glutamicum

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Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala  
                   20                  25                  30

Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu  
                   35                  40                  45

Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro  
                   50                  55                  60

Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys  
                   65                  70                  75                  80

Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly

85										90					95				
Ala	His	Lys	Thr	Asn	Gln	Val	Ile	Gly	Gln	Val	Leu	Leu	Ala	Lys	Arg				
			100					105					110						
Met	Gly	Lys	Thr	Arg	Ile	Ile	Ala	Glu	Thr	Gly	Ala	Gly	Gln	His	Gly				
		115					120					125							
Thr	Ala	Thr	Ala	Leu	Ala	Cys	Ala	Leu	Met	Gly	Leu	Glu	Cys	Val	Val				
	130					135					140								
Tyr	Met	Gly	Ala	Lys	Asp	Val	Ala	Arg	Gln	Gln	Pro	Asn	Val	Tyr	Arg				
145					150					155					160				
Met	Gln	Leu	His	Gly	Ala	Lys	Val	Ile	Pro	Val	Glu	Ser	Gly	Ser	Gly				
				165					170					175					
Thr	Leu	Lys	Asp	Ala	Val	Asn	Glu	Ala	Leu	Arg	Asp	Trp	Thr	Ala	Thr				
			180					185					190						
Phe	His	Glu	Ser	His	Tyr	Leu	Leu	Gly	Thr	Pro	Ala	Gly	Pro	His	Pro				
		195					200					205							
Phe	Pro	Thr	Ile	Val	Arg	Glu	Phe	His	Lys	Val	Ile	Ser	Glu	Glu	Ala				
	210					215					220								
Lys	Ala	Gln	Met	Leu	Glu	Arg	Thr	Gly	Lys	Leu	Pro	Asp	Val	Val	Val				
225					230					235				240					
Ala	Cys	Val	Gly	Gly	Gly	Ser	Asn	Ala	Ile	Gly	Met	Phe	Ala	Asp	Phe				
				245					250					255					
Ile	Asp	Asp	Glu	Gly	Val	Glu	Leu	Val	Gly	Ala	Glu	Pro	Ala	Gly	Glu				
			260					265					270						
Gly	Leu	Asp	Ser	Gly	Lys	His	Gly	Ala	Thr	Ile	Thr	Asn	Gly	Gln	Ile				
		275					280					285							
Gly	Ile	Leu	His	Gly	Thr	Arg	Ser	Tyr	Leu	Met	Arg	Asn	Ser	Asp	Gly				
	290					295					300								
Gln	Val	Glu	Glu	Ser	Tyr	Ser	Ile	Ser	Ala	Gly	Leu	Asp	Tyr	Pro	Gly				
305					310					315					320				
Val	Gly	Pro	Gln	His	Ala	His	Leu	His	Ala	Thr	Gly	Arg	Ala	Thr	Tyr				
				325					330					335					
Val	Gly	Ile	Thr	Asp	Ala	Glu	Ala	Leu	Gln	Ala	Phe	Gln	Tyr	Leu	Ala				
			340					345					350						
Arg	Tyr	Glu	Gly	Ile	Ile	Pro	Ala	Leu	Glu	Ser	Ser	His	Ala	Phe	Ala				
		355					360					365							
Tyr	Ala	Leu	Lys	Arg	Ala	Lys	Thr	Ala	Glu	Val									
	370					375													

&lt;210&gt; 447

&lt;211&gt; 1231

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1231)

&lt;223&gt; FRXA00956

&lt;400&gt; 447

```

gccggtgcag gcacgtgggc tggggcgaaa gacgccggcg cgctgctgaa aatttttagcg 60

accatctcca cattccatta ctaaagggttt aaataggatc atg act gaa aaa gaa 115
                                         Met Thr Glu Lys Glu
                                         1                               5

aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163
Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly
                               10                               15                               20

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag 211
Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu
                               25                               30                               35

aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc 259
Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu
                               40                               45                               50

ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa 307
Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu
                               55                               60                               65

tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc 355
Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile
                               70                               75                               80                               85

ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac 403
Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn
                               90                               95                               100

cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc 451
Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg
                               105                               110                               115

atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc 499
Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu
                               120                               125                               130

gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag 547
Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys
                               135                               140                               145

gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc 595
Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly
                               150                               155                               160                               165

gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc 643
Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala
                               170                               175                               180

gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac 691
Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His
                               185                               190                               195

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tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg 739  
 Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val  
 200 205 210

cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta 787  
 Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu  
 215 220 225

gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt 835  
 Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly  
 230 235 240 245

ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt 883  
 Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly  
 250 255 260

gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc ggc 931  
 Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly  
 265 270 275

aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc 979  
 Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly  
 280 285 290

acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc  
 1027  
 Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser  
 295 300 305

tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac  
 1075  
 Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His  
 310 315 320 325

gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac  
 1123  
 Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp  
 330 335 340

gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc  
 1171  
 Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile  
 345 350 355

atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc  
 1219  
 Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg  
 360 365 370

gcc aag acc gcc  
 1231  
 Ala Lys Thr Ala  
 375

&lt;210&gt; 448

&lt;211&gt; 377

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 448

Met Thr Glu Lys Glu Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr  
 1 5 10 15  
 Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala  
 20 25 30  
 Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu  
 35 40 45  
 Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro  
 50 55 60  
 Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys  
 65 70 75 80  
 Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly  
 85 90 95  
 Ala His Lys Thr Asn Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg  
 100 105 110  
 Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly  
 115 120 125  
 Thr Ala Thr Ala Leu Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val  
 130 135 140  
 Tyr Met Gly Ala Lys Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg  
 145 150 155 160  
 Met Gln Leu His Gly Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly  
 165 170 175  
 Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr  
 180 185 190  
 Phe His Glu Ser His Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro  
 195 200 205  
 Phe Pro Thr Ile Val Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala  
 210 215 220  
 Lys Ala Gln Met Leu Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val  
 225 230 235 240  
 Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe  
 245 250 255  
 Ile Asp Asp Glu Gly Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu  
 260 265 270  
 Gly Leu Asp Ser Gly Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile  
 275 280 285  
 Gly Ile Leu His Gly Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly  
 290 295 300  
 Gln Val Glu Glu Ser Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly  
 305 310 315 320  
 Val Gly Pro Gln His Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr

	325		330		335
Val Gly Ile Thr Asp Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala					
	340		345		350
Arg Tyr Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala					
	355		360		365
Tyr Ala Leu Lys Arg Ala Lys Thr Ala					
	370		375		

&lt;210&gt; 449

&lt;211&gt; 1401

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1378)

&lt;223&gt; RXA00064

&lt;400&gt; 449

tcccctaataa cgtctagagt agtggccttga ggtcactgct cttttttttgt gccctttttt 60

gggccgtcta	ttttgccacc	acatgcggag	gtacgcagtt	atg	agt	tca	ggt	tcg	115
				Met	Ser	Ser	Val	Ser	
				1				5	

ctg	cag	gat	ttt	gat	gca	gag	cga	att	ggc	ttg	ttc	cac	gag	gac	att	163
Leu	Gln	Asp	Phe	Asp	Ala	Glu	Arg	Ile	Gly	Leu	Phe	His	Glu	Asp	Ile	
				10					15					20		

aag	cgc	aag	ttt	gat	gag	ctc	aag	tca	aaa	aat	ctg	aag	ctg	gat	ctt	211
Lys	Arg	Lys	Phe	Asp	Glu	Leu	Lys	Ser	Lys	Asn	Leu	Lys	Leu	Asp	Leu	
			25					30					35			

act	cgc	ggc	aag	cct	tcg	tcg	gag	cag	ttg	gat	ttc	gct	gat	gag	ttg	259
Thr	Arg	Gly	Lys	Pro	Ser	Ser	Glu	Gln	Leu	Asp	Phe	Ala	Asp	Glu	Leu	
		40					45					50				

ttg	gcg	ttg	cct	ggc	aag	ggc	gat	ttc	aag	gct	gcg	gat	ggc	act	gat	307
Leu	Ala	Leu	Pro	Gly	Lys	Gly	Asp	Phe	Lys	Ala	Ala	Asp	Gly	Thr	Asp	
	55					60					65					

gtc	cgt	aac	tat	ggc	ggg	ctg	gat	ggc	atc	ggt	gat	att	cgc	cag	att	355
Val	Arg	Asn	Tyr	Gly	Gly	Leu	Asp	Gly	Ile	Val	Asp	Ile	Arg	Gln	Ile	
	70				75					80					85	

tgg	gcg	gat	ttg	ctg	ggc	ggt	ggt	cct	gtg	gag	cag	gtc	ttg	gcg	ggg	gat	403
Trp	Ala	Asp	Leu	Leu	Gly	Val	Pro	Val	Glu	Gln	Val	Leu	Ala	Gly	Asp		
				90					95					100			

gct	tcg	agc	ttg	aac	atc	atg	ttt	gat	gtg	atc	agc	tgg	tcg	tac	att	451
Ala	Ser	Ser	Leu	Asn	Ile	Met	Phe	Asp	Val	Ile	Ser	Trp	Ser	Tyr	Ile	
			105					110					115			

ttc	ggc	aac	aat	gat	tcg	ggt	cag	cct	tgg	tcg	aag	gaa	gaa	acc	ggt	499
Phe	Gly	Asn	Asn	Asp	Ser	Val	Gln	Pro	Trp	Ser	Lys	Glu	Glu	Thr	Val	
		120					125					130				

aag tgg att tgc cct gtt ccg ggc tat gat cgc cat ttc tcc atc acg Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg His Phe Ser Ile Thr 135 140 145	547
gag cgt ttc ggc ttt gag atg att tct gtg cca atg aat gaa gac ggc Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro Met Asn Glu Asp Gly 150 155 160 165	595
cct gat atg gat gct gtt gag gaa ttg gtg aag aat ccg cag gtt aag Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys Asn Pro Gln Val Lys 170 175 180	643
ggc atg tgg gtt gtt ccg gtg ttt tct aac ccg act ggt ttc acg gtg Gly Met Trp Val Val Pro Val Phe Ser Asn Pro Thr Gly Phe Thr Val 185 190 195	691
aca gaa gac gtc gca aag cgt cta agc gca atg gaa acc gca gct ccg Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met Glu Thr Ala Ala Pro 200 205 210	739
gac ttc cgc gtt gtg tgg gat aat gcc tac gcc gtt cat acg ctg acc Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala Val His Thr Leu Thr 215 220 225	787
gat gaa ttc cct gag gtt atc gat atc gtc ggg ctt ggt gag gcc gct Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly Leu Gly Glu Ala Ala 230 235 240 245	835
ggc aac ccg aac cgt ttc tgg gcg ttc act tct act tcg aag atc act Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser Thr Ser Lys Ile Thr 250 255 260	883
ctc gcg ggt gcg ggc gtg tcg ttc ttc ctc acc tct gcg gag aac cgc Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr Ser Ala Glu Asn Arg 265 270 275	931
aag tgg tac acc ggc cat gcg ggt atc cgt ggc att ggc cct aac aag Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly Ile Gly Pro Asn Lys 280 285 290	979
gtc aat cag ttg gct cat gcg cgt tac ttt ggc gat gct gag gga gtg 1027 Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly Asp Ala Glu Gly Val 295 300 305	
cgc gcg gtg atg cgt aag cat gct gcg tcg ttg gct ccg aag ttc aac 1075 Arg Ala Val Met Arg Lys His Ala Ala Ser Leu Ala Pro Lys Phe Asn 310 315 320 325	
aag gtt ctg gag att ctg gat tct cgc ctt gct gag tac ggt gtc gcg 1123 Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala Glu Tyr Gly Val Ala 330 335 340	
cag tgg act gtc cct gcg ggc ggt tac ttc att tcc ctt gat gtg gtt 1171 Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile Ser Leu Asp Val Val 345 350 355	

cct ggt acg gcg tct cgc gtg gct gag ttg gct aag gaa gcc ggc atc  
 1219  
 Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala Lys Glu Ala Gly Ile  
           360                          365                          370

gcg ttg acg ggt gcg ggt tct tct tac ccg ctg cgt cag gat ccg gag  
 1267  
 Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu Arg Gln Asp Pro Glu  
           375                          380                          385

aac aaa aat ctc cgt ttg gca ccg tcg ctg cct cca gtt gag gaa ctt  
 1315  
 Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro Pro Val Glu Glu Leu  
 390                          395                          400                          405

gag gtt gcc atg gat ggc gtg gct acc tgt gtg ctg ttg gca gca gcg  
 1363  
 Glu Val Ala Met Asp Gly Val Ala Thr Cys Val Leu Leu Ala Ala Ala  
                           410                          415                          420

gag cat tac gct aac taaaagtgaac tacagcggag aca  
 1401  
 Glu His Tyr Ala Asn  
                           425

<210> 450

<211> 426

<212> PRT

<213> Corynebacterium glutamicum

<400> 450

Met Ser Ser Val Ser Leu Gln Asp Phe Asp Ala Glu Arg Ile Gly Leu  
   1                          5                          10                          15

Phe His Glu Asp Ile Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn  
                           20                          25                          30

Leu Lys Leu Asp Leu Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp  
                           35                          40                          45

Phe Ala Asp Glu Leu Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala  
                           50                          55                          60

Ala Asp Gly Thr Asp Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val  
   65                          70                          75                          80

Asp Ile Arg Gln Ile Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln  
                           85                          90                          95

Val Leu Ala Gly Asp Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile  
                           100                          105                          110

Ser Trp Ser Tyr Ile Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser  
                           115                          120                          125

Lys Glu Glu Thr Val Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg  
                           130                          135                          140

His Phe Ser Ile Thr Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro  
   145                          150                          155                          160

Met Asn Glu Asp Gly Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys  
 165 170 175  
 Asn Pro Gln Val Lys Gly Met Trp Val Val Pro Val Phe Ser Asn Pro  
 180 185 190  
 Thr Gly Phe Thr Val Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met  
 195 200 205  
 Glu Thr Ala Ala Pro Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala  
 210 215 220  
 Val His Thr Leu Thr Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly  
 225 230 235 240  
 Leu Gly Glu Ala Ala Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser  
 245 250 255  
 Thr Ser Lys Ile Thr Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr  
 260 265 270  
 Ser Ala Glu Asn Arg Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly  
 275 280 285  
 Ile Gly Pro Asn Lys Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly  
 290 295 300  
 Asp Ala Glu Gly Val Arg Ala Val Met Arg Lys His Ala Ala Ser Leu  
 305 310 315 320  
 Ala Pro Lys Phe Asn Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala  
 325 330 335  
 Glu Tyr Gly Val Ala Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile  
 340 345 350  
 Ser Leu Asp Val Val Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala  
 355 360 365  
 Lys Glu Ala Gly Ile Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu  
 370 375 380  
 Arg Gln Asp Pro Glu Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro  
 385 390 395 400  
 Pro Val Glu Glu Leu Glu Val Ala Met Asp Gly Val Ala Thr Cys Val  
 405 410 415  
 Leu Leu Ala Ala Ala Glu His Tyr Ala Asn  
 420 425

&lt;210&gt; 451

&lt;211&gt; 1143

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1120)

&lt;223&gt; RXN00448

&lt;400&gt; 451

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ccatttacct tcaactaagg tagccgtaac tgcaaagctc aggccatcct cttcagtggt 60

catagagata accgtagtag gtatgtgccca cacttggtcag gtg act acc aaa gac 115
                               Val Thr Thr Lys Asp
                               1                               5

att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163
Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser
                10                15                20

ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211
Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
                25                30                35

cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val
                40                45                50

tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala
                55                60                65

ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg ctt ctc gac 355
Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser Leu Leu Asp
                70                75                80                85

gcc gtc cac acc cac gca cca aac aac ggc ttc acc gac gtc gta tcc 403
Ala Val His Thr His Ala Pro Asn Asn Gly Phe Thr Asp Val Val Ser
                90                95                100

gta aaa acc gcc gtc tac gac gca gta aaa gcc cgc aac atg caa cac 451
Val Lys Thr Ala Val Tyr Asp Ala Val Lys Ala Arg Asn Met Gln His
                105                110                115

cgt tat gtg gga tcc cac ccc atg gca ggc acc gcc aac tcc ggc tgg 499
Arg Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp
                120                125                130

agc gca tcc atg gac gga ctg ttc aaa cga gca gta tgg gtg gtc acc 547
Ser Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr
                135                140                145

ttc gac cag ctt ttc gac ggc acc gac atc aac tcc acc tgg atc agc 595
Phe Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser
                150                155                160                165

atc tgg aaa gac gtc gtc caa atg gca ctc gcc gtg ggc gct gaa gtt 643
Ile Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val
                170                175                180

gtc cca tcc cga gtt ggc cca cac gat gca gca gca gca cga gtg tct 691
Val Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Ala Arg Val Ser
                185                190                195

cat tta aca cac atc ctg gct gaa acc ctc gcc atc gtc ggt gac aac 739
His Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn
                200                205                210

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ggt ggc gca ctg tct ctc tct tta gcc gct ggc agc tac cgc gac tcc 787  
 Gly Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser  
 215 220 225  
  
 acc cgc gtt gca ggc acc gac cca gga ctc gtc cgc gcc atg tgt gaa 835  
 Thr Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala M t Cys Glu  
 230 235 240 245  
  
 agc aac gcc ggc cca ctg gtc aaa gcc ctc gac gaa gca ctg gcg atc 883  
 Ser Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile  
 250 255 260  
  
 ctc cac gaa gcc cgc gaa ggc ctc acc gca gaa cag cca aac atc gag 931  
 Leu His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu  
 265 270 275  
  
 caa ctt gcc gac aac ggc tac cga tcc cgc atc cgc tac gaa gcc cgc 979  
 Gln Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg  
 280 285 290  
  
 tcc ggc cag cga cgc gcc aaa gaa tcc gtt agc cct acc atc acc tca  
 1027  
 Ser Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser  
 295 300 305  
  
 tcc agg cca gtg ctc cgt ctc cac ccg ggc aca cca aac tgg gag aag  
 1075  
 Ser Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys  
 310 315 320 325  
  
 cag ctc atc cac gct gaa acc ctc ggc gca cgg atc gaa gtg ttc  
 1120  
 Gln Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe  
 330 335 340

tagttttatc ggctgatgat tct  
 1143

<210> 452  
 <211> 340  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 452  
 Val Thr Thr Lys Asp Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly  
 1 5 10 15  
  
 Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser  
 20 25 30  
  
 Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp  
 35 40 45  
  
 Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala  
 50 55 60  
  
 Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile  
 65 70 75 80  
  
 Asp Ser Leu Leu Asp Ala Val His Thr His Ala Pro Asn Asn Gly Phe



85										90					95				
Thr	Asp	Val	Val	Ser	Val	Lys	Thr	Ala	Val	Tyr	Asp	Ala	Val	Lys	Ala				
			100					105					110						
Arg	Asn	Met	Gln	His	Arg	Tyr	Val	Gly	Ser	His	Pro	Met	Ala	Gly	Thr				
		115					120					125							
Ala	Asn	Ser	Gly	Trp	Ser	Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala				
		130				135					140								
Val	Trp	Val	Val	Thr	Phe	Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn				
					150					155				160					
Ser	Thr	Trp	Ile	Ser	Ile	Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala				
				165					170					175					
Val	Gly	Ala	Glu	Val	Val	Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala				
			180					185					190						
Ala	Ala	Arg	Val	Ser	His	Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala				
		195					200					205							
Ile	Val	Gly	Asp	Asn	Gly	Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly				
		210				215					220								
Ser	Tyr	Arg	Asp	Ser	Thr	Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val				
					230					235				240					
Arg	Ala	Met	Cys	Glu	Ser	Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp				
				245					250					255					
Glu	Ala	Leu	Ala	Ile	Leu	His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu				
			260					265					270						
Gln	Pro	Asn	Ile	Glu	Gln	Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile				
		275					280					285							
Arg	Tyr	Glu	Ala	Arg	Ser	Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser				
		290				295					300								
Pro	Thr	Ile	Thr	Ser	Ser	Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr				
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Pro	Asn	Trp	Glu	Lys	Gln	Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg				
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Ile	Glu	Val	Phe																
			340																

&lt;210&gt; 453

&lt;211&gt; 689

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(666)

&lt;223&gt; FRXA00448

&lt;400&gt; 453

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Tyr	Val	Gly	Ser	His	Pro	Met	Ala	Gly	Thr	Ala	Asn	Ser	Gly	Trp	Ser		
1				5				10					15				
gca	tcc	atg	gac	gga	ctg	ttc	aaa	cga	gca	gta	tgg	gtg	gtc	acc	ttc		96
Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala	Val	Trp	Val	Val	Thr	Phe		
			20				25					30					
gac	cag	ctt	ttc	gac	ggc	acc	gac	atc	aac	tcc	acc	tgg	atc	agc	atc		144
Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn	Ser	Thr	Trp	Ile	Ser	Ile		
		35				40					45						
tgg	aaa	gac	gtc	gtc	caa	atg	gca	ctc	gcc	gtg	ggc	gct	gaa	gtt	gtc		192
Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala	Val	Gly	Ala	Glu	Val	Val		
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cca	tcc	cga	gtt	ggc	cca	cac	gat	gca	gca	gca	gca	cga	gtg	tct	cat		240
Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala	Ala	Ala	Arg	Val	Ser	His		
	65				70					75					80		
tta	aca	cac	atc	ctg	gct	gaa	acc	ctc	gcc	atc	gtc	ggt	gac	aac	ggt		288
Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala	Ile	Val	Gly	Asp	Asn	Gly		
			85						90					95			
ggc	gca	ctg	tct	ctc	tct	tta	gcc	gct	ggc	agc	tac	cgc	gac	tcc	acc		336
Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly	Ser	Tyr	Arg	Asp	Ser	Thr		
			100				105						110				
cgc	gtt	gca	ggc	acc	gac	cca	gga	ctc	gtc	cgc	gcc	atg	tgt	gaa	agc		384
Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val	Arg	Ala	Met	Cys	Glu	Ser		
	115						120					125					
aac	gcc	ggc	cca	ctg	gtc	aaa	gcc	ctc	gac	gaa	gca	ctg	gcg	atc	ctc		432
Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Ile	Leu		
	130					135					140						
cac	gaa	gcc	cgc	gaa	ggc	ctc	acc	gca	gaa	cag	cca	aac	atc	gag	caa		480
His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu	Gln	Pro	Asn	Ile	Glu	Gln		
	145				150					155					160		
ctt	gcc	gac	aac	ggc	tac	cga	tcc	cgc	atc	cgc	tac	gaa	gcc	cgc	tcc		528
Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile	Arg	Tyr	Glu	Ala	Arg	Ser		
			165					170						175			
ggc	cag	cga	cgc	gcc	aaa	gaa	tcc	gtt	agc	cct	acc	atc	acc	tca	tcc		576
Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser	Pro	Thr	Ile	Thr	Ser	Ser		
			180				185						190				
agg	cca	gtg	ctc	cgt	ctc	cac	ccg	ggc	aca	cca	aac	tgg	gag	aag	cag		624
Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr	Pro	Asn	Trp	Glu	Lys	Gln		
		195				200					205						
ctc	atc	cac	gct	gaa	acc	ctc	ggc	gca	cgg	atc	gaa	gtg	ttc				666
Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg	Ile	Glu	Val	Phe				
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 <213> Corynebacterium glutamicum

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 Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr Phe  
                   20                  25                  30  
 Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser Ile  
                   35                  40                  45  
 Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val Val  
                   50                  55                  60  
 Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Ala Arg Val Ser His  
   65                  70                  75                  80  
 Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn Gly  
                   85                  90                  95  
 Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser Thr  
                   100                  105                  110  
 Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu Ser  
                   115                  120                  125  
 Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile Leu  
   130                  135                  140  
 His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu Gln  
   145                  150                  155                  160  
 Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg Ser  
                   165                  170                  175  
 Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser Ser  
                   180                  185                  190  
 Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys Gln  
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 Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe  
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 <223> FRXA00452

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Val Thr Thr Lys Asp  
1 5

att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163  
Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly S r  
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ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211  
Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn  
25 30 35

cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259  
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val  
40 45 50

tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307  
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala  
55 60 65

ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg 346  
Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser  
70 75 80

&lt;210&gt; 456

&lt;211&gt; 82

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 456

Val Thr Thr Lys Asp Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly  
1 5 10 15

Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser  
20 25 30

Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp  
35 40 45

Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala  
50 55 60

Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile  
65 70 75 80

Asp Ser

&lt;210&gt; 457

&lt;211&gt; 1248

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (1225)

&lt;223&gt; RXA00584

&lt;400&gt; 457

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				Met	His	Ser	Pro	Glu	5							
				1												
agg	caa	gaa	aaa	atg	agt	tct	cca	gtc	tca	ctc	gaa	aac	gcg	gcg	tca	163
Arg	Gln	Glu	Lys	Met	Ser	Ser	Pro	Val	Ser	Leu	Glu	Asn	Ala	Ala	Ser	
				10					15					20		
acc	agc	aac	aag	cgc	gtc	gtg	gct	ttc	cac	gag	ctg	cct	agc	cct	aca	211
Thr	Ser	Asn	Lys	Arg	Val	Val	Ala	Phe	His	Glu	Leu	Pro	Ser	Pro	Thr	
			25					30					35			
gat	ctc	atc	gcc	gca	aac	cca	ctg	aca	cca	aag	cag	gct	tcc	aag	gtg	259
Asp	Leu	Ile	Ala	Ala	Asn	Pro	Leu	Thr	Pro	Lys	Gln	Ala	Ser	Lys	Val	
		40					45					50				
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Glu	Gln	Asp	Arg	Gln	Asp	Ile	Ala	Asp	Ile	Phe	Ala	Gly	Asp	Asp	Asp	
	55					60					65					
cgc	ctc	gtt	gtc	gtt	gtg	gga	cct	tgc	tca	gtt	cac	gat	cct	gaa	gca	355
Arg	Leu	Val	Val	Val	Val	Gly	Pro	Cys	Ser	Val	His	Asp	Pro	Glu	Ala	
	70				75					80					85	
gcc	atc	gat	tac	gca	aac	cgc	ctg	gct	ccg	ctg	gca	aag	cgc	ctt	gat	403
Ala	Ile	Asp	Tyr	Ala	Asn	Arg	Leu	Ala	Pro	Leu	Ala	Lys	Arg	Leu	Asp	
				90					95					100		
cag	gac	ctc	aag	att	gtc	atg	cgc	gtg	tac	ttc	gag	aag	cct	cgc	acc	451
Gln	Asp	Leu	Lys	Ile	Val	Met	Arg	Val	Tyr	Phe	Glu	Lys	Pro	Arg	Thr	
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atc	gtc	gga	tgg	aag	gga	ttg	atc	aat	gat	cct	cac	ctc	aac	gaa	acc	499
Ile	Val	Gly	Trp	Lys	Gly	Leu	Ile	Asn	Asp	Pro	His	Leu	Asn	Glu	Thr	
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Tyr	Asp	Ile	Pro	Glu	Gly	Leu	Arg	Ile	Ala	Arg	Lys	Val	Leu	Ile	Asp	
	135					140					145					
gtt	gtg	aac	ctt	gat	ctc	cca	gtc	ggc	tgc	gaa	ttc	ctc	gaa	cca	aac	595
Val	Val	Asn	Leu	Asp	Leu	Pro	Val	Gly	Cys	Glu	Phe	Leu	Glu	Pro	Asn	
	150				155					160					165	
agc	cct	cag	tac	tac	gcc	gac	act	gtc	gca	tgg	gga	gca	atc	ggc	gct	643
Ser	Pro	Gln	Tyr	Tyr	Ala	Asp	Thr	Val	Ala	Trp	Gly	Ala	Ile	Gly	Ala	
				170					175					180		
cgt	acc	acc	gaa	tct	cag	gtg	cac	cgc	cag	ctg	gct	tct	ggg	atg	tct	691
Arg	Thr	Thr	Glu	Ser	Gln	Val	His	Arg	Gln	Leu	Ala	Ser	Gly	Met	Ser	
			185					190					195			
atg	cca	att	ggt	ttc	aag	aac	gga	act	gac	gga	aac	atc	cag	gtt	gca	739
Met	Pro	Ile														

tcc gac gac ggc gcg ctg agc gtc gtg gag acc gca ggc aac agc aac 835  
 Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr Ala Gly Asn Ser Asn  
 230 235 240 245

tcc cac atc att ttg cgc ggc ggt acc tcc ggc ccg aat cat gat gca 883  
 Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly Pro Asn His Asp Ala  
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 Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu  
 265 270 275

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 Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln  
 280 285 290

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 1027  
 Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu  
 295 300 305

gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag  
 1075  
 Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln  
 310 315 320 325

aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg  
 1123  
 Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val  
 330 335 340

tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc  
 1171  
 Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile  
 345 350 355

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 Ala Lys  
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<210> 458  
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His	Asp	Pro	Glu	Ala	Ala	Ile	Asp	Tyr	Ala	Asn	Arg	Leu	Ala	Pro	Leu	
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Ala	Lys	Arg	Leu	Asp	Gln	Asp	Leu	Lys	Ile	Val	Met	Arg	Val	Tyr	Phe	
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Glu	Lys	Pro	Arg	Thr	Ile	Val	Gly	Trp	Lys	Gly	Leu	Ile	Asn	Asp	Pro	
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His	Leu	Asn	Glu	Thr	Tyr	Asp	Ile	Pro	Glu	Gly	Leu	Arg	Ile	Ala	Arg	
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Lys	Val	Leu	Ile	Asp	Val	Val	Asn	Leu	Asp	Leu	Pro	Val	Gly	Cys	Glu	
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Phe	Leu	Glu	Pro	Asn	Ser	Pro	Gln	Tyr	Tyr	Ala	Asp	Thr	Val	Ala	Trp	
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Gly	Ala	Ile	Gly	Ala	Arg	Thr	Thr	Glu	Ser	Gln	Val	His	Arg	Gln	Leu	
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Ala	Ser	Gly	Met	Ser	Met	Pro	Ile	Gly	Phe	Lys	Asn	Gly	Thr	Asp	Gly	
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210					215					220						
Phe	Phe	Phe	Gly	Thr	Ser	Asp	Asp	Gly	Ala	Leu	Ser	Val	Val	Glu	Thr	
225					230					235					240	
Ala	Gly	Asn	Ser	Asn	Ser	His	Ile	Ile	Leu	Arg	Gly	Gly	Thr	Ser	Gly	
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Pro	Asn	His	Asp	Ala	Ala	Ser	Val	Glu	Ala	Val	Val	Glu	Lys	Leu	Gly	
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275					280					285						
Asp	His	Ile	Arg	Gln	Val	Glu	Val	Val	Arg	Glu	Ile	Ala	Glu	Gln	Ile	
290					295					300						
Ser	Gly	Gly	Ser	Glu	Ala	Val	Ala	Gly	Ile	Met	Ile	Glu	Ser	Phe	Leu	
305					310					315					320	
Val	Gly	Gly	Ala	Gln	Asn	Leu	Asp	Pro	Ala	Lys	Leu	Arg	Ile	Asn	Gly	
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Ile	Asp	Thr	Thr	Ile	Asp	Leu	Leu	Ala	Glu	Leu	Ala	Ala	Ala	Val	Arg	
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<223> RXA00579

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Met Arg Val Leu Ile  
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Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu  
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Glu Val Thr Gly Gln Ala Pro Val Val Val Pro Asn Asp Gln Glu Ile  
25 30 35  
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Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His  
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Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala Gly Val Ile Glu Arg  
55 60 65  
gca cgc gtt ccg att ttg ggt gtg tgt tta ggc cac cag ggc att gcg 355  
Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly His Gln Gly Ile Ala  
70 75 80 85  
ttg gcc tat ggc ggt gat gtt gat ttg gcg ccc agg ccg gtc cac ggt 403  
Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro Arg Pro Val His Gly  
90 95 100  
gag gtt tcg cag atc acc cat gat ggt tca ggt tta ttt gca ggc atc 451  
Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly Leu Phe Ala Gly Ile  
105 110 115  
cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc 499  
Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg  
120 125 130  
ttg ccg gag tca ttg aaa gct aca gct acc agc gat gat ggt ttg atc 547  
Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile  
135 140 145  
atg gca ttg gca cat gaa gtg ctt ccg cag tgg ggt gtg caa ttt cat 595  
Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His  
150 155 160 165



ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc 643  
 Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe  
 170 175 180

ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att 691  
 Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile  
 185 190 195

ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat 739  
 Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His  
 200 205 210

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ggt gat gcc agc ggt cct ctc gca cgc aca aaa acc cat aat gtc ggc 835  
 Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly  
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gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca 883  
 Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser  
 250 255 260

gtt gcg ccc ggt caa ggt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt 931  
 Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly  
 265 270 275

tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt 979  
 Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser  
 280 285 290

ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa  
 1027  
 Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu  
 295 300 305

tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt  
 1075  
 Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe  
 310 315 320 325

gaa gaa acc atc aag aag ctg cat aat ctt gtc gcc ccg cgg ata cct  
 1123  
 Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro  
 330 335 340

gcg tcc gga cac ctc gct ttg cag gtt cga gat tcc aaa gat gag tat  
 1171  
 Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr  
 345 350 355

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 1219  
 Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser  
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 Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala

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 gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc  
 1411  
 Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro  
 425                                      430                                      435  
 att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa  
 1459  
 Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu  
 440                                      445                                      450  
 atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg  
 1507  
 Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu  
 455                                      460                                      465  
 atg atc gtg gat ttg gtc cgc aac gac tta gcc cgc ggc gct ttg ccc  
 1555  
 Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro  
 470                                      475                                      480                                      485  
 acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca  
 1603  
 Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr  
 490                                      495                                      500  
 gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt  
 1651  
 Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser  
 505                                      510                                      515  
 ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt  
 1699  
 Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly  
 520                                      525                                      530  
 gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct  
 1747  
 Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala  
 535                                      540                                      545  
 cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc  
 1795  
 Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly  
 550                                      555                                      560                                      565  
 gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat  
 1843  
 Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn  
 570                                      575                                      580

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg  
1891

His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro  
585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat  
1939

Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn  
600 605 610

ttg ttt ggg gtt gaa ttc cca tgacgtacct cgtgtgggac ggt  
1983

Leu Phe Gly Val Glu Phe Pro  
615 620

<210> 460

<211> 620

<212> PRT

<213> Corynebacterium glutamicum

<400> 460

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20 25 30

Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser  
35 40 45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala  
50 55 60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly  
65 70 75 80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro  
85 90 95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly  
100 105 110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser  
115 120 125

Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser  
130 135 140

Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp  
145 150 155 160

Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln  
165 170 175

Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu  
180 185 190

Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu  
195 200 205

Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln  
 210 215 220  
 Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys  
 225 230 235 240  
 Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp  
 245 250 255  
 Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp  
 260 265 270  
 Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala  
 275 280 285  
 Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg  
 290 295 300  
 Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu  
 305 310 315 320  
 Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val  
 325 330 335  
 Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp  
 340 345 350  
 Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile  
 355 360 365  
 Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly  
 370 375 380  
 Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala  
 385 390 395 400  
 Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile  
 405 410 415  
 Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr  
 420 425 430  
 Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala  
 435 440 445  
 Gln Glu Asp Gln Glu Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp  
 450 455 460  
 Arg Ala Glu Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala  
 465 470 475 480  
 Arg Gly Ala Leu Pro Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val  
 485 490 495  
 Glu Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Glu  
 500 505 510  
 Leu Gly Pro Arg Ser Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly  
 515 520 525

Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp  
530 535 540

Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr  
545 550 555 560

Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu  
565 570 575

Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu  
580 585 590

Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser  
595 600 605

Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro  
610 615 620

<210> 461

<211> 747

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(724)

<223> RXA00958

<400> 461

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ccattgcgct tgctgctggg tccactttgg aggtcatccg atg aca cac gtt gtt 115  
Met Thr His Val Val  
1 5

ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163  
Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe  
10 15 20

gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211  
Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val  
25 30 35

gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259  
Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly  
40 45 50

cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307  
Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg  
55 60 65

aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355  
Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala  
70 75 80 85

ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403  
Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His  
90 95 100

ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451

Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro  
 105 110 115  
 gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499  
 Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile  
 120 125 130  
 cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547  
 Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val  
 135 140 145  
 gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595  
 Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile  
 150 155 160 165  
 ggt gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643  
 Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly  
 170 175 180  
 ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691  
 Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile  
 185 190 195  
 ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744  
 Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn  
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 tca 747  
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 <211> 208  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 462  
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 20 25 30  
 Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile  
 35 40 45  
 Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met  
 50 55 60  
 Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys  
 65 70 75 80  
 Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro  
 85 90 95  
 Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala  
 100 105 110  
 Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro  
 115 120 125  
 Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His

130	135	140
Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr		
145	150	155 160
Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp		
	165	170 175
Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro		
	180	185 190
Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn		
	195	200 205

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXN03007

<400> 463  
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 Met Thr Ser Pro Ala  
 1 5  
 aca ctg aaa gtt ctc aac gcc tac ttg gat aac ccc act cca acc ctg 163  
 Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn Pro Thr Pro Thr Leu  
 10 15 20  
 gag gag gca att gag gtg ttc acc ccg ctg acc gtg ggt gaa tac gat 211  
 Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr Val Gly Glu Tyr Asp  
 25 30 35  
 gac gtg cac atc gca gcg ctg ctt gcc acc atc cgt act cgc ggt gag 259  
 Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile Arg Thr Arg Gly Glu  
 40 45 50  
 cag ttc gct gat att gcc ggc gct gcc aag gcg ttc ctc gcg gcg gct 307  
 Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala Phe Leu Ala Ala Ala  
 55 60 65  
 cgt ccg ttc ccg att act ggc gca ggt ttg cta gat tcc gct ggt act 355  
 Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu Asp Ser Ala Gly Thr  
 70 75 80 85  
 ggt ggc gac ggt gcc aac acc atc aac atc acc acc ggc gca tcc ctg 403  
 Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr Thr Gly Ala Ser Leu  
 90 95 100  
 atc gca gca tcc ggt gga gtg aag ctg gtt aag cac ggc aac cgt tcg 451  
 Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys His Gly Asn Arg S r

105 110 115

gtg agc tcc aag tcc ggc 469  
Val Ser Ser Lys Ser Gly  
120

<210> 464  
<211> 123  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 464  
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Val Gly Glu Tyr Asp Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile  
35 40 45  
Arg Thr Arg Gly Glu Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala  
50 55 60  
Phe Leu Ala Ala Ala Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu  
65 70 75 80  
Asp Ser Ala Gly Thr Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr  
85 90 95  
Thr Gly Ala Ser Leu Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys  
100 105 110  
His Gly Asn Arg Ser Val Ser Ser Lys Ser Gly  
115 120

<210> 465  
<211> 564  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
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<222> (101)..(541)  
<223> RXN02918

<400> 465  
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tgattctatt attgccaaat cagaaagcag gagagaccgc atg agc gaa atc cta 115  
Met Ser Glu Ile Leu  
1 5  
gaa acc tat tgg gca ccc cac ttt gga aaa acc gaa gaa gcc aca gca 163  
Glu Thr Tyr Trp Ala Pro His Phe Gly Lys Thr Glu Glu Ala Thr Ala  
10 15 20  
ctc gtt tca tac ctg gca caa gct tcc ggc gat ccc att gag gtt cac 211  
Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp Pro Ile Glu Val His



	25	30	35	
acc ctg ttc ggg gat tta ggt tta gac gga ctc tct gga aac tac acc				259
Thr Leu Phe Gly Asp Leu Gly Leu Asp Gly Leu Ser Gly Asn Tyr Thr				
	40	45	50	
gac act gag att gac ggc tac ggc gac gca ttc ctg ctg gtt gca gcg				307
Asp Thr Glu Ile Asp Gly Tyr Gly Asp Ala Phe Leu Leu Val Ala Ala				
	55	60	65	
cta tcc gtg ttg atg gct gaa aac aaa gca aca ggt ggc gtg aat ctg				355
Leu Ser Val Leu Met Ala Glu Asn Lys Ala Thr Gly Gly Val Asn Leu				
	70	75	80	85
ggt gag ctt ggg gga gct gat aaa tcg atc cgg ctg cat gtt gaa tcc				403
Gly Glu Leu Gly Gly Ala Asp Lys Ser Ile Arg Leu His Val Glu Ser				
	90	95	100	
aag gag aac acc caa atc aac acc gca ttg aag tat ttt gcg ctc tcc				451
Lys Glu Asn Thr Gln Ile Asn Thr Ala Leu Lys Tyr Phe Ala Leu Ser				
	105	110	115	
cca gaa gac cac gca gca gca gat cgc ttc gat gag gat gac ctg tct				499
Pro Glu Asp His Ala Ala Ala Asp Arg Phe Asp Glu Asp Asp Leu Ser				
	120	125	130	
gag ctt gcc aac ttg agt gaa gag ctg cgc gga cag ctg gac				541
Glu Leu Ala Asn Leu Ser Glu Glu Leu Arg Gly Gln Leu Asp				
	135	140	145	
taattgtctc ccatttaagg agt				564

&lt;210&gt; 466

&lt;211&gt; 147

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 466

Met Ser Glu Ile Leu Glu Thr Tyr Trp Ala Pro His Phe Gly Lys Thr				
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Glu Glu Ala Thr Ala Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp				
	20	25	30	
Pro Ile Glu Val His Thr Leu Phe Gly Asp Leu Gly Leu Asp Gly Leu				
	35	40	45	
Ser Gly Asn Tyr Thr Asp Thr Glu Ile Asp Gly Tyr Gly Asp Ala Phe				
	50	55	60	
Leu Leu Val Ala Ala Leu Ser Val Leu Met Ala Glu Asn Lys Ala Thr				
	65	70	75	80
Gly Gly Val Asn Leu Gly Glu Leu Gly Gly Ala Asp Lys Ser Ile Arg				
	85	90	95	
Leu His Val Glu Ser Lys Glu Asn Thr Gln Ile Asn Thr Ala Leu Lys				
	100	105	110	
Tyr Phe Ala Leu Ser Pro Glu Asp His Ala Ala Ala Asp Arg Phe Asp				

115	120	125	
Glu Asp Asp Leu Ser Glu	Leu Ala Asn Leu Ser	Glu Glu Leu Arg Gly	
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Gln Leu Asp			
145			
<210> 467			
<211> 735			
<212> DNA			
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<222> (101)..(712)			
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	Met Ala Ala Arg Val	1 5	
gcc cag gaa ctt gaa gac ggc cag tac gtc aac ctc ggc atc ggc atg	163		
Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn Leu Gly Ile Gly Met	10 15 20		
cct aca ctt atc ccc ggc tac ctg cct gag gga cta gag gtt atc ctt	211		
Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly Leu Glu Val Ile Leu	25 30 35		
cac tcc gaa aac ggt gtg ctg ggc gtt gga cct tac cca act gaa gag	259		
His Ser Glu Asn Gly Val Leu Gly Val Gly Pro Tyr Pro Thr Glu Glu	40 45 50		
gaa ctt gat cct gag ctg atc aac gcc ggc aag gaa acc atc acg gtt	307		
Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys Glu Thr Ile Thr Val	55 60 65		
gca cct ggc gca tcc tac ttc tcc tct tct gat tct ttc gcc atg atc	355		
Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp Ser Phe Ala Met Ile	70 75 80 85		
cgc tcc aag tct gtc gac gtt gca gtc ttg ggc gtt atg gaa gtc tcc	403		
Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly Val Met Glu Val Ser	90 95 100		
cag tac ggc gac ctg gcc aac tgg atg att ccc ggc aag ctg gtc aag	451		
Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro Gly Lys Leu Val Lys	105 110 115		
ggt atg ggt ggc gca atg gat ctg gtg cac ggc gca tcc aag atc atc	499		
Gly Met Gly Gly Ala Met Asp Leu Val His Gly Ala Ser Lys Ile Ile	120 125 130		
gcc atg acc gat cac atc acc aag aag ggc gct ccg aag atc ctt aag	547		
Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala Pro Lys Ile Leu Lys	135 140 145		

gag tgt cgc ctc cca ctg act ggc gcg aag tgc gtg gac atg att gtc 595  
 Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys Val Asp Met Ile Val  
 150 155 160 165

acc acc cac gct gtg ttc tct gtg gac cct gaa gaa ggc ctc acg ctc 643  
 Thr Thr His Ala Val Phe Ser Val Asp Pro Glu Glu Gly Leu Thr Leu  
 170 175 180

atc gag tgc gcc gac ggt gtc acc gtt gag gaa ctc cgc gaa atc acc 691  
 Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu Leu Arg Glu Ile Thr  
 185 190 195

gaa gcc gat ttc aaa gtt gct taagcaaacg ctgcgcaatt aag 735  
 Glu Ala Asp Phe Lys Val Ala  
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<210> 468

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 468

Met Ala Ala Arg Val Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn  
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Leu Gly Ile Gly Met Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly  
 20 25 30

Leu Glu Val Ile Leu His Ser Glu Asn Gly Val Leu Gly Val Gly Pro  
 35 40 45

Tyr Pro Thr Glu Glu Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys  
 50 55 60

Glu Thr Ile Thr Val Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp  
 65 70 75 80

Ser Phe Ala Met Ile Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly  
 85 90 95

Val Met Glu Val Ser Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro  
 100 105 110

Gly Lys Leu Val Lys Gly Met Gly Gly Ala Met Asp Leu Val His Gly  
 115 120 125

Ala Ser Lys Ile Ile Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala  
 130 135 140

Pro Lys Ile Leu Lys Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys  
 145 150 155 160

Val Asp Met Ile Val Thr Thr His Ala Val Phe Ser Val Asp Pro Glu  
 165 170 175

Glu Gly Leu Thr Leu Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu  
 180 185 190

Leu Arg Glu Ile Thr Glu Ala Asp Phe Lys Val Ala

195

200

<210> 469  
 <211> 876  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(853)  
 <223> RXN01115

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gccaggggtct tgcagctgtc tttgaaaagg agaactaaaa atg gct att ttg cac 115  
 Met Ala Ile Leu His  
 1 5

agc gtt tcc tac gga act tcc gac aac acc ttg gtg ttc att ggc tcg 163  
 Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu Val Phe Ile Gly Ser  
 10 15 20

ttg ggt tcc acc acc gac atg tgg ctg cca cag ctg gat gcc ttg cat 211  
 Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln Leu Asp Ala Leu His  
 25 30 35

aag gat ttc cgc gtc atc gct gtt gat cac cgc gga cat ggt ctg tct 259  
 Lys Asp Phe Arg Val Ile Ala Val Asp His Arg Gly His Gly Leu Ser  
 40 45 50

gaa ctc atc gaa ggc acc ccc act gtg gcg gat ctg gcg cag gat gtg 307  
 Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp Leu Ala Gln Asp Val  
 55 60 65

ctg gat acc ctc gat gac ctg ggt gtc gga aac ttc ggc gtc atc gga 355  
 Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn Phe Gly Val Ile Gly  
 70 75 80 85

cta tct ctc ggc gga gcg gtt gca caa tac ttg gcg gcc acc tct gat 403  
 Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu Ala Ala Thr Ser Asp  
 90 95 100

cgt gtc acc aag gca gca ttc atg tgt acc gct gca aaa ttc ggc gag 451  
 Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala Ala Lys Phe Gly Glu  
 105 110 115

ccc cag ggc tgg cta gat cgc gcc gca gcg tgc cgc gaa aac ggc act 499  
 Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys Arg Glu Asn Gly Thr  
 120 125 130

ggt tct ctg tcc gaa gct gtg atc cag cgc tgg ttc tcc ccc act tgg 547  
 Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp Phe Ser Pro Thr Trp  
 135 140 145

ttg gag aac aac cca gcg tcc cgc gag cac ttc gaa gcc atg gtt gcc 595  
 Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe Glu Ala Met Val Ala  
 150 155 160 165

ggc acc cca tct gag ggt tac gcg ctg tgc tgc gag gcg ttg gca acc 643

Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys Glu Ala Leu Ala Thr  
 170 175 180  
 tgg gat ttc acc gat cgc ctg gga gaa atc acc gtg cca gtg ctc acc 691  
 Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr Val Pro Val Leu Thr  
 185 190 195  
 atc gca ggt gcc gat gac ccc tcc act cct cca gca acc gtg cag atc 739  
 Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro Ala Thr Val Gln Ile  
 200 205 210  
 att gcc gat ggc gtt ggc ggc gag tcc cgc gca gag gtc cta agc cca 787  
 Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala Glu Val Leu Ser Pro  
 215 220 225  
 gcc gcg cac gta cca acc gtg gaa cgt cca aac gag gta aat gaa ctg 835  
 Ala Ala His Val Pro Thr Val Glu Arg Pro Asn Glu Val Asn Glu Leu  
 230 235 240 245  
 cta gca cag cat ttc gct taatgttgta ggcatgttca caa 876  
 Leu Ala Gln His Phe Ala  
 250

&lt;210&gt; 470

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 470

Met Ala Ile Leu His Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu  
 1 5 10 15  
 Val Phe Ile Gly Ser Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln  
 20 25 30  
 Leu Asp Ala Leu His Lys Asp Phe Arg Val Ile Ala Val Asp His Arg  
 35 40 45  
 Gly His Gly Leu Ser Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp  
 50 55 60  
 Leu Ala Gln Asp Val Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn  
 65 70 75 80  
 Phe Gly Val Ile Gly Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu  
 85 90 95  
 Ala Ala Thr Ser Asp Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala  
 100 105 110  
 Ala Lys Phe Gly Glu Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys  
 115 120 125  
 Arg Glu Asn Gly Thr Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp  
 130 135 140  
 Phe Ser Pro Thr Trp Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe  
 145 150 155 160  
 Glu Ala Met Val Ala Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys

	165		170		175
Glu Ala Leu Ala Thr Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr	180	185	190		
Val Pro Val Leu Thr Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro	195	200	205		
Ala Thr Val Gln Ile Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala	210	215	220		
Glu Val Leu Ser Pro Ala Ala His Val Pro Thr Val Glu Arg Pro Asn	225	230	235	240	
Glu Val Asn Glu Leu Leu Ala Gln His Phe Ala	245	250			

<210> 471  
 <211> 1284  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1261)  
 <223> RXS00116

<400> 471  
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 tttgcgccacc aatcaatggg ggatcaaata tagtagctgc atg agt aat gac ttc 115  
 Met Ser Asn Asp Phe  
 1 5  
 gtc gtt tct agg ctt aga ccc ttt ggt gaa acg att ttt gca acc atg 163  
 Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr Ile Phe Ala Thr Met  
 10 15 20  
 acc cag cga gct gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt 211  
 Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe  
 25 30 35  
 cct gat gag gat ggt cct cgt cgg atg tta gag atc gcg tcg gag cag 259  
 Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln  
 40 45 50  
 att ctc ggg gga aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg 307  
 Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser  
 55 60 65  
 ttg agg gca gct gtg gct cgt gat cat ttg gag agg ttt gat ctg gag 355  
 Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu  
 70 75 80 85  
 tac aac cct gat tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg 403  
 Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala  
 90 95 100  
 att acg gcg act gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc 451  
 Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile

105				110				115								
gtt	ttg	gaa	ccg	tat	tac	gat	gcg	tat	gcg	gcg	gct	att	gcg	ttg	gcg	499
Val	Leu	Glu	Pro	Tyr	Tyr	Asp	Ala	Tyr	Ala	Ala	Ala	Ile	Ala	Leu	Ala	
		120					125					130				
ggg	gcg	acg	cgg	gtg	gcg	gtt	cct	ttg	cag	gag	gtg	gag	aac	tcg	tgg	547
Gly	Ala	Thr	Arg	Val	Ala	Val	Pro	Leu	Gln	Glu	Val	Glu	Asn	Ser	Trp	
		135				140					145					
gat	gtg	gat	gtc	gat	aag	ttg	cat	gcg	gcg	gtg	act	aag	aag	acg	cgg	595
Asp	Val	Asp	Val	Asp	Lys	Leu	His	Ala	Ala	Val	Thr	Lys	Lys	Thr	Arg	
150					155					160					165	
atg	att	atc	gtt	aat	tcg	ccg	cat	aat	ccg	acg	ggt	tcg	gtg	ttt	tct	643
Met	Ile	Ile	Val	Asn	Ser	Pro	His	Asn	Pro	Thr	Gly	Ser	Val	Phe	Ser	
				170					175					180		
aag	aag	gcg	ttg	aag	cag	ttg	gcg	ggt	gtt	gct	cgt	gcg	tat	gac	ttg	691
Lys	Lys	Ala	Leu	Lys	Gln	Leu	Ala	Gly	Val	Ala	Arg	Ala	Tyr	Asp	Leu	
			185					190					195			
ttg	gtg	ttg	tca	gat	gag	gtg	tat	gag	cat	ctt	gtt	ttt	gat	gat	cag	739
Leu	Val	Leu	Ser	Asp	Glu	Val	Tyr	Glu	His	Leu	Val	Phe	Asp	Asp	Gln	
		200					205					210				
aag	cat	gtg	agt	gtc	gcg	aag	ctg	ccc	ggt	atg	tgg	gat	cgc	acg	gtg	787
Lys	His	Val	Ser	Val	Ala	Lys	Leu	Pro	Gly	Met	Trp	Asp	Arg	Thr	Val	
	215					220					225					
acg	gtg	tcg	tcg	gcg	gcg	aaa	acg	ttc	aat	gtg	act	ggt	tgg	aag	acg	835
Thr	Val	Ser	Ser	Ala	Ala	Lys	Thr	Phe	Asn	Val	Thr	Gly	Trp	Lys	Thr	
230					235					240					245	
ggg	tgg	gcg	ttg	gca	ccg	gag	ccg	ttg	ttg	gag	gcg	gtg	ttg	aag	gcg	883
Gly	Trp	Ala	Leu	Ala	Pro	Glu	Pro	Leu	Leu	Glu	Ala	Val	Leu	Lys	Ala	
				250					255					260		
aag	cag	ttt	atg	tct	tat	gtg	ggg	gct	aca	cct	ttt	cag	ccg	gct	gtg	931
Lys	Gln	Phe	Met	Ser	Tyr	Val	Gly	Ala	Thr	Pro	Phe	Gln	Pro	Ala	Val	
			265					270					275			
gcg	cat	gcg	att	gaa	cat	gag	cag	aag	tgg	gtg	tca	aag	atg	tct	aag	979
Ala	His	Ala	Ile	Glu	His	Glu	Gln	Lys	Trp	Val	Ser	Lys	Met	Ser	Lys	
		280					285					290				
ggg	ctt	gag	ctc	aag	cgg	gat	att	ttg	cgt	act	gcg	tta	gat	aag	gcg	
1027																
Gly	Leu	Glu	Leu	Lys	Arg	Asp	Ile	Leu	Arg	Thr	Ala	Leu	Asp	Lys	Ala	
		295				300					305					
ggg	ctg	aag	act	cat	gac	agt	atg	ggc	acg	tat	ttc	atc	gtt	gcg	gat	
1075																
Gly	Leu	Lys	Thr	His	Asp	Ser	Met	Gly	Thr	Tyr	Phe	Ile	Val	Ala	Asp	
310					315					320					325	
att	ggg	gat	cgt	gat	ggt	gcg	gag	ttc	tgt	ttt	gag	ttg	att	gag	aag	
1123																
Ile	Gly	Asp	Arg	Asp	Gly	Ala	Glu	Phe	Cys	Phe	Glu	Leu	Ile	Glu	Lys	
				330					335					340		

gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag  
1171

Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys  
345 350 355

aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg  
1219

Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr  
360 365 370

ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta  
1261

Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu  
375 380 385

tagtttgaac aggttggttg ggg  
1284

<210> 472

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 472

Met Ser Asn Asp Phe Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr  
1 5 10 15

Ile Phe Ala Thr Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn  
20 25 30

Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu  
35 40 45

Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly  
50 55 60

Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu  
65 70 75 80

Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val  
85 90 95

Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro  
100 105 110

Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala  
115 120 125

Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu  
130 135 140

Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val  
145 150 155 160

Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr  
165 170 175

Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala  
180 185 190



Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu  
195 200 205

Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met  
210 215 220

Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val  
225 230 235 240

Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu  
245 250 255

Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro  
260 265 270

Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val  
275 280 285

Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr  
290 295 300

Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr  
305 310 315 320

Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe  
325 330 335

Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe  
340 345 350

Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys  
355 360 365

Lys Lys Glu Glu Thr Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile  
370 375 380

Lys Lys Leu  
385

<210> 473

<211> 607

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(607)

<223> FRXA00116

<400> 473

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ttctaggcctt agaccctttg gtgaaacgat ttttgcaacc atg acc cag cga gct 115  
Met Thr Gln Arg Ala  
1 5

gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt cct gat gag gat 163  
Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp  
10 15 20

ggt cct cgt cgg atg tta gag atc gcg tcg gag cag att ctc ggg gga 211  
 Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly  
                   25                                  30                                  35

aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg ttg agg gca gct 259  
 Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala  
                   40                                  45                                  50

gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat 307  
 Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp  
                   55                                  60                                  65

tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act 355  
 Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr  
                   70                                  75                                  80                                  85

gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg 403  
 Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro  
                                   90                                  95                                  100

tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg cgg 451  
 Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg  
                   105                                  110                                  115

gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg gat gtg gat gtc 499  
 Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val  
                   120                                  125                                  130

gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt 547  
 Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val  
                   135                                  140                                  145

aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg 595  
 Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu  
                   150                                  155                                  160                                  165

aag cag ttg gcg 607  
 Lys Gln Leu Ala

&lt;210&gt; 474

&lt;211&gt; 169

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 474

Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly  
   1                                  5                                  10                                  15

Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu  
                   20                                  25                                  30

Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala  
                   35                                  40                                  45

Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu  
                   50                                  55                                  60

Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu  
                   65                                  70                                  75                                  80

Ala	Ile	Thr	Ala	Thr 85	Val	Leu	Gly	Leu	Val 90	Glu	Pro	Gly	Asp	Glu 95	Val
Ile	Val	Leu	Glu 100	Pro	Tyr	Tyr	Asp	Ala 105	Tyr	Ala	Ala	Ala	Ile 110	Ala	Leu
Ala	Gly	Ala 115	Thr	Arg	Val	Ala	Val 120	Pro	Leu	Gln	Glu	Val 125	Glu	Asn	Ser
Trp 130	Asp	Val	Asp	Val	Asp	Lys 135	Leu	His	Ala	Ala	Val 140	Thr	Lys	Lys	Thr
Arg 145	Met	Ile	Ile	Val	Asn 150	Ser	Pro	His	Asn	Pro 155	Thr	Gly	Ser	Val	Phe 160
Ser	Lys	Lys	Ala	Leu 165	Lys	Gln	Leu	Ala							

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<210> 475
<211> 843
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (101)..(820)  
<223> RXS00391
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tttctcccc atccctgtac aagataaaaac ccgtgcacag																115
											Leu	Leu	Arg	Asp	Ser	
											1				5	
caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc																163
Gln	Arg	Val	Gly	Leu	Ala	Ile	Asp	Pro	Ser	Ile	Ala	Leu	Val	Met	Ala	
				10					15					20		
act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg																211
Thr	Ser	Gly	Ser	Thr	Gly	Thr	Pro	Lys	Gly	Ala	Gln	Leu	Thr	Pro	Leu	
			25					30					35			
aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa																259
Asn	Leu	Val	Ser	Ser	Ala	Asp	Ala	Thr	His	Gln	Phe	Leu	Gly	Gly	Glu	
		40					45					50				
ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag																307
Gly	Gln	Trp	Leu	Leu	Ala	Met	Pro	Ala	His	His	Ile	Ala	Gly	Met	Gln	
	55					60					65					
gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat																355
Val	Leu	Leu	Arg	Ser	Leu	Ile	Ala	Gly	Val	Glu	Pro	Leu	Ala	Ile	Asp	
	70				75					80				85		
ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa																403
Leu	Ser	Thr	Gly	Phe	His	Ile	Asp	Ala	Phe	Ala	Gly	Ala	Ala	Ala	Glu	
			90						95					100		

ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451  
 Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln  
                   105                                  110                                  115

tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499  
 Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu  
                   120                                  125                                  130

ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547  
 Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg  
                   135                                  140                                  145

att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595  
 Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser  
 150                                  155                                  160                                  165

tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643  
 Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly  
                                   170                                  175                                  180

gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691  
 Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met  
                                   185                                  190                                  195

att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739  
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn  
                   200                                  205                                  210

gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787  
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile  
                   215                                  220                                  225

ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840  
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His  
 230                                  235                                  240

tgc 843

<210> 476

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 476

Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile  
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Ala Leu Val Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala  
                   20                                  25                                  30

Gln Leu Thr Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln  
                   35                                  40                                  45

Phe Leu Gly Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His  
           50                                  55                                  60

Ile Ala Gly Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu  
           65                                  70                                  75                                  80

Pro Leu Ala Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala

85								90				95					
Gly	Ala	Ala	Ala	Glu	Leu	Lys	Asn	Thr	Gly	Asp	Arg	Val	Tyr	Thr	Ser		
100								105				110					
Leu	Thr	Pro	Met	Gln	Leu	Leu	Lys	Ala	Met	Asp	Ser	Leu	Gln	Gly	Ile		
115								120				125					
Glu	Ala	Leu	Lys	Leu	Phe	Asp	Val	Ile	Leu	Val	Gly	Gly	Ala	Ala	Leu		
130								135				140					
Ser	Lys	Gln	Ala	Arg	Ile	Ser	Ala	Glu	Gln	Leu	Asp	Ile	Asn	Ile	Val		
145								150				155				160	
Thr	Thr	Tyr	Gly	Ser	Ser	Glu	Thr	Ser	Gly	Gly	Cys	Val	Tyr	Asp	Gly		
165								170				175					
Lys	Pro	Ile	Pro	Gly	Ala	Lys	Val	Arg	Ile	Ser	Asp	Glu	Arg	Ile	Glu		
180								185				190					
Leu	Gly	Gly	Pro	Met	Ile	Ala	Gln	Gly	Tyr	Arg	Asn	Ala	Pro	Glu	His		
195								200				205					
Pro	Asp	Phe	Ala	Asn	Glu	Gly	Trp	Phe	Thr	Thr	Ser	Asp	Ser	Gly	Glu		
210								215				220					
Leu	His	Asp	Gly	Ile	Leu	Thr	Val	Thr	Gly	Arg	Val	Asp	Thr	Arg	His		
225								230				235				240	

<210> 477  
 <211> 1017  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(994)  
 <223> RXS00393

<400> 477  
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 aattgcgcgga tcgagtatgt gatgggggaaa gatagagggtt atg tct cac acg gaa 115  
 Met Ser His Thr Glu  
 1 5  
 ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163  
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg  
 10 15 20  
 ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211  
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly  
 25 30 35  
 gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259  
 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala  
 40 45 50

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat	307
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp	
55 60 65	
tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg	355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu	
70 75 80 85	
cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg	403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala	
90 95 100	
gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc	451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser	
105 110 115	
ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg	499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu	
120 125 130	
ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggc	547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly	
135 140 145	
ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg	595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met	
150 155 160 165	
gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc	643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala	
170 175 180	
gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac	691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn	
185 190 195	
aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc	739
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu	
200 205 210	
gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg	787
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu	
215 220 225	
att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg	835
Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp	
230 235 240 245	
cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca	883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala	
250 255 260	
ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc	931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile	
265 270 275	
ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg	979
Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu	
280 285 290	

gca tta gcg ttt agc taaaacgctt ttcgacgctc ccc

1017

Ala Leu Ala Phe Ser

295

<210> 478

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 478

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Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val  
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Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp  
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Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys  
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Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala  
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Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly  
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Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly  
145 150 155 160

Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser  
165 170 175

Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly  
180 185 190

Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr  
195 200 205

Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys  
210 215 220

Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu  
225 230 235 240

Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu  
245 250 255

Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp

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 Met Ser His Thr Glu  
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 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg  
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 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly  
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 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala  
 40 45 50  
  
 ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307  
 Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp  
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 Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu  
 70 75 80 85  
  
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 Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala  
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 Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser  
 105 110 115  
  
 ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499  
 Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu  
 120 125 130  
  
 ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547  
 Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly  
 135 140 145



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 Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala  
 170 175 180  
  
 gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691  
 Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn  
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 gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787  
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu  
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 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp  
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 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala  
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 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser  
 265 270 275  
  
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 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val  
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Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp  
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 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala  
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 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly  
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 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly  
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 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly  
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 195 200 205  
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys  
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 225 230 235 240  
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu  
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 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp  
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 Cys Ser Arg Ala Trp His  
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 Met Gly Ala Val Glu

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Leu	Arg	Glu	Ala	Leu	Ala	Glu	His	L u	Glu	Val	Glu	Phe	Asp	Gln	Val	
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acg	gta	ggt	tgc	ggc	tcg	tct	gcg	ctg	tgt	caa	cag	ctg	ggt	cag	gca	211
Thr	Val	Gly	Cys	Gly	Ser	Ser	Ala	Leu	Cys	Gln	Gln	Leu	Val	Gln	Ala	
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Thr	Cys	Ala	Gln	Gly	Asp	Glu	Val	Ile	Phe	Pro	Trp	Arg	Ser	Phe	Glu	
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Ala	Tyr	Pro	Ile	Phe	Ala	Gln	Val	Ala	Gly	Ala	Thr	Pro	Val	Ala	Ile	
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Pro	Leu	Thr	Ala	Asp	Gln	Asn	His	Asp	Leu	Asp	Ala	Met	Ala	Ala	Ala	
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Ile	Thr	Asp	Lys	Thr	Arg	Leu	Ile	Phe	Ile	Cys	Asn	Pro	Asn	Asn	Pro	
90					95					100						
tcg	ggc	acc	acc	atc	acc	cag	gcg	cag	ttt	gat	aat	ttc	atg	gaa	aag	451
Ser	Gly	Thr	Thr	Ile	Thr	Gln	Ala	Gln	Phe	Asp	Asn	Phe	Met	Glu	Lys	
105					110					115						
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Val	Pro	Asn	Asp	Val	Val	Val	Gly	Leu	Asp	Glu	Ala	Tyr	Phe	Glu	Phe	
120					125					130						
aac	cgc	gcg	gac	gac	acc	cca	ggt	gcc	act	gag	gaa	atc	cac	cgc	cac	547
Asn	Arg	Ala	Asp	Asp	Thr	Pro	Val	Ala	Thr	Glu	Glu	Ile	His	Arg	His	
135					140					145						
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Asp	Asn	Val	Ile	Gly	Leu	Arg	Thr	Phe	Ser	Lys	Ala	Tyr	Gly	Leu	Ala	
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Gly	Leu	Arg	Val	Gly	Tyr	Ala	Phe	Gly	Asn	Ala	Glu	Ile	Ile	Ala	Ala	
170					175					180						
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Met	Asn	Lys	Val	Ala	Ile	Pro	Phe	Ala	Val	Asn	Ser	Ala	Ala	Gln	Ala	
185					190					195						
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Ala	Ala	Leu	Ala	Ser	Leu	Asn	Ser	Ala	Asp	Glu	Leu	Met	Glu	Arg	Val	
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Glu	Glu	Thr	Val	Glu	Lys	Arg	Asp	Ala	Val	Val	Ser	Ala	Leu	Gly	Ala	
215					220					225						
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Ala	Pro	Thr	Gln	Ala	Asn	Phe	Val	Trp	Leu	Pro	Gly	Glu	Gly	Ala	Ala	
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 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe  
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ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931  
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys  
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ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtctttgg cgttttgcgg 984  
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Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro  
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Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala  
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Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp  
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Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys  
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Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp  
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Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu  
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Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu  
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Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys  
                   145                  150                  155                  160

Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala  
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Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn  
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Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu  
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Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val  
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 Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro  
 225 230 235 240  
 Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile  
 245 250 255  
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Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile	
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His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr	
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ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc	192
Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile	
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Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala	
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Ala Gln Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met	
85 90 95	
gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg	336
Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala	
100 105 110	
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Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu	
115 120 125	

ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432  
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
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cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480  
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
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act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522  
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 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
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 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
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 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
       65                          70                          75                          80  
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
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 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
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 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
           115                          120                          125  
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
       130                          135                          140  
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
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Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
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gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
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gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
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gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
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Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
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Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu Asp His Gly Asp Tyr
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Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr Arg Asn Ile Leu Glu
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tct ttg ggg gcg aag gtt ctg aac ctg cgc tgt act gca gag act cgt 499
Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys Thr Ala Glu Thr Arg
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Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu Pro His Lys Pro Lys
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gct gtt att gtc acc agc cca gga aac cca acg ggc acc atc att gat 595
Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr Gly Thr Ile Ile Asp
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ccg gaa gag cta gag cgc atc gcc aag tgg tgc gat gac aat gat gct 643
Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys Asp Asp Asn Asp Ala
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gtt ctt atc tct gat gag gac tac cac ggc atg agc ttt ggt cgt ccg 691
Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met Ser Phe Gly Arg Pro
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ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt acc 739

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 230 235 240 245  
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 Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala Phe  
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 Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr Arg  
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 gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt ggc 979  
 Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu Gly  
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Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala  
 20 25 30  
 Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr  
 35 40 45  
 Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp  
 50 55 60  
 His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val  
 65 70 75 80  
 Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu  
 85 90 95  
 Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr  
 100 105 110  
 Arg Asn Ile Leu Glu Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys  
 115 120 125  
 Thr Ala Glu Thr Arg Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu  
 130 135 140  
 Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr  
 145 150 155 160  
 Gly Thr Ile Ile Asp Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys  
 165 170 175  
 Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met  
 180 185 190  
 Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala  
 195 200 205  
 Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg  
 210 215 220  
 Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn  
 225 230 235 240  
 Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala  
 245 250 255  
 Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His  
 260 265 270  
 Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro  
 275 280 285  
 Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu  
 290 295 300  
 Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu  
 305 310 315 320  
 Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe  
 325 330 335  
 Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser

340                                      345                                      350  
 Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys  
       355                                      360                                      365

Lys

<210> 487  
 <211> 657  
 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(634)  
 <223> FRXA00618

<400> 487  
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caatgatgct gttcttatct ctgatgagga ctaccacggc atg agc ttt ggt cgt 115  
    Met Ser Phe Gly Arg  
    1                                      5

ccg ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt 163  
 Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly  
    10                                      15                                      20

acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc 211  
 Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile  
    25                                      30                                      35

atc gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct 259  
 Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser  
    40                                      45                                      50

ctt tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc 307  
 Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala  
    55                                      60                                      65

ttc act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat 355  
 Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr  
    70                                      75                                      80                                      85

cgc gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt 403  
 Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu  
    90                                      95                                      100

ggc act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt 451  
 Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val  
    105                                      110                                      115

tct gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat 499  
 Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp  
    120                                      125                                      130

gaa gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa 547  
 Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu  
    135                                      140                                      145

ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595  
 Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr  
 150 155 160 165

att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644  
 Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys  
 170 175

taggttagtt tcg 657

<210> 488

<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 488

Met Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn  
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Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp  
 20 25 30

Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu  
 35 40 45

Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala  
 50 55 60

Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala  
 65 70 75 80

His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu  
 85 90 95

Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr  
 100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala  
 115 120 125

Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp  
 130 135 140

Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala  
 145 150 155 160

Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile  
 165 170 175

Lys Lys

<210> 489

<211> 385

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS  
 <222> (101)..(385)  
 <223> FRXA00627

<400> 489

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gaagccaagc actagaagca atgttcagcc gtttcgcgtc atg cag atg ttg gac 115
                               Met Gln Met Leu Asp
                               1                               5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
                               10                               15                               20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
                               25                               30                               35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
                               40                               45                               50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
                               55                               60                               65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
70                               75                               80                               85

ggt gga ttc gtg gca tcg ttt atc gcc acc 385
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
                               90                               95

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<210> 490  
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 <213> Corynebacterium glutamicum

<400> 490

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Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
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Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
                35                               40                               45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
                50                               55                               60

His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
65                               70                               75                               80

Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
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<210> 491  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1198)  
 <223> RXS01105

<400> 491

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gctttgaaaa cctccccacc accgacgagg cctaagaaaa atg acc aaa att act 115
                                         Met Thr Lys Ile Thr
                                         1                               5

ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163
Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr
                               10                               15                               20

ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211
Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn
                               25                               30                               35

cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259
Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val
                               40                               45                               50

gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307
Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val
                               55                               60                               65

gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355
Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val
                               70                               75                               80                               85

gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403
Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile
                               90                               95                               100

ctg cag cag ctg ctg cag gct ttt ggt gga cct gga cgc acc gcg ttg 451
Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro Gly Arg Thr Ala Leu
                               105                               110                               115

gga ttc caa ccc agc tat tcc atg cac cca att ttg gct aaa ggc acc 499
Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile Leu Ala Lys Gly Thr
                               120                               125                               130

cac act gaa ttc att gcg gtg tcc cga ggt gct gat ttc cgc atc gat 547
His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala Asp Phe Arg Ile Asp
                               135                               140                               145

atg gat gtg gcg ctg gaa gaa att cgt gca aag cag cct gac att gtt 595
Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys Gln Pro Asp Ile Val
                               150                               155                               160                               165

ttt gtc acc acc ccg aac aac ccg acc ggt gat gtg acc tcg ctg gac 643
Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp Val Thr Ser Leu Asp
                               170                               175                               180

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gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat 691  
 Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp  
 185 190 195

gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg 739  
 Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu  
 200 205 210

gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct 787  
 Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala  
 215 220 225

ttt gat ttc gca ggt gga cgc ctc ggc tac ttc gtg gcc aac cca gcg 835  
 Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala  
 230 235 240 245

ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg 883  
 Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala  
 250 255 260

ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg 931  
 Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr  
 265 270 275

ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca 979  
 Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala  
 280 285 290

cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt  
 1027  
 Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe  
 295 300 305

gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt  
 1075  
 Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe  
 310 315 320 325

ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg  
 1123  
 Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu  
 330 335 340

cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca  
 1171  
 Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala  
 345 350 355

gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca  
 1218  
 Ala Ala Glu Ile Ile Lys Leu Asn Leu  
 360 365

tga  
 1221

&lt;210&gt; 492

&lt;211&gt; 366

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 492

Met	Thr	Lys	Ile	Thr	Leu	Ser	Asp	Leu	Pro	Leu	Arg	Glu	Glu	Leu	Arg	1	5	10	15
Gly	Glu	His	Ala	Tyr	Gly	Ala	Pro	Gln	Leu	Asn	Val	Asp	Ile	Arg	Leu	20	25	30	
Asn	Thr	Asn	Glu	Asn	Pro	Tyr	Pro	Pro	Ser	Glu	Ala	Leu	Val	Ala	Asp	35	40	45	
Leu	Val	Ala	Thr	Val	Asp	Lys	Ile	Ala	Thr	Glu	Leu	Asn	Arg	Tyr	Pro	50	55	60	
Glu	Arg	Asp	Ala	Val	Glu	Leu	Arg	Asp	Glu	Leu	Ala	Ala	Tyr	Ile	Thr	65	70	75	80
Lys	Gln	Thr	Gly	Val	Ala	Val	Thr	Arg	Asp	Asn	Leu	Trp	Ala	Ala	Asn	85	90	95	
Gly	Ser	Asn	Glu	Ile	Leu	Gln	Gln	Leu	Leu	Gln	Ala	Phe	Gly	Gly	Pro	100	105	110	
Gly	Arg	Thr	Ala	Leu	Gly	Phe	Gln	Pro	Ser	Tyr	Ser	Met	His	Pro	Ile	115	120	125	
Leu	Ala	Lys	Gly	Thr	His	Thr	Glu	Phe	Ile	Ala	Val	Ser	Arg	Gly	Ala	130	135	140	
Asp	Phe	Arg	Ile	Asp	Met	Asp	Val	Ala	Leu	Glu	Glu	Ile	Arg	Ala	Lys	145	150	155	160
Gln	Pro	Asp	Ile	Val	Phe	Val	Thr	Thr	Pro	Asn	Asn	Pro	Thr	Gly	Asp	165	170	175	
Val	Thr	Ser	Leu	Asp	Asp	Val	Glu	Arg	Ile	Ile	Asn	Val	Ala	Pro	Gly	180	185	190	
Ile	Val	Ile	Val	Asp	Glu	Ala	Tyr	Ala	Glu	Phe	Ser	Pro	Ser	Pro	Ser	195	200	205	
Ala	Thr	Thr	Leu	Leu	Glu	Lys	Tyr	Pro	Thr	Lys	Leu	Val	Val	Ser	Arg	210	215	220	
Thr	Met	Ser	Lys	Ala	Phe	Asp	Phe	Ala	Gly	Gly	Arg	Leu	Gly	Tyr	Phe	225	230	235	240
Val	Ala	Asn	Pro	Ala	Phe	Ile	Asp	Ala	Val	Met	Leu	Val	Arg	Leu	Pro	245	250	255	
Tyr	His	Leu	Ser	Ala	Leu	Ser	Gln	Ala	Ala	Ala	Ile	Val	Ala	Leu	Arg	260	265	270	
His	Ser	Ala	Asp	Thr	Leu	Gly	Thr	Val	Glu	Lys	Leu	Ser	Val	Glu	Arg	275	280	285	
Val	Arg	Val	Ala	Ala	Arg	Leu	Glu	Glu	Leu	Gly	Tyr	Ala	Val	Val	Pro	290	295	300	
Ser	Glu	Ser	Asn	Phe	Val	Phe	Phe	Gly	Asp	Phe	Ser	Asp	Gln	His	Ala	305	310	315	320

Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly  
 325 330 335

Ile Ala Gly His Leu Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp  
 340 345 350

Ala Phe Leu Asp Ala Ala Ala Glu Ile Ile Lys Leu Asn Leu  
 355 360 365

<210> 493

<211> 1752

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1729)

<223> RXS02315

<400> 493

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 Met Ser Ser Thr Pro  
 1 5  
 gct caa gat ctt gcc cgc gcc gtt att gat tcc ctc gca cca cac gtc 163  
 Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser Leu Ala Pro His Val  
 10 15 20  
 act gac gtg gtg tta tgc cca gga tcc agg aac tca ccg ttg tcg ctt 211  
 Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn Ser Pro Leu Ser Leu  
 25 30 35  
 gag ttg ctg gcg cgg cag gat ctg cgt gtc cat gtg cgt atc gac gag 259  
 Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His Val Arg Ile Asp Glu  
 40 45 50  
 cgc agc gcc tca ttt ttg gcg ctg tcc cta gcg cgt acc cag gcc cgg 307  
 Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala Arg Thr Gln Ala Arg  
 55 60 65  
 ccg gtg gct gtg gtg atg acc tcc ggc acg gct gta gct aac tgc ctg 355  
 Pro Val Ala Val Val Met Thr Ser Gly Thr Ala Val Ala Asn Cys Leu  
 70 75 80 85  
 cct gct gtt gct gaa gct gcg cat gcc cat atc ccg ttg att gtg ctc 403  
 Pro Ala Val Ala Glu Ala Ala His Ala His Ile Pro Leu Ile Val Leu  
 90 95 100  
 tct gct gac cgt cct gca cat ttg gtg gga acg ggg gcg agc caa acg 451  
 Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr Gly Ala Ser Gln Thr  
 105 110 115  
 att aac cag acc ggt att ttt ggt gat ctt gca ccg acg gtc ggt atc 499  
 Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala Pro Thr Val Gly Ile  
 120 125 130  
 act gag ctg gat cag gta gcg cag att gct gaa agc ctt gct cag ggg 547



Thr	Glu	Leu	Asp	Gln	Val	Ala	Gln	Ile	Ala	Glu	Ser	Leu	Ala	Gln	Gly		
135						140					145						
gct	tcc	cag	att	ccg	cgt	cat	ttc	aat	ctt	gca	ctt	gat	gtt	cct	ttg	595	
Ala	Ser	Gln	Ile	Pro	Arg	His	Phe	Asn	Leu	Ala	Leu	Asp	Val	Pro	Leu		
150					155					160					165		
gtt	gct	cct	gaa	ctg	cca	gag	ctt	cat	ggg	gag	gca	gtt	gga	gca	tca	643	
Val	Ala	Pro	Glu	Leu	Pro	Glu	Leu	His	Gly	Glu	Ala	Val	Gly	Ala	Ser		
				170					175					180			
tgg	acg	cat	cgc	tgg	atc	aac	cac	ggg	gag	gtg	acc	gtg	gac	ctg	ggg	691	
Trp	Thr	His	Arg	Trp	Ile	Asn	His	Gly	Glu	Val	Thr	Val	Asp	Leu	Gly		
			185					190					195				
gag	cac	acc	ctc	gtg	att	gcc	ggg	gat	gaa	gca	tgg	gaa	gtg	gaa	ggg	739	
Glu	His	Thr	Leu	Val	Ile	Ala	Gly	Asp	Glu	Ala	Trp	Glu	Val	Glu	Gly		
		200					205					210					
ctg	gaa	gat	gtg	ccc	acc	atc	gct	gaa	cct	act	gca	cca	aag	cct	tat	787	
Leu	Glu	Asp	Val	Pro	Thr	Ile	Ala	Glu	Pro	Thr	Ala	Pro	Lys	Pro	Tyr		
	215					220					225						
aat	ccg	gtg	cac	cca	ctg	gct	gct	gaa	atc	ttg	ctg	aag	gag	cag	gtc	835	
Asn	Pro	Val	His	Pro	Leu	Ala	Ala	Glu	Ile	Leu	Leu	Lys	Glu	Gln	Val		
230					235					240					245		
tcc	gcg	gaa	ggc	tat	gtg	gta	aac	acc	agg	cct	gat	cat	gtg	atc	gtg	883	
Ser	Ala	Glu	Gly	Tyr	Val	Val	Asn	Thr	Arg	Pro	Asp	His	Val	Ile	Val		
				250					255					260			
gtg	gga	cac	ccc	acg	ctg	cac	cgc	gga	gtg	ttg	aag	ttg	atg	tca	gat	931	
Val	Gly	His	Pro	Thr	Leu	His	Arg	Gly	Val	Leu	Lys	Leu	Met	Ser	Asp		
			265					270					275				
cct	ggc	att	aaa	tta	act	gtg	ctt	tca	cgc	acc	gat	atc	atc	act	gat	979	
Pro	Gly	Ile	Lys	Leu	Thr	Val	Leu	Ser	Arg	Thr	Asp	Ile	Ile	Thr	Asp		
		280					285					290					
ccc	ggc	cgc	cat	gcc	gat	cag	gtg	ggc	agc	aca	gtg	aaa	gtc	acc	ggc		
1027																	
Pro	Gly	Arg	His	Ala	Asp	Gln	Val	Gly	Ser	Thr	Val	Lys	Val	Thr	Gly		
	295					300					305						
acc	cag	gaa	aag	cag	tgg	cta	aag	atc	tgt	tcg	gca	gca	tca	gaa	ctt		
1075																	
Thr	Gln	Glu	Lys	Gln	Trp	Leu	Lys	Ile	Cys	Ser	Ala	Ala	Ser	Glu	Leu		
310					315					320					325		
gcg	gcc	gat	ggg	gtg	cgt	gac	gtc	ctg	gac	aac	caa	gaa	ttc	ggg	ttc		
1123																	
Ala	Ala	Asp	Gly	Val	Arg	Asp	Val	Leu	Asp	Asn	Gln	Glu	Phe	Gly	Phe		
				330					335					340			
acc	ggc	ctc	cat	gtt	gcc	gca	gcc	gtg	gcg	gat	acc	tta	ggc	acc	ggc		
1171																	
Thr	Gly	Leu	His	Val	Ala	Ala	Ala	Val	Ala	Asp	Thr	Leu	Gly	Thr	Gly		
			345					350					355				
gat	act	ctc	ttt	gct	gca	gca	tcc	aac	tca	atc	cgt	gac	ctc	tcc	ctg		
1219																	

Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu  
 360 365 370  
 gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc  
 1267  
 Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val  
 375 380 385  
 gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct  
 1315  
 Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala  
 390 395 400 405  
 gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc  
 1363  
 Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala  
 410 415 420  
 ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc  
 1411  
 Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile  
 425 430 435  
 ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac  
 1459  
 Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn  
 440 445 450  
 gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt  
 1507  
 Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly  
 455 460 465  
 ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc  
 1555  
 Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser  
 470 475 480 485  
 atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac  
 1603  
 Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp  
 490 495 500  
 aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc  
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 Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser  
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 1699  
 Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala  
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 Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His  
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 Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala  
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 Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala  
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 Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile  
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 Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr  
                   100                  105                  110  
 Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala  
           115                  120                  125  
 Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu  
   130                  135                  140  
 Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala  
  145                  150                  155                  160  
 Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu  
                   165                  170                  175  
 Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val  
                   180                  185                  190  
 Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala  
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 Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr  
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 Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu  
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 Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro  
                   245                  250                  255  
 Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu  
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 Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr  
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Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr  
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 Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser  
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 Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn  
 325 330 335  
 Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp  
 340 345 350  
 Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile  
 355 360 365  
 Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe  
 370 375 380  
 Ser Pro Arg Gly Val Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile  
 385 390 395 400  
 Gly Thr Ser Leu Ala Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala  
 405 410 415  
 Pro Arg Thr Val Ala Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile  
 420 425 430  
 Gly Gly Leu Leu Ile Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr  
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 Ile Val Val Ser Asn Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu  
 450 455 460  
 Thr Gly Ala Asp Gly Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr  
 465 470 475 480  
 Pro His Asp Ala Ser Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu  
 485 490 495  
 His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp  
 500 505 510  
 Thr Thr Glu Val Ser Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg  
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 Asp Thr Arg Arg Ala Gln Gln Gln Ala Leu Met Asp Thr Val His  
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&lt;210&gt; 495

&lt;211&gt; 1434

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (1411)

&lt;223&gt; RXS02550

&lt;400&gt; 495

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	Val Thr Thr Asp Lys	
	1 5	
cgc aaa acc tct aag acc acc gac acc gcc aac aag gct gtg ggc gcg	163	
Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn Lys Ala Val Gly Ala		
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Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr Arg Arg Ile Phe Asp		
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cag tcg gag aag atg aag gac gtg ctg tac gag atc cgt ggc ccg gtg	259	
Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu Ile Arg Gly Pro Val		
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gcc gcg gag gcg gaa cgc atg gag ctt gat ggg cat aac atc tta aag	307	
Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly His Asn Ile Leu Lys		
	55 60 65	
ctc aac acg gga aat cca gcc gtg ttc gga ttc gat gcc ccc gac gtg	355	
Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe Asp Ala Pro Asp Val		
	70 75 80 85	
att atg cgt gac atg atc gcc aac ctt cca act tcc caa ggg tat tcc	403	
Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr Ser Gln Gly Tyr Ser		
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acc tcc aaa ggc att att ccg gcc cgg cga gca gtg gtc acc cgc tac	451	
Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala Val Val Thr Arg Tyr		
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gaa gtt gtg ccc gga ttc ccc cac ttc gat gtt gat gat gtg ttc tta	499	
Glu Val Val Pro Gly Phe Pro His Phe Asp Val Asp Asp Val Phe Leu		
	120 125 130	
ggc aac ggt gtc tca gaa cta atc acc atg acc acc caa gca ctc ctc	547	
Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr Thr Gln Ala Leu Leu		
	135 140 145	
aac gac ggc gat gaa gtt ctt atc ccc gca ccg gac tac cca ctg tgg	595	
Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro Asp Tyr Pro Leu Trp		
	150 155 160 165	
act gcc gca acc tcc ctg gct ggt ggt aag cct gtg cac tac ctc tgt	643	
Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro Val His Tyr Leu Cys		
	170 175 180	
gat gag gaa gat gac tgg aac cca tcc atc gaa gac atc aag tcc aaa	691	
Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu Asp Ile Lys Ser Lys		
	185 190 195	
atc tca gag aaa acc aaa gct att gtg gtg atc aac ccc aac aac ccc	739	
Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile Asn Pro Asn Asn Pro		
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acg gga gct gtc tac ccg cgc cgg gtg ttg gaa caa atc gtc gag att	787	
Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu Gln Ile Val Glu Ile		
	215 220 225	

gca cgc gag cat gac ctg ctg att ttg gcc gat gaa atc tac gac cgc 835  
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att ctc tac gat gat gcc gag cac atc agc ctg gca acc ctt gca cca 883  
 Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu Ala Thr Leu Ala Pro  
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gat ctc ctt tgc atc aca tac aac ggt cta tcc aag gca tac cgc gtc 931  
 Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser Lys Ala Tyr Arg Val  
 265 270 275

gca gga tac cga gct ggc tgg atg gta ttg act gga cca aag caa tac 979  
 Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr Gly Pro Lys Gln Tyr  
 280 285 290

gca cgt gga ttt att gag ggc ctc gaa ctc ctc gca ggc act cga ctc  
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 Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu Ala Gly Thr Arg Leu  
 295 300 305

tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga  
 1075  
 Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly  
 310 315 320 325

cgc cag tcc atc tac gac ctc act ggc gaa cac ggc cga ctc ctg gaa  
 1123  
 Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu  
 330 335 340

cag cgc aac atg gca tgg acg aaa ctc aac gaa atc cca ggt gtc agc  
 1171  
 Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser  
 345 350 355

tgt gtg aaa cca atg gga gct cta tac gcg ttc ccc aag ctc gac ccc  
 1219  
 Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro  
 360 365 370

aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc  
 1267  
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 375 380 385

cgt gcc gag aaa atc ctc atg gtt cag ggc act ggc ttc aac tgg cca  
 1315  
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 390 395 400 405

cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg  
 1363  
 His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu  
 410 415 420

gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag  
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<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 496

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Arg Arg Ile Phe Asp Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu  
35 40 45

Ile Arg Gly Pro Val Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly  
50 55 60

His Asn Ile Leu Lys Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe  
65 70 75 80

Asp Ala Pro Asp Val Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr  
85 90 95

Ser Gln Gly Tyr Ser Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala  
100 105 110

Val Val Thr Arg Tyr Glu Val Val Pro Gly Phe Pro His Phe Asp Val  
115 120 125

Asp Asp Val Phe Leu Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr  
130 135 140

Thr Gln Ala Leu Leu Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro  
145 150 155 160

Asp Tyr Pro Leu Trp Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro  
165 170 175

Val His Tyr Leu Cys Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu  
180 185 190

Asp Ile Lys Ser Lys Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile  
195 200 205

Asn Pro Asn Asn Pro Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu  
210 215 220

Gln Ile Val Glu Ile Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp  
225 230 235 240

Glu Ile Tyr Asp Arg Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu  
245 250 255

Ala Thr Leu Ala Pro Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser  
260 265 270

Lys Ala Tyr Arg Val Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr  
 275 280 285

Gly Pro Lys Gln Tyr Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu  
 290 295 300

Ala Gly Thr Arg Leu Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln  
 305 310 315 320

Val Ala Leu Gly Gly Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His  
 325 330 335

Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu  
 340 345 350

Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe  
 355 360 365

Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu  
 370 375 380

Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr  
 385 390 395 400

Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro  
 405 410 415

Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu  
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Ser Thr Tyr Lys Gln  
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<210> 497

<211> 1080

<212> DNA

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<222> (101)..(1057)

<223> RXS02319

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 Met Ser Asn Tyr Ser  
 1 5

acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163  
 Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe  
 10 15 20

gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211  
 Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg  
 25 30 35

gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259  
 Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn



40	45	50	
gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His 55 60 65			307
gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly 70 75 80 85			355
ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln 90 95 100			403
cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg 105 110 115			451
gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys 120 125 130			499
gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg 135 140 145			547
acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly 150 155 160 165			595
ggt ggg cac tcc ctc cat gtc gtt tgc gac ctc acc atc gct tcc cgc Gly Gly His Ser Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg 170 175 180			643
caa gaa gca cgc ttc aag caa acc gac gct gac gtg gga tcc ttc gac Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp 185 190 195			691
gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn 200 205 210			739
gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met 215 220 225			787
caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu 230 235 240 245			835
aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr 250 255 260			883
ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu 265 270 275			931
atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met 280 285 290			979

acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa  
1027

Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu  
295 300 305

ccc aac tgg aat gaa ttc cct tac tac tac tagtgagttc atggggtcct  
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Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr  
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1080

<210> 498

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 498

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Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg  
35 40 45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr  
50 55 60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu  
65 70 75 80

Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys  
85 90 95

Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala  
100 105 110

Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp  
115 120 125

Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val  
130 135 140

Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn  
145 150 155 160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu  
165 170 175

Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp  
180 185 190

Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met  
195 200 205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr

210					215					220					
Asp 225	Ala	Glu	Arg	Met	Gln 230	Gln	Met	Gly	Ala	Val 235	Asn	Ile	Val	Ala	Asp 240
His	Gly	Asp	Leu	Glu 245	Lys	Glu	Ala	Ile	Gln 250	Ala	Ala	Arg	Glu	Ile 255	Asn
Thr	Lys	Ser	Pro 260	Thr	Gly	Gln	Arg	Met 265	Leu	Lys	Phe	Ala	Phe 270	Asn	Leu
Thr	Asp	Asp 275	Gly	Leu	Met	Gly	Gln 280	Gln	Val	Phe	Ala	Gly 285	Glu	Ala	Thr
Arg 290	Leu	Ala	Tyr	Met	Thr	Asp 295	Glu	Ala	Val	Glu	Gly 300	Lys	Glu	Ala	Phe
Leu 305	Glu	Lys	Arg	Glu	Pro 310	Asn	Trp	Asn	Glu	Phe 315	Pro	Tyr	Tyr	Tyr	

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<223> RXS02908
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											Leu	Lys	Leu	His	Pro	
											1				5	
gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg																163
Glu	Val	Leu	Glu	Arg	Ala	Ile	Ala	Asp	Ile	Lys	Gly	Val	Thr	Ala	Ala	
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tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc																211
Cys	Val	Val	Gly	Ile	Pro	Asp	Pro	Arg	Leu	Gly	Gln	Ala	Ile	Val	Ala	
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Ala	Tyr	Ser	Gly	Ser	Ile	Ser	Pro	Ser	Glu	Val	Ile	Glu	Gly	Leu	Asp	
		40					45					50				
gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct																307
Asp	Leu	Pro	Arg	Trp	Gln	Leu	Pro	Lys	Arg	Leu	Lys	His	Leu	Glu	Ser	
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ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag																355
Leu	Pro	Ser	Ile	Gly	Pro	Gly	Lys	Ala	Asp	Arg	Arg	Ala	Ile	Ala	Lys	
70					75					80					85	
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Leu Phe																

<210> 500  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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                   20                  25                  30  
 Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val  
                   35                  40                  45  
 Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu  
   50                  55                  60  
 Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg  
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 Arg Ala Ile Ala Lys Leu Phe  
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 <223> RXS03003

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   Met Thr Ser Arg Thr  
   1                  5  
 ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tcg ctc gct tcc 163  
 Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser  
                   10                  15                  20  
 gca aaa gcc aaa gct gcg tct cac ccg gat ggg atc gtg aat ctt tct 211  
 Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser  
                   25                  30                  35  
 gtt ggc act ccg gtt gat ccg gtc gcg ccc agc att cag atc gcg ttg 259  
 Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser Ile Gln Ile Ala Leu  
                   40                  45                  50  
 gca gaa gca gcg ggg ttt tcg ggt tac cct caa acc atc ggc acc ccg 307  
 Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln Thr Ile Gly Thr Pro  
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 gaa ctc cgc gca gcc atc agg ggc gcg ctt gag cgg cgc tac aac atg 355

Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu Arg Arg Tyr Asn Met  
 70 75 80 85  
 aca aag ctt gtc gac gcc tcc ctc ctc ccc gtc gtg ggt acc aag gag 403  
 Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val Val Gly Thr Lys Glu  
 90 95 100  
 gca att gcc ctt ctt cca ttc gcg ttg ggt att tcc ggc acc gtt gtc 451  
 Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile Ser Gly Thr Val Val  
 105 110 115  
 atc cca gag att gcg tac cca acc tac gaa gtc gct gtc gtg gcc gca 499  
 Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val Ala Val Val Ala Ala  
 120 125 130  
 gga tgc acc gtg ttg cgt tct gat tcg ctg ttt aag ctc ggc ccg cag 547  
 Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln  
 135 140 145  
 atc ccg tcg atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag 595  
 Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys  
 150 155 160 165  
 gtt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643  
 Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu  
 170 175 180  
 aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691  
 Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp  
 185 190 195  
 gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat 739  
 Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp  
 200 205 210  
 ggc gac cac acc aac ttg atc gcc att cac tcg ctg 775  
 Gly Asp His Thr Asn Leu Ile Ala Ile His Ser Leu  
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 <213> *Corynebacterium glutamicum*  
 <400> 502  
 Met Thr Ser Arg Thr Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp  
 1 5 10 15  
 Asp Ser Leu Ala Ser Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly  
 20 25 30  
 Ile Val Asn Leu Ser Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser  
 35 40 45  
 Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln  
 50 55 60  
 Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu  
 65 70 75 80

[illegible]

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<211> 390
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<213> Corynebacterium glutamicum
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<223> RXS03026
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cgaactagcc cccaacaac aattagaaat ggaacctaaa atg cct gga aaa att 115
                                         Met Pro Gly Lys Ile
                                         1                               5
ctc ctt ctc aac ggc cca aac ctg aac atg ctg ggc aaa cgc gag cct 163
Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu Gly Lys Arg Glu Pro
                        10                        15                        20
gac att tac gga cac gac acc ttg gaa gac gtc gtc gcg ctg gca acc 211
Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val Val Ala Leu Ala Thr
                        25                        30                        35
gct gag gct gcg aaa cac ggc ctt gag gtt gag gcg ctg cag agc aat 259
Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu Ala Leu Gln Ser Asn
                        40                        45                        50
cac caa ggt gag cta atc gat gcg ctg cac aac gct cgc ggg acc cac 307

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His Gln Gly Glu Leu Ile Asp Ala Leu His Asn Ala Arg Gly Thr His  
 55 60 65

atc ggt tgc gtg att aac ccc ggc ggc ctg act aca ctt cgg tgg cgc 355  
 Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr Thr Leu Arg Trp Arg  
 70 75 80 85

ttt tgg atg ctg tgaaggcgtc tgagcttcct acc 390  
 Phe Trp Met Leu

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 504  
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 Gly Lys Arg Glu Pro Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val  
 20 25 30  
 Val Ala Leu Ala Thr Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu  
 35 40 45  
 Ala Leu Gln Ser Asn His Gln Gly Glu Leu Ile Asp Ala Leu His Asn  
 50 55 60  
 Ala Arg Gly Thr His Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr  
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 Thr Leu Arg Trp Arg Phe Trp Met Leu  
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 Met Thr Gln Ser Ala  
 1 5  
 cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163  
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
 10 15 20  
 gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211  
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259  
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
           40                          45                          50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307  
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
           55                          60                          65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355  
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala  
           70                          75                          80                          85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403  
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
                           90                          95                          100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
                           105                          110                          115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499  
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
           120                          125                          130

gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547  
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
           135                          140                          145

gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
           150                          155                          160                          165

cag taatttggtt tgacgacgca gta 621  
 Gln

&lt;210&gt; 506

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 506

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   1                          5                          10                          15

Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu  
           20                          25                          30

Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
           35                          40                          45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
           50                          55                          60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
           65                          70                          75                          80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
           85                          90                          95



Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr  
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr  
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe  
 130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr  
 145 150 155 160

Glu Ala Pro Ile Lys Gln  
 165

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(3052)  
 <223> RXC01434

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 Val Leu Gly Ala Val  
 1 5

ctg aca tcg ctg gtt att ccg gtc ctt acc cgc gcg gaa aaa gaa gac 163  
 Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg Ala Glu Lys Glu Asp  
 10 15 20

gcc gac ggc ggt tcc ggg ttc ttc agg cgg ctg ctc acc ctg tcg gtg 211  
 Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu Leu Thr Leu Ser Val  
 25 30 35

acg ctg ctg ggt ggt gtc acc atc ctg tcg att atc ggc gcg ccg ctg 259  
 Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu  
 40 45 50

ctg aca cgg atg atg ctg tcc tct gag gga caa gtc aac gtg gtc atg 307  
 Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln Val Asn Val Val Met  
 55 60 65

tcc acg gcc ttt gcg tat tgg ctg ctg cca cag att ttc ttc tac ggc 355  
 Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln Ile Phe Phe Tyr Gly  
 70 75 80 85

ctg ttt gcc ctg ttc atg gct gtg ttg aac acc cgt gaa gtg ttc aaa 403  
 Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr Arg Glu Val Phe Lys  
 90 95 100

ccc ggc gcg tgg gca cct gtt gtc aac aat gtg atc acc ttg acc gtg 451  
 Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val Ile Thr Leu Thr Val  
 105 110 115

ctg ggc gtg tac atg gtg ctg cct gcg cgt ttg cac ccg cat gag cag	499
Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln	
120 125 130	
gtg ggc att ttt gat ccg cag atc att ttc ctc ggc gtg ggc acc acc	547
Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr	
135 140 145	
ctt ggt gtg gtt gca cag tgt cta atc atg att ccg tac ctg cgt cgc	595
Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile Pro Tyr Leu Arg Arg	
150 155 160 165	
gcg ggc att gat atg cgc cct ctg tgg ggt atc gat gcg cgt ttg aag	643
Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile Asp Ala Arg Leu Lys	
170 175 180	
caa ttc ggt ggc atg gcg atg gcg atc atc gtg tac gtg gca atc tcc	691
Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser	
185 190 195	
cag ttc ggt tac atc atc acc act cgc att gcg tcg att gca gac gat	739
Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp	
200 205 210	
gct gcg ccg ttt att tat cag cag cac tgg atg ttg ctg caa gtt cct	787
Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro	
215 220 225	
tat ggc atc atc ggc gtc acc ttg ctc acc gcg att atg ccg cga ctg	835
Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu	
230 235 240 245	
tcc cgc aac gcg gca gac ggc gat gat agg gca gta gtc tct gac ctt	883
Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu	
250 255 260	
cag ttg ggt tcc aag cta acc ttc atc gca ctg atc ccc atc gtg gtg	931
Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val	
265 270 275	
ttc ttc acc gcc ttc ggt gtc cct att gcc aat ggc ctt ttt gcc tac	979
Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr	
280 285 290	
ggc caa ttc gat gcc aac gcc gcc aac atc ctt ggt tgg act ctg agc	
1027	
Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser	
295 300 305	
ttc tct gct ttc acg ctg att cct tac gct ttg gtg ctg cta cat ctg	
1075	
Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu	
310 315 320 325	
cgt gtg ttt tat gcg cgt gaa gag gtc tgg acc cca acc ttc atc atc	
1123	
Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr Pro Thr Phe Ile Ile	
330 335 340	

gcc ggc atc acc gcc acc aag gtc gtg ctt tcc ctg ttg gca ccg ctg  
 1171  
 Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu  
 345 350 355

ctg tcg agc tcc ccg gag cgt gtg gtg gtg ctt ctt ggt gcg gcc aac  
 1219  
 Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn  
 360 365 370

ggt ttc agt ttc atc acc ggc gcg gtc atc ggc gcg tat ctg ttg cgc  
 1267  
 Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg  
 375 380 385

aac aaa ctc ggc ctg ttg ggt atg cgc tct ttg gct aaa acc tcc ctg  
 1315  
 Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu  
 390 395 400 405

tgg gcg ttg ggc tct gcg gcg gtt ggt gca gca gca gca tgg gcg ttg  
 1363  
 Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Ala Trp Ala Leu  
 410 415 420

ggg tgg ctg att caa gcc gtc gtg ggc gat ttc ttg ctg ggc act cta  
 1411  
 Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu  
 425 430 435

agc tcc gta ggc tac ttg ttg aac ctg gct gtg ttg ggt gtc ttc ttc  
 1459  
 Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe  
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atc ttc gtc acc ggc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc  
 1507  
 Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val  
 455 460 465

caa aac ttg ggc cag gca ctg acc cgc atc cca ggt ttg agc cgg ttt  
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 Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe  
 470 475 480 485

att cgc ccg aat acc aag atc tct ttg gat gtc ggc gaa gtc tcc gag  
 1603  
 Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu  
 490 495 500

cag gat ttc tcc acc cag ctg gtc gcg cca agc gag ttc gca gca acc  
 1651  
 Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr  
 505 510 515

cct gtg ccg cca ccg atg tcc gcc ggt att gtc cgc gga cct cgc ctg  
 1699  
 Pro Val Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu  
 520 525 530

gtt ccc ggc gcc cca gtc ggc gac ggt cgt ttc cgt ctg ctc gcc gat  
1747  
Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp  
535 540 545

cac ggc ggc gtc caa ggc gcg cgt ttc tgg cag gcc cgc gag atc gcc  
1795  
His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala  
550 555 560 565

acc ggc aag gaa gtc gcg ctg atc ttt gtg gat act tcc ggc aac gcc  
1843  
Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala  
570 575 580

cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag  
1891  
Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu  
585 590 595

gtg cag cgc cgc acc aag aag ctg gcc agc ttg ggc agc ttg gcg gta  
1939  
Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val  
600 605 610

gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg  
1987  
Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val  
615 620 625

gcc gat tgg gtg cct ggc tcc agc ttg agc gcc gtc gcg gaa tcc ggt  
2035  
Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala Val Ala Glu Ser Gly  
630 635 640 645

gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc  
2083  
Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr  
650 655 660

atc ggc gag gcc cac gag atg ggt atc ccg gcc ggc ttg gac aac aag  
2131  
Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys  
665 670 675

tgc cga att cgt atc aac acc gac ggc cat gcc gtc ctc gcc ttg ccg  
2179  
Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro  
680 685 690

gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc  
2227  
Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala  
695 700 705

tcg gcc gcc gag atg ctt atc gac gcg acc ctc gct ccc agc gac gtc  
2275  
Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val  
710 715 720 725

aag gca atg gtc act gaa gcc cag ggg cta gct aca gaa gac aat ccc  
2323

Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro  
730 735 740

gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc  
2371

Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr  
745 750 755

gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct  
2419

Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro  
760 765 770

gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg  
2467

Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met  
775 780 785

gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc  
2515

Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala  
790 795 800 805

ggt acc gcg ttc ctc acc agc ttc ttc ggc agc agc acc aac gaa caa  
2563

Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln  
810 815 820

tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct  
2611

Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro  
825 830 835

gtg ggg cca ccg gtc tac ctg gat ctg gat caa gcc cgc acg tgg gat  
2659

Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp  
840 845 850

gac ggt gca gga aca gat gtc acc gac gtc acc gac ggc aac acc tcc  
2707

Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser  
855 860 865

acc gca tgg acc tcc acc ggc ggc gac ggc ctc cta gtt gac ctg tcc  
2755

Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser  
870 875 880 885

acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc  
2803

Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser  
890 895 900

gac agc aac gtg acc tcg acc gtg aag atc tac gca ttc aac gac gcc  
2851

Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala  
905 910 915

tca cca cac tcc ctg tcg gaa ggc atc gag atc ggc acc gtg gat tat  
2899

Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr  
920 925 930

tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg  
2947

Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro  
935 940 945

ggt cag gtg gaa tcc gtg gtg att ctg gtc gat gag gtt cgt tcc tca  
2995

Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser  
950 955 960 965

caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt  
3043

Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu  
970 975 980

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Val Gly Trp

<210> 508

<211> 984

<212> PRT

<213> Corynebacterium glutamicum

<400> 508

Val Leu Gly Ala Val Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg  
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Ala Glu Lys Glu Asp Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu  
20 25 30

Leu Thr Leu Ser Val Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile  
35 40 45

Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln  
50 55 60

Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln  
65 70 75 80

Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr  
85 90 95

Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val  
100 105 110

Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu  
115 120 125

His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu  
130 135 140

Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile  
145 150 155 160

Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile  
 165 170 175  
 Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val  
 180 185 190  
 Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala  
 195 200 205  
 Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met  
 210 215 220  
 Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala  
 225 230 235 240  
 Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala  
 245 250 255  
 Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu  
 260 265 270  
 Ile Pro Ile Val Val Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn  
 275 280 285  
 Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu  
 290 295 300  
 Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu  
 305 310 315 320  
 Val Leu Leu His Leu Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr  
 325 330 335  
 Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser  
 340 345 350  
 Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu  
 355 360 365  
 Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly  
 370 375 380  
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu  
 385 390 395 400  
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala  
 405 410 415  
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe  
 420 425 430  
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val  
 435 440 445  
 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser  
 450 455 460  
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro  
 465 470 475 480

Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val  
 485 490 495  
 Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser  
 500 505 510  
 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val  
 515 520 525  
 Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe  
 530 535 540  
 Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln  
 545 550 555 560  
 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp  
 565 570 575  
 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala  
 580 585 590  
 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu  
 595 600 605  
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn  
 610 615 620  
 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala  
 625 630 635 640  
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala  
 645 650 655  
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala  
 660 665 670  
 Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala  
 675 680 685  
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp  
 690 695 700  
 Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu  
 705 710 715 720  
 Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala  
 725 730 735  
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr  
 740 745 750  
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu  
 755 760 765  
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr  
 770 775 780  
 Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val  
 785 790 795 800  
 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser



805 810 815  
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 Ala Thr Pro Glu Pro Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln  
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 Ala Arg Thr Trp Asp Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr  
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 Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr  
 900 905 910  
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 Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp  
 930 935 940  
 Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu Val Asp  
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 Met Ser Ile Glu Trp  
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 Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr Leu Val Ser Phe Pro  
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Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr Ala Thr Ile Ala Asn	
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Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly Val Val Ala Tyr Arg	
55 60 65	
cgt gaa cta cac gcc cat gta aaa acc atc aga ttt ctg ctg cca gca	355
Arg Glu Leu His Ala His Val Lys Thr Ile Arg Phe Leu Leu Pro Ala	
70 75 80 85	
tca atc ctc gga ggg atc acc ggc gcc tcg ctc ttg ctg cat ttc tcc	403
Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu Leu Leu His Phe Ser	
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gca gat gtt ttt aca gca gta att ccc tgg ctg att gga ttc ggc acg	451
Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu Ile Gly Phe Gly Thr	
105 110 115	
ctg ttg gtt atc gca ggt cca tca att aag aag cat gtt ggc gct cat	499
Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys His Val Gly Ala His	
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act tca ggt ggc atc tct gct ggg ttt agg caa ttg cct ttc ccg agc	547
Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln Leu Pro Phe Pro Ser	
135 140 145	
cga acc acc ttc atc gtc tca gta tgt ggt gcc ctg ttg ctg ggc atg	595
Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala Leu Leu Leu Gly Met	
150 155 160 165	
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Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile Leu Leu Ile Ala Leu	
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Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu Leu Asn Ala Ile Lys	
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Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala Ala Ser Val Phe Ile	
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Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly Arg Tyr Ala Arg Arg	
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ctt cgc ccc agt gtt ttt aga gca ttt gtg gtc atc gtc gga atc acc	883
Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val Ile Val Gly Ile Thr	
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 Ala Thr Ile Ala Asn Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly  
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 Phe Leu Leu Pro Ala Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu  
                   85                  90                  95  
 Leu Leu His Phe Ser Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu  
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 Ile Gly Phe Gly Thr Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys  
                   115                  120                  125  
 His Val Gly Ala His Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln  
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 Leu Pro Phe Pro Ser Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala  
 145                  150                  155                  160  
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 Leu Leu Ile Ala Leu Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu  
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 Leu Asn Ala Ile Lys Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala  
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 Ala Ser Val Phe Ile Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr  
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 Val Ala Leu Ile Ala Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly  
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 Arg Tyr Ala Arg Arg Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val  
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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(646)

&lt;223&gt; RXC02789

&lt;400&gt; 511

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                                   Met Lys Val Ser Ala
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gat aca ccc ggt cac gat gat cca ggc cca ggc cgg cgc ctt ggc tta 163
Asp Thr Pro Gly His Asp Asp Pro Gly Pro Gly Arg Arg Leu Gly Leu
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gat gtc ggc acc gtg cgc atc gga gtg gca gcc tct gac cgc gat gcc 211
Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala Ser Asp Arg Asp Ala
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aag ctt gcc atg cct gtg gaa acc gtt ccg cgg gaa act gga ttc aaa 259
Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg Glu Thr Gly Phe Lys
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ggg cca gac ctg gcc gat att gat cgg ttg gtc gcc atc gtt gag gaa 307
Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val Ala Ile Val Glu Glu
                                   55                               60                               65

tac aac gcc gtg gaa gtc att gtt ggt cta ccc aca gat ctg cag gga 355
Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro Thr Asp Leu Gln Gly
                                   70                               75                               80                               85

aat ggc tcc gcc agt gtg aag cat gca aag gaa att gct ttc cgc gtc 403
Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu Ile Ala Phe Arg Val
                                   90                               95                               100

cgt cgg cgc ctc acc aat gct gga aag aac att ccg gta cgg ctt ggc 451
Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile Pro Val Arg Leu Gly
                                   105                               110                               115

gac gaa cgc ctc acc acc gtc gtg gcc acc caa gcc ttg cgg gcc tca 499
Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln Ala Leu Arg Ala Ser
                                   120                               125                               130

gga gtc agc gaa aaa gcg gga cgt aaa gtt att gat caa gct gcc gca 547
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gta gaa atc ctt caa acc tgg ttg gat gct cgc acc cga gcc ctt gaa 595
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cca caa tcc aca gac acc caa gat ttc gac gag aag gga aat ttc cca 643
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Gly

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                   20                  25                  30  
 Ser Asp Arg Asp Ala Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg  
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 Glu Thr Gly Phe Lys Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val  
   50                  55                  60  
 Ala Ile Val Glu Glu Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro  
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 Thr Asp Leu Gln Gly Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu  
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 Ile Ala Phe Arg Val Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile  
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 Pro Val Arg Leu Gly Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln  
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 Ala Leu Arg Ala Ser Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile  
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 Asp Gln Ala Ala Ala Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg  
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 <223> RXC02295

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   1                  5

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atc ctc gcg gtc atg ccg caa ctc gca cct gtg aca gcg ctg gcc tcc Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val Thr Ala Leu Ala Ser	40 45 50	259
aac aaa ctg gca gcc gtc acc ggc acg gca tcg gcg gca ttc acc ctg Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser Ala Ala Phe Thr Leu	55 60 65	307
gtc agg cgc gtc aaa ccc gac aaa aaa ctg ctt gcg ctc tac gtt ctg Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu Ala Leu Tyr Val Leu	70 75 80 85	355
gtg gca gct gtg tgc tcc ggt gca ggc gcc ctg gct gcg agt ctc att Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu Ala Ala Ser Leu Ile	90 95 100	403
gac aaa caa atc atg cga ccg ctg atc atc gtg ttg atg ctg gtc gtt Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val Leu Met Leu Val Val	105 110 115	451
ggc ctg atc gtg gtg ttc aaa cca aac ttc gga acc ggc gaa agc aaa Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly Thr Gly Glu Ser Lys	120 125 130	499
gcc ctg ccc acc gga tgg aaa cgc tgg gcc gcc atc gtt gca gtc gga Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala Ile Val Ala Val Gly	135 140 145	547
ctc atc gca gcc tac gac ggc atc ttc gga ccc gga acc ggc atg ttc Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro Gly Thr Gly Met Phe	150 155 160 165	595
ctc atc atg gcg ttc acc gca ctg ctc tcc caa aat ttc ctg tcc tcc Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln Asn Phe Leu Ser Ser	170 175 180	643
gca gcc atg gcg aag gtc gta aac acc gca aca aac ctg ggt gcg cta Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr Asn Leu Gly Ala Leu	185 190 195	691
att gta ttc atc atc ggc ggc cac atg tgg tgg acc cta gga ctc gtg Ile Val Phe Ile Ile Gly Gly His Met Trp Trp Thr Leu Gly Leu Val	200 205 210	739
ctg gca gtc gcc aat gtc gca ggc gca caa ctc ggt gcc cga acg gtg Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu Gly Ala Arg Thr Val	215 220 225	787
ctt ggt ggc ggt acc agg cta att aga tac gca cta cta acc ctg gtt Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala Leu Leu Thr Leu Val	230 235 240 245	835

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 Thr Ala Leu Ala Ser Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser  
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 Ala Ala Phe Thr Leu Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu  
                   65                                  70                                  75                                  80  
 Ala Leu Tyr Val Leu Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu  
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 Ala Ala Ser Leu Ile Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val  
                   100                                  105                                  110  
 Leu Met Leu Val Val Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly  
                   115                                  120                                  125  
 Thr Gly Glu Ser Lys Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala  
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 Ile Val Ala Val Gly Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro  
                   145                                  150                                  155                                  160  
 Gly Thr Gly Met Phe Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln  
                   165                                  170                                  175  
 Asn Phe Leu Ser Ser Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr  
                   180                                  185                                  190  
 Asn Leu Gly Ala Leu Ile Val Phe Ile Ile Gly Gly His Met Trp Trp  
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 Thr Leu Gly Leu Val Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu  
                   210                                  215                                  220  
 Gly Ala Arg Thr Val Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala  
                   225                                  230                                  235                                  240  
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Val Glu Asp Leu Ser  
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Tyr Arg Ile Pro Gln Ser Arg Thr Val Ala Glu Gln Val Pro Gly Pro  
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Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala Ala Val Ala Arg Ala  
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Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp Ala Asp Gly Gly Ile  
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Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr Thr Gly Lys Gly Ala  
135 140 145  
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Val Val Val Phe Asp Asn Ala Tyr His Gly Arg Thr Asn Leu Thr Met  
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 130 135 140  
 Thr Gly Lys Gly Ala Val Val Val Phe Asp Asn Ala Tyr His Gly Arg  
 145 150 155 160  
 Thr Asn Leu Thr Met Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser  
 165 170 175  
 Gly Phe Gly Pro Leu Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr  
 180 185 190  
 Pro Leu Arg Asp Gly Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile  
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 210 215 220  
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 225 230 235 240  
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<220>  
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<223> RXN02970

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Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
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Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
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His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
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Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
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Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
                                   70 75 80 85
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
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ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
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tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
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gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
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cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
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Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
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Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
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Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
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His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
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Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
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Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
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ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
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1027	
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
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Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys	
330 335 340	
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Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
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Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu	
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Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala	
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1315

Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
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Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His  
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Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu  
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1459

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Ala Leu Phe  
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<212> PRT

<213> Corynebacterium glutamicum

<400> 518

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Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
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Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
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His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr

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His Gly Ala Thr Gly Ser Ala Met M t Leu Thr Gly Glu His Arg Arg						
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Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro						
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Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys						
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Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala						
	210			215		220
Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly						
	225			230		235
Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys						
	245			250		255
Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe						
	260			265		270
Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe						
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Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala						
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Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly						
	305			310		315
Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala						
	325			330		335
Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile						
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Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu						
	355			360		365
Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile						
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Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala						
	385			390		395
Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser						
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Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu						
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Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
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Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
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Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
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cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
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1219																	
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gaa	aac	gta	gcg	atc	gct	gac	gtg	cgg	ggc	atc	gga	ttc	ttc	tgg	gca		
1267																	
Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile	Gly	Phe	Phe	Trp	Ala		
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 Phe Lys Glu Arg Gly  
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 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
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 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
 65 70 75 80  
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
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 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
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 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
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 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
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 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
 145 150 155 160  
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
 165 170 175  
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
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 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
 195 200 205  
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
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 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
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Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
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 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
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 <222> (101)..(1975)  
 <223> RXA01551

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 Thr Gly Ala Arg Ala Arg Ala Glu Ile Ala Leu Ile Ala Ala Arg Ala  
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 Pro Phe Glu Pro Val Arg Leu Ala Pro Ala Lys Glu Glu Arg Asn Gly  
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Gly	Lys	Arg	Val	Thr	Gln	Met	Ala	Tyr	Ala	Arg	Ala	Gly	Val	Ile	Thr	
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Asn	His	Pro	Glu	Ser	Glu	Pro	Met	Ile	Ile	Gly	Arg	Lys	Phe	Leu	Thr	
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 425 430 435  
 ttt tac act ctt gga cca cta gtt acc gac atc gct cca ggt tat gac  
 1459  
 Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile Ala Pro Gly Tyr Asp  
 440 445 450  
 cac atc act tct gcc att ggt gca gct cac atc gcc atg ggt ggc acc  
 1507  
 His Ile Thr Ser Ala Ile Gly Ala Ala His Ile Ala Met Gly Gly Thr  
 455 460 465  
 gcc atg ctg tgt tat gtc acc ccg aaa gaa cac ctt ggc ctg ccc aac  
 1555  
 Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His Leu Gly Leu Pro Asn  
 470 475 480 485  
 cgt gac gac gtc aaa acc ggc gta atc acc tac aag ctc gct gcc cac  
 1603  
 Arg Asp Asp Val Lys Thr Gly Val Ile Thr Tyr Lys Leu Ala Ala His

490 495 500  
 gca gca gat gtg gcc aag ggt cat ccc ggc gcg cgt gcc tgg gac gac  
 1651  
 Ala Ala Asp Val Ala Lys Gly His Pro Gly Ala Arg Ala Trp Asp Asp  
 505 510 515  
 gcc atg agt aaa gcg cgt ttt gaa ttc cgt tgg aat gat cag ttt gcg  
 1699  
 Ala Met Ser Lys Ala Arg Phe Glu Phe Arg Trp Asn Asp Gln Phe Ala  
 520 525 530  
 ctc tcc ctc gac ccc gac act gca atc gct tat cac gac gaa acc ctg  
 1747  
 Leu Ser Leu Asp Pro Asp Thr Ala Ile Ala Tyr His Asp Glu Thr Leu  
 535 540 545  
 ccg gca gag cct gcg aaa acc gca cac ttc tgt tca atg tgt ggc ccg  
 1795  
 Pro Ala Glu Pro Ala Lys Thr Ala His Phe Cys Ser Met Cys Gly Pro  
 550 555 560 565  
 aag ttc tgc tcc atg cga att agc cag gac att cgc gat atg ttt ggc  
 1843  
 Lys Phe Cys Ser Met Arg Ile Ser Gln Asp Ile Arg Asp Met Phe Gly  
 570 575 580  
 gat caa atc gcg gaa ttg ggg atg cct ggg gtt ggg gat tct tct agt  
 1891  
 Asp Gln Ile Ala Glu Leu Gly Met Pro Gly Val Gly Asp Ser Ser Ser  
 585 590 595  
 gct gtt gct tct agt ggg gca cgg gag ggg atg gct gag aaa tcc cgg  
 1939  
 Ala Val Ala Ser Ser Gly Ala Arg Glu Gly Met Ala Glu Lys Ser Arg  
 600 605 610  
 gaa ttt att gct ggt ggt gcg gag gtt tat cgg cgt tagacagagc  
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 35 40 45

Lys His Ser Tyr Ser Pro Ile Arg Lys Asp Gly Leu Glu Val Pro Glu  
 50 55 60  
 Thr Glu Ile Arg Leu Asp Asp Ser Pro Ser Gly Pro Asn Glu Pro Phe  
 65 70 75 80  
 Arg Ile Tyr Arg Thr Arg Gly Pro Glu Thr Asn Pro Lys Gln Gly Leu  
 85 90 95  
 Pro Arg Leu Arg Glu Ser Trp Ile Thr Ala Arg Gly Asp Val Ala Thr  
 100 105 110  
 Tyr Gln Gly Arg Glu Arg Leu Leu Ile Asp Asp Gly Arg Ser Ala Met  
 115 120 125  
 Arg Arg Gly Gln Ala Ser Ala Glu Trp Lys Gly Gln Lys Pro Ala Pro  
 130 135 140  
 Leu Lys Ala Leu Pro Gly Lys Arg Val Thr Gln Met Ala Tyr Ala Arg  
 145 150 155 160  
 Ala Gly Val Ile Thr Arg Glu Met Glu Phe Val Ala Leu Arg Glu His  
 165 170 175  
 Val Asp Ala Glu Phe Val Arg Ser Glu Val Ala Arg Gly Arg Ala Ile  
 180 185 190  
 Ile Pro Asn Asn Val Asn His Pro Glu Ser Glu Pro Met Ile Ile Gly  
 195 200 205  
 Arg Lys Phe Leu Thr Lys Ile Asn Ala Asn Ile Gly Asn Ser Ala Val  
 210 215 220  
 Thr Ser Ser Ile Glu Glu Glu Val Ser Lys Leu Gln Trp Ala Thr Arg  
 225 230 235 240  
 Trp Gly Ala Asp Thr Val Met Asp Leu Ser Thr Gly Asp Asp Ile His  
 245 250 255  
 Thr Thr Arg Glu Trp Ile Ile Arg Asn Ser Pro Val Pro Ile Gly Thr  
 260 265 270  
 Val Pro Ile Tyr Gln Ala Leu Glu Lys Val Asn Gly Val Ala Ala Asp  
 275 280 285  
 Leu Asn Trp Glu Val Phe Arg Asp Thr Ile Ile Glu Gln Cys Glu Gln  
 290 295 300  
 Gly Val Asp Tyr Met Thr Ile His Ala Gly Val Leu Leu Ala Tyr Ile  
 305 310 315 320  
 Pro Leu Thr Thr Arg Arg Val Thr Gly Ile Val Ser Arg Gly Gly Ser  
 325 330 335  
 Ile Met Ala Gly Trp Cys Leu Ala His His Arg Glu Ser Phe Leu Tyr  
 340 345 350  
 Glu His Phe Asp Glu Leu Cys Glu Ile Phe Ala Gln Tyr Asp Val Ala  
 355 360 365  
 Phe Ser Leu Gly Asp Gly Leu Arg Pro Gly Ser Leu Ala Asp Ala Asn

370	375	380
Asp Ala Ala Gln Phe Ala Glu Leu Lys Thr Ile Gly Glu Leu Thr Gln 385 390 395 400		
Arg Ala Trp Glu Tyr Asp Val Gln Val Met Val Glu Gly Pro Gly His 405 410 415		
Val Pro Leu Asn Met Ile Gln Glu Asn Asn Glu Leu Glu Gln Lys Trp 420 425 430		
Ala Ala Asp Ala Pro Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile 435 440 445		
Ala Pro Gly Tyr Asp His Ile Thr Ser Ala Ile Gly Ala Ala His Ile 450 455 460		
Ala Met Gly Gly Thr Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His 465 470 475 480		
Leu Gly Leu Pro Asn Arg Asp Asp Val Lys Thr Gly Val Ile Thr Tyr 485 490 495		
Lys Leu Ala Ala His Ala Ala Asp Val Ala Lys Gly His Pro Gly Ala 500 505 510		
Arg Ala Trp Asp Asp Ala Met Ser Lys Ala Arg Phe Glu Phe Arg Trp 515 520 525		
Asn Asp Gln Phe Ala Leu Ser Leu Asp Pro Asp Thr Ala Ile Ala Tyr 530 535 540		
His Asp Glu Thr Leu Pro Ala Glu Pro Ala Lys Thr Ala His Phe Cys 545 550 555 560		
Ser Met Cys Gly Pro Lys Phe Cys Ser Met Arg Ile Ser Gln Asp Ile 565 570 575		
Arg Asp Met Phe Gly Asp Gln Ile Ala Glu Leu Gly Met Pro Gly Val 580 585 590		
Gly Asp Ser Ser Ser Ala Val Ala Ser Ser Gly Ala Arg Glu Gly Met 595 600 605		
Ala Glu Lys Ser Arg Glu Phe Ile Ala Gly Gly Ala Glu Val Tyr Arg 610 615 620		
Arg 625		

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA01019

&lt;400&gt; 523

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Thr Leu Ala His Ser Leu Ser Phe Pro Asp Ser Leu Arg Asp Gly Pro	
1 5 10 15	
acc gtt gga gac ctc ggg gaa ttt gaa gtg att cgg gta atc acg gag	96
Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu	
20 25 30	
caa gct gga tca tct ctc aac ggc gat gac gca gct gtg ctt cgg cat	144
Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His	
35 40 45	
gca tca ccc aat tcc agg gct gtt gtc acc acc gac atg ttg gtt gcg	192
Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala	
50 55 60	
ggt agg cat ttc caa ttg gat tgg tcc acc ccg gaa caa ata ggg cag	240
Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln	
65 70 75 80	
aag gcg att gtg cag aac ttt gct gat att gag gcg atg ggt gca cgt	288
Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg	
85 90 95	
cca gta gcc gca ttg ttg gcg att tcc gcc ccc aca cac acc ccc gtg	336
Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val	
100 105 110	
gag ttt gtc cga ggc tta gcc cgt ggc atg aat caa cgc ttg gag gag	384
Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu	
115 120 125	
tac tcc gcg gaa ctt gtt ggc gga gac atc acc agc ggg gac tcc ttg	432
Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu	
130 135 140	
gtt att gct gta act gca att ggt caa ctg ggt gga tcc ttg cca gag	480
Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu	
145 150 155 160	
ctg acg ttg gga cgt gcc cga cca gga cag acc ctg gtg gcc cac gga	528
Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly	
165 170 175	
aag atc ggt tac tcc gca gca ggc ctt gct cta ctg cag cac ttt ggt	576
Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly	
180 185 190	
cca gac aac gtt cca gag cac ctt cgc ccc ttg gtg gat gca cac tgc	624
Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys	
195 200 205	
gca cca gtt ctc acc cca ggc cga ggc atg gtg gca cgc gct gct gga	672
Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly	
210 215 220	
gcg acc gcc atg act gat aac tcg gac gga ctg att gtg gat ctt aac	720
Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn	
225 230 235 240	



caa atg gcc atg aag tct ggt gtg cgc atc gat gtg gat tcc tgt agc 768  
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser  
                   245                                  250                                  255

atc agc ccc gat gaa ctc ctt agc gaa gcc gct tcc gta ctc gga aca 816  
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr  
                   260                                  265                                  270

gac gcc tgg cga tgg atc tta agc ggc ggg gaa gac cac acc ctg ctc 864  
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu  
                   275                                  280                                  285

tct acg acg ttt ggc gat gcc ccc tct gga ttc cgc acc atc ggc caa 912  
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln  
                   290                                  295                                  300

gtc acc aaa aca cgc cac gaa gac ctc gtc acc gta gat aag aaa acc 960  
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr  
                   305                                  310                                  315                                  320

ccc gca ttt tcc gat gga tgg aga agc ttc taatgaccaa caccctatgg  
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 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe  
                                   325                                  330

aat  
 1013

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 <213> Corynebacterium glutamicum

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 Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu  
                   20                                  25                                  30  
 Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His  
                   35                                  40                                  45  
 Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala  
                   50                                  55                                  60  
 Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln  
   65                                  70                                  75                                  80  
 Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg  
                   85                                  90                                  95  
 Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val  
                   100                                  105                                  110  
 Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu  
                   115                                  120                                  125  
 Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu  
   130                                  135                                  140

Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu  
 145 150 155 160  
 Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly  
 165 170 175  
 Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly  
 180 185 190  
 Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys  
 195 200 205  
 Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly  
 210 215 220  
 Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn  
 225 230 235 240  
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser  
 245 250 255  
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr  
 260 265 270  
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu  
 275 280 285  
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln  
 290 295 300  
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr  
 305 310 315 320  
 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe  
 325 330

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(706)  
 <223> RXA01352

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 ctggttaaca ccagcgaagg aagcgaggat tgattgtccc gtg ttt gaa aat cgt 115  
 Val Phe Glu Asn Arg  
 1 5  
 ttt gac ctg cgt tgt tat gtt gtg act ggt gcg ggc tcg gtg gat gag 163  
 Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala Gly Ser Val Asp Glu  
 10 15 20  
 gtt gtg cac act gcg tct gct gcg gct cgt ggt ggc gcg ggt gtg gtg 211  
 Val Val His Thr Ala Ser Ala Ala Ala Arg Gly Gly Ala Gly Val Val

25										30					35					
cag	gtg	cgt	tca	aag	cct	att	tcg	cca	gaa	gcg	atg	agg	gag	ttg	gca	259				
Gln	Val	Arg	Ser	Lys	Pro	Ile	Ser	Pro	Glu	Ala	Met	Arg	Glu	Leu	Ala					
40					45					50										
tca	aag	gtt	gcg	ctt	gag	gtt	gcg	cgg	tgc	agc	cca	aca	acg	agg	gtg	307				
Ser	Lys	Val	Ala	Leu	Glu	Val	Ala	Arg	Cys	Ser	Pro	Thr	Thr	Arg	Val					
55					60					65										
ctt	atc	gac	gac	cac	ctc	cac	gtt	gct	tct	tcc	tta	atg	cgc	gaa	gga	355				
Leu	Ile	Asp	Asp	His	Leu	His	Val	Ala	Ser	Ser	Leu	Met	Arg	Glu	Gly					
70					75					80					85					
ctc	ccg	att	cac	ggg	gtg	cat	ctt	ggg	cag	gat	gat	atg	tgc	gtg	ctt	403				
Leu	Pro	Ile	His	Gly	Val	His	Leu	Gly	Gln	Asp	Asp	Met	Ser	Val	Leu					
90					95					100										
gag	gct	cgt	gag	ttg	ttg	ggg	cct	gag	gcg	atc	att	ggg	ttg	act	act	451				
Glu	Ala	Arg	Glu	Leu	Leu	Gly	Pro	Glu	Ala	Ile	Ile	Gly	Leu	Thr	Thr					
105					110					115										
gga	acc	cta	gaa	ctt	gtg	gcg	gcg	gcg	aat	gag	ctg	tcc	gat	gtg	ttg	499				
Gly	Thr	Leu	Glu	Leu	Val	Ala	Ala	Ala	Asn	Glu	Leu	Ser	Asp	Val	Leu					
120					125					130										
gat	tac	atc	ggg	gct	ggg	ccg	ttt	cgg	aag	act	ccc	acc	aag	gat	tca	547				
Asp	Tyr	Ile	Gly	Ala	Gly	Pro	Phe	Arg	Lys	Thr	Pro	Thr	Lys	Asp	Ser					
135					140					145										
ggg	cgg	cca	ccg	att	ggc	ctt	gcg	ggg	tat	ccc	cct	ttg	gtg	gaa	ttg	595				
Gly	Arg	Pro	Pro	Ile	Gly	Leu	Ala	Gly	Tyr	Pro	Pro	Leu	Val	Glu	Leu					
150					155					160					165					
tcc	aag	gtg	ccg	atc	gtt	gcg	att	ggg	gat	gtc	acc	cct	gcc	gat	gtg	643				
Ser	Lys	Val	Pro	Ile	Val	Ala	Ile	Gly	Asp	Val	Thr	Pro	Ala	Asp	Val					
170					175					180										
cgc	gct	ctc	agc	gca	acc	ggg	gtg	gct	ggc	gtt	gcc	atg	gtg	cgg	gct	691				
Arg	Ala	Leu	Ser	Ala	Thr	Gly	Val	Ala	Gly	Val	Ala	Met	Val	Arg	Ala					
185					190					195										
ttt	tct	gaa	tct	gat												706				
Phe	Ser	Glu	Ser	Asp																
200																				

&lt;210&gt; 526

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 526

Val	Phe	Glu	Asn	Arg	Phe	Asp	Leu	Arg	Cys	Tyr	Val	Val	Thr	Gly	Ala
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Gly	Ser	Val	Asp	Glu	Val	Val	His	Thr	Ala	Ser	Ala	Ala	Ala	Arg	Gly
		20					25					30			

Gly	Ala	Gly	Val	Val	Gln	Val	Arg	Ser	Lys	Pro	Ile	Ser	Pro	Glu	Ala
		35				40						45			

Met Arg Glu Leu Ala Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser  
50 55 60

Pro Thr Thr Arg Val Leu Ile Asp Asp His Leu His Val Ala Ser Ser  
65 70 75 80

Leu Met Arg Glu Gly Leu Pro Ile His Gly Val His Leu Gly Gln Asp  
85 90 95

Asp Met Ser Val Leu Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile  
100 105 110

Ile Gly Leu Thr Thr Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu  
115 120 125

Leu Ser Asp Val Leu Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr  
130 135 140

Pro Thr Lys Asp Ser Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro  
145 150 155 160

Pro Leu Val Glu Leu Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val  
165 170 175

Thr Pro Ala Asp Val Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val  
180 185 190

Ala Met Val Arg Ala Phe Ser Glu Ser Asp  
195 200

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<211> 944

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(921)

<223> RXA01381

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Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp  
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att tcc aac att cac cgc caa atc ctc ttc ggc gca agc gat gtc ggt 96  
Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly  
20 25 30

cga ccc aag gtc gag gtt gcc gcc gag cgc ctc aaa gaa ctc caa cca 144  
Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro  
35 40 45

gac atc acc gtc aac gcg ttg cac gaa cgg atc act cca gaa aac gcc 192  
Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala  
50 55 60

tgc gag ctg ctc aat tcc gtg gac ctc gtc tta gac ggc tcc gat tct 240  
Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser

65	70	75	80	
ttc tcc aca aaa tac tta gtg tct gat gcc gcc gaa atc acc gga act				288
Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr				
	85	90	95	
ccc ctc atc tgg gca acg gta ctg cgc ttt cac ggc gaa ctg gca ctc				336
Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu				
	100	105	110	
ttc aac tct ggc ccc gac cac cgc gga gtc ggc ctg cgc gac gtc ttc				384
Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe				
	115	120	125	
ccc gaa caa ccc tcc gcc gat ttc gtc cct gac tgc gcc acc gct ggt				432
Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly				
	130	135	140	
gtt ctt ggc gcc acc aca gcc acc atc ggc gca ctc atg gcc act cac				480
Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His				
	145	150	155	160
gcc atc gga ttt ctc aca gaa atc ggc gac gtc caa cca ggc aca atc				528
Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile				
	165	170	175	
ctc tcc tac gac gca ttc ccc gcc gcc acg cgc agc ttc cgc gtc tcc				576
Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser				
	180	185	190	
gcc gac ccg gcg cgc cca ctg gtc acc cgc ctc cgc gcc tcc tac gag				624
Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu				
	195	200	205	
gca gcg cgc acc gat aca act tcg ctt atc gac gcc acc ctc aac ggc				672
Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly				
	210	215	220	
tcc ctc acc gcc ctc gat atc cga gag cca cat gaa gtt ctg ctc aaa				720
Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys				
	225	230	235	240
gac ctc ccc gag ggc gca acg tca ctg aag ctc ccc tta agc cag atc				768
Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile				
	245	250	255	
acc tcg gac agc gac att tta gag gca ctg tct gga atc gac ggc gac				816
Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp				
	260	265	270	
att ttg gtc tac tgc gct tcg gga atc cgc agt tcc gac ttc atc gac				864
Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp				
	275	280	285	
aac tac tcc cac ctc ggc cac aaa ttt gtg aat ctt ccc ggt ggg gtc				912
Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val				
	290	295	300	
aac gcg ctg tagctgtcaa tttaagaggc cag				944
Asn Ala Leu				
305				

&lt;210&gt; 528

&lt;211&gt; 307

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 528

Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp  
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Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly  
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Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro  
 35 40 45

Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala  
 50 55 60

Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser  
 65 70 75 80

Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr  
 85 90 95

Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu  
 100 105 110

Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe  
 115 120 125

Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly  
 130 135 140

Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His  
 145 150 155 160

Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile  
 165 170 175

Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser  
 180 185 190

Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu  
 195 200 205

Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly  
 210 215 220

Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys  
 225 230 235 240

Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile  
 245 250 255

Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp  
 260 265 270

Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp  
 275 280 285

Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val  
 290 295 300

Asn Ala Leu  
 305

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 <213> Corynebacterium glutamicum

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 <223> RXA01360

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 Met Leu His Ile Ala  
 1 5  
 gat aaa act ttc gat tcc cac ctc atc atg ggc acc ggc gga gcc acc 163  
 Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly Thr Gly Gly Ala Thr  
 10 15 20  
 tct cag gcg ttg ctg gag gaa tcc ctt gtc gcc agt gga act caa ttg 211  
 Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala Ser Gly Thr Gln Leu  
 25 30 35  
 acc acc gtg gcg atg cgt cga cac caa gca acc acc tct agc gga gaa 259  
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 40 45 50

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 530  
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 Ser Gly Thr Gln Leu Thr Thr Val Ala Met Arg Arg His Gln Ala Thr  
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 Thr Ser Ser Gly Glu  
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 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(606)

&lt;223&gt; RXA01361

&lt;400&gt; 531

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Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val	
1 5 10 15	
acg atg aat tcg ggg gtg agg gtt gcg tcg aaa agc gtt gtt gtt ttg	96
Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu	
20 25 30	
gcg gcg ggc ctg ggc gcc gca agc att ccc ggc tgg ttt gag ggc gcg	144
Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala	
35 40 45	
aac cca ttg cag ttg agg ccg gtg tac ggc gat att gtg cgc gtg cgc	192
Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg	
50 55 60	
gtg ccg gag cga ctg cag ccg atg gtc acc aag gtg gtg cgc ggg ttt	240
Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe	
65 70 75 80	
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Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu	
85 90 95	
gcg atc ggc gcg aca agc cgt gag gat cac ccg caa cct cga acg ggc	336
Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly	
100 105 110	
gca gtg cat gat ttg cta cgc gat gct atc cgt ttg att ccg ggc att	384
Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile	
115 120 125	
gaa gaa acc gaa ttt atc gaa gtc acc tgc ggc gcc cgc ccc ggc acc	432
Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr	
130 135 140	
ccg gat gac ctg ccg tac ctg gga tgg gtt gga tcc aat gtg att gcg	480
Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala	
145 150 155 160	
tcc aca gga tat ttc cgc cat gga att ttg ctg tca gcc ctt ggt gca	528
Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala	
165 170 175	
cgc gct gcc gtt gat atg gca acc aac cag cca ctg ttc ccc act ctt	576
Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu	
180 185 190	
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Asp Val Cys Asp Pro Phe Arg His Gln Ile	
195 200	
tta	629



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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 532  
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             20                    25                    30  
 Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala  
             35                    40                    45  
 Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg  
     50                    55                    60  
 Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe  
     65                    70                    75                    80  
 Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu  
             85                    90                    95  
 Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly  
             100                    105                    110  
 Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile  
             115                    120                    125  
 Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr  
     130                    135                    140  
 Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala  
     145                    150                    155                    160  
 Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala  
             165                    170                    175  
 Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu  
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 Asp Val Cys Asp Pro Phe Arg His Gln Ile  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(904)  
 <223> RXA01208

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																Val	Ala	Asn	Ser	Phe	
																1				5	
ttg	gat	tct	tta	act	ctt	gtt	cga	caa	aac	act	ccc	ctt	gtt	cag	tgt	163					
Leu	Asp	Ser	Leu	Thr	Leu	Val	Arg	Gln	Asn	Thr	Pro	Leu	Val	Gln	Cys						
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ttg	acc	aac	tct	gtg	gtc	atg	caa	ttc	acg	gcc	aat	gtg	ttg	ctt	gcc	211					
Leu	Thr	Asn	Ser	Val	Val	Met	Gln	Phe	Thr	Ala	Asn	Val	Leu	Leu	Ala						
				25					30					35							
gcg	ggt	gcg	acc	cct	gcg	atg	gtg	gat	act	cca	gct	gaa	tcg	gca	gaa	259					
Ala	Gly	Ala	Thr	Pro	Ala	Met	Val	Asp	Thr	Pro	Ala	Glu	Ser	Ala	Glu						
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ttc	gcc	gct	gtg	gcc	aat	gga	gtg	ctc	atc	aat	gcg	gga	act	cct	tct	307					
Phe	Ala	Ala	Val	Ala	Asn	Gly	Val	Leu	Ile	Asn	Ala	Gly	Thr	Pro	Ser						
				55					60					65							
gcg	gag	caa	tac	caa	ggc	atg	acc	aag	gcc	att	gag	ggt	gca	cga	aaa	355					
Ala	Glu	Gln	Tyr	Gln	Gly	Met	Thr	Lys	Ala	Ile	Glu	Gly	Ala	Arg	Lys						
				70					75					80							
gct	ggc	aca	cca	tgg	gtg	tta	gac	cca	gtt	gct	gtg	ggt	ggg	ttg	tcg	403					
Ala	Gly	Thr	Pro	Trp	Val	Leu	Asp	Pro	Val	Ala	Val	Gly	Gly	Leu	Ser						
				90					95					100							
gag	agg	acc	aag	tat	gcg	gag	gga	atc	gtc	gat	aag	cag	cct	gcc	gca	451					
Glu	Arg	Thr	Lys	Tyr	Ala	Glu	Gly	Ile	Val	Asp	Lys	Gln	Pro	Ala	Ala						
				105					110					115							
att	cgt	gga	aac	gcc	tca	gag	gtc	gtg	gcg	ctt	gcg	ggg	ctc	ggt	gcc	499					
Ile	Arg	Gly	Asn	Ala	Ser	Glu	Val	Val	Ala	Leu	Ala	Gly	Leu	Gly	Ala						
				120					125					130							
ggt	ggg	cgc	ggc	gta	gac	gcg	acc	gat	tcc	gtg	gaa	gtg	gcg	ttg	gag	547					
Gly	Gly	Arg	Gly	Val	Asp	Ala	Thr	Asp	Ser	Val	Glu	Val	Ala	Leu	Glu						
				135					140					145							
gcg	gcg	caa	ttg	ttg	gcc	aag	cgc	act	ggt	ggc	gtc	gtg	gct	gtc	tct	595					
Ala	Ala	Gln	Leu	Leu	Ala	Lys	Arg	Thr	Gly	Gly	Val	Val	Ala	Val	Ser						
				150					155					160							
ggt	gcg	gag	gac	ttg	att	gtg	tct	gcg	gat	cgg	gtg	acg	tgg	ttg	cgt	643					
Gly	Ala	Glu	Asp	Leu	Ile	Val	Ser	Ala	Asp	Arg	Val	Thr	Trp	Leu	Arg						
				170					175					180							
tcg	ggg	gat	ccg	atg	ttg	cag	ctg	gtg	att	ggc	act	gga	tgc	tct	ttg	691					
Ser	Gly	Asp	Pro	Met	Leu	Gln	Leu	Val	Ile	Gly	Thr	Gly	Cys	Ser	Leu						
				185					190					195							
ggc	gcg	ctg	aca	gct	gca	tat	cta	ggc	gcc	acg	gtt	gac	tca	gat	att	739					
Gly	Ala	Leu	Thr	Ala	Ala	Tyr	Leu	Gly	Ala	Thr	Val	Asp	Ser	Asp	Ile						
				200					205					210							
tcc	gcg	cac	gat	gct	gtg	ttg	gct	gcg	cat	gcc	cat	gtg	ggt	gct	gct	787					
Ser	Ala	His	Asp	Ala	Val	Leu	Ala	Ala	His	Ala	His	Val	Gly	Ala	Ala						
				215					220					225							
ggc	cag	att	gca	gca	cag	aag	gca	tcg	gcg	cca	ggc	agc	ttt	gcg	gtg	835					
Gly	Gln	Ile	Ala	Ala	Gln	Lys	Ala	Ser	Ala	Pro	Gly	Ser	Phe	Ala	Val						

230                      235                      240                      245  
 gcg ttt att gat gcg ctt tat gac gtg gat gcc cag gct gtg gcc tcg 883  
 Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala Gln Ala Val Ala Ser  
                          250                                      255                                      260  
  
 ttg gtt gat gtg cga gag gcc tgaaaagtac gtgactgatt ttt 927  
 Leu Val Asp Val Arg Glu Ala  
                          265  
  
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 <211> 268  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
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 Pro Leu Val Gln Cys Leu Thr Asn Ser Val Val Met Gln Phe Thr Ala  
                          20                                      25                                      30  
 Asn Val Leu Leu Ala Ala Gly Ala Thr Pro Ala Met Val Asp Thr Pro  
                          35                                      40                                      45  
 Ala Glu Ser Ala Glu Phe Ala Ala Val Ala Asn Gly Val Leu Ile Asn  
                          50                                      55                                      60  
 Ala Gly Thr Pro Ser Ala Glu Gln Tyr Gln Gly Met Thr Lys Ala Ile  
                          65                                      70                                      75                                      80  
 Glu Gly Ala Arg Lys Ala Gly Thr Pro Trp Val Leu Asp Pro Val Ala  
                          85                                      90                                      95  
 Val Gly Gly Leu Ser Glu Arg Thr Lys Tyr Ala Glu Gly Ile Val Asp  
                          100                                      105                                      110  
 Lys Gln Pro Ala Ala Ile Arg Gly Asn Ala Ser Glu Val Val Ala Leu  
                          115                                      120                                      125  
 Ala Gly Leu Gly Ala Gly Gly Arg Gly Val Asp Ala Thr Asp Ser Val  
                          130                                      135                                      140  
 Glu Val Ala Leu Glu Ala Ala Gln Leu Leu Ala Lys Arg Thr Gly Gly  
                          145                                      150                                      155                                      160  
 Val Val Ala Val Ser Gly Ala Glu Asp Leu Ile Val Ser Ala Asp Arg  
                          165                                      170                                      175  
 Val Thr Trp Leu Arg Ser Gly Asp Pro Met Leu Gln Leu Val Ile Gly  
                          180                                      185                                      190  
 Thr Gly Cys Ser Leu Gly Ala Leu Thr Ala Ala Tyr Leu Gly Ala Thr  
                          195                                      200                                      205  
 Val Asp Ser Asp Ile Ser Ala His Asp Ala Val Leu Ala Ala His Ala  
                          210                                      215                                      220  
 His Val Gly Ala Ala Gly Gln Ile Ala Ala Gln Lys Ala Ser Ala Pro  
                          225                                      230                                      235                                      240



tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt 595  
 Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly  
 150 155 160 165

att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa 643  
 Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys  
 170 175 180

gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag 691  
 Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys  
 185 190 195

caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg 739  
 Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu  
 200 205 210

atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg 787  
 Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro  
 215 220 225

agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag 835  
 Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu  
 230 235 240 245

aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt 883  
 Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser  
 250 255 260

gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg 931  
 Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val  
 265 270 275

ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg 979  
 Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu  
 280 285 290

aaa gaa gag gaa aat tca ctt tagggataga atcaagatcc atg  
 1023  
 Lys Glu Glu Glu Asn Ser Leu  
 295 300

<210> 536  
 <211> 300  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 536  
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 Ala Leu Leu Gln Glu Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly  
 20 25 30  
 Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala  
 35 40 45  
 Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu  
 50 55 60  
 Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg

65	70	75	80
Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val	85	90	95
Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys	100	105	110
Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe	115	120	125
Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser	130	135	140
Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr	145	150	155
Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val	165	170	175
Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly	180	185	190
Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala	195	200	205
Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala	210	215	220
Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala	225	230	235
Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala	245	250	255
Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg	260	265	270
Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr	275	280	285
Ala Gly Leu Lys Leu Lys Glu Glu Glu Asn Ser Leu	290	295	300

&lt;210&gt; 537

&lt;211&gt; 693

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(670)

&lt;223&gt; RXA02400

&lt;400&gt; 537

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tttaagtcgc cagattaaag tcgtcaatga aaggacatac atg tct att tcc cgc 115  
 Met Ser Ile Ser Arg  
 1 5

acc gtc ttc ggc atc gca gcc acc gca gcc ctg tct gca gct ctc gtt 163  
 Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu Ser Ala Ala Leu Val  
                     10                    15                    20

gcg tgt tct cca cct cac cag cag gat tcc cca gtc cag cgc acc aat 211  
 Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro Val Gln Arg Thr Asn  
                     25                    30                    35

gag atc ttg act act tct cag aac cca act tct gcg agc agc acc tca 259  
 Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser Ala Ser Ser Thr Ser  
                     40                    45                    50

acc tct tcc gca acg act act tcc tca gct cct gtg gaa gag gac gta 307  
 Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro Val Glu Glu Asp Val  
                     55                    60                    65

gag atc gtt gtt tca cca gca gcg ttg gtg gac ggt gag cag gtt acc 355  
 Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp Gly Glu Gln Val Thr  
                     70                    75                    80                    85

ttc gaa atc tct gga ctt gat cca gag ggc ggc tac tac gca gcg atc 403  
 Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly Tyr Tyr Ala Ala Ile  
                     90                    95                    100

tgc gat tcc gta gcg aac cct ggt aac cca gtt cct tct tgc acc ggc 451  
 Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val Pro Ser Cys Thr Gly  
                     105                    110                    115

gaa atg gct gat ttc acg tcc cag gca tgg ttg agc aac tcc cag ccc 499  
 Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu Ser Asn Ser Gln Pro  
                     120                    125                    130

ggc gcg act gta gag atc gca gaa gac ggc acc gca act gtg gag ctt 547  
 Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr Ala Thr Val Glu Leu  
                     135                    140                    145

gaa gct acc gca acc ggc act ggc ttg gac tgc acc act cag gct tgt 595  
 Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys Thr Thr Gln Ala Cys  
                     150                    155                    160                    165

gta gcg aag gtc ttc ggc gat cat acc gaa ggt ttc cgc gat gtt gct 643  
 Val Ala Lys Val Phe Gly Asp His Thr Glu Gly Phe Arg Asp Val Ala  
                     170                    175                    180

gaa gtc cca gtt act ttc gca gcc gct taagtttttct taaaacgcac 690  
 Glu Val Pro Val Thr Phe Ala Ala Ala  
                     185                    190

tca 693

<210> 538  
 <211> 190  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 538  
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<210> 539
<211> 1528
<212> DNA
<213> Corynebacterium glutamicum
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                                         Met Cys Glu Arg Pro
                                         1           5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
                        10                        15                        20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
                        25                        30                        35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val

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40	45	50	
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cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu 70 75 80 85			355
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln 90 95 100			403
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu 105 110 115			451
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly 120 125 130			499
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala 135 140 145			547
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu 150 155 160 165			595
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly 170 175 180			643
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp 185 190 195			691
ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala 200 205 210			739
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu 215 220 225			787
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn 230 235 240 245			835
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr 250 255 260			883
ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly 265 270 275			931
ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His 280 285 290			979

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag  
1027

Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln  
295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc  
1075

Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly  
310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt  
1123

Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly  
330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc  
1171

Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc  
1219

Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc  
1267

Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct  
1315

Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
1363

Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc  
1411

Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac  
1459

Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc  
1507

Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile  
455 460 465

gcc gcc ggc gaa agc gtg gaa  
1528

Ala Ala Gly Glu Ser Val Glu  
470 475

&lt;210&gt; 540

&lt;211&gt; 476

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 540

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu  
 1 5 10 15

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile  
 20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp  
 35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys  
 50 55 60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
 65 70 75 80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
 85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
 100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
 115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
 130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
 145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
 165 170 175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
 180 185 190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
 195 200 205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
 210 215 220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
 225 230 235 240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
 245 250 255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
 260 265 270

Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val  
 275 280 285

Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
 290 295 300  
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
 305 310 315 320  
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
 325 330 335  
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350  
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu  
 355 360 365  
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn  
 370 375 380  
 Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met  
 385 390 395 400  
 Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr  
 405 410 415  
 Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn  
 420 425 430  
 Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg  
 435 440 445  
 Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser  
 450 455 460  
 Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu  
 465 470 475

<210> 541  
 <211> 1528  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1528)  
 <223> FRXA01209

<400> 541  
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 Met Cys Glu Arg Pro  
 1 5  
 gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163  
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val  
 10 15 20  
 ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211  
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile  
 25 30 35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg	259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val	
40 45 50	
gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct	307
Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	
55 60 65	
cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag	355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu	
70 75 80 85	
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa	403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln	
90 95 100	
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa	451
Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu	
105 110 115	
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt	499
Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	
120 125 130	
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg	547
Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala	
135 140 145	
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag	595
Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu	
150 155 160 165	
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga	643
Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly	
170 175 180	
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac	691
Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp	
185 190 195	
ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct	739
Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala	
200 205 210	
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa	787
Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu	
215 220 225	
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat	835
Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn	
230 235 240 245	
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca	883
Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	
250 255 260	
ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc	931
Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	
265 270 275	

ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979  
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His  
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag  
 1027  
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln  
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc  
 1075  
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly  
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt  
 1123  
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly  
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc  
 1171  
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
 345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc  
 1219  
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
 360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc  
 1267  
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
 375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct  
 1315  
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
 1363  
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
 410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc  
 1411  
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac  
 1459  
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc  
 1507  
 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile  
 455 460 465

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Ala Ala Gly Glu Ser Val Glu  
470 475

<210> 542

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 542

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu  
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Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile  
20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp  
35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys  
50 55 60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
65 70 75 80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
165 170 175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
180 185 190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
195 200 205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
210 215 220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
225 230 235 240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
245 250 255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
260 265 270

Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val  
 275 280 285

Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
 290 295 300

Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
 305 310 315 320

Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
 325 330 335

Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350

Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu  
 355 360 365

Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn  
 370 375 380

Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met  
 385 390 395 400

Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr  
 405 410 415

Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn  
 420 425 430

Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg  
 435 440 445

Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser  
 450 455 460

Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu  
 465 470 475

<210> 543

<211> 723

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(700)

<223> RXN01413

<400> 543

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cgggtttcct cagcgtttaa ccatctgaaa ccatctgaga ttg acc cat ctg ttc 115  
 Leu Thr His Leu Phe  
 1 5

tta gaa ctc gat gag cgt tta gta ctg ggt gtt cag caa gat ggt tac 163  
 Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val Gln Gln Asp Gly Tyr  
 10 15 20



caa tgg act gag cat ttg ttc cgg ctg cca ctg caa cat ctc cgt aac 211  
 Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu Gln His Leu Arg Asn  
                   25                                  30                                  35

tcg ccc aat gac ctg cag gga ttg aag ata cga tgg tgt gaa ctt tat 259  
 Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg Trp Cys Glu Leu Tyr  
                   40                                  45                                  50

tcc aca acg ggg aaa gat caa ggg gta gaa ctt ctg cct caa gca acc 307  
 Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu Leu Pro Gln Ala Thr  
                   55                                  60                                  65

gtc gtt acc cca aat aac ttc gag gct tcc acc ctc tcc ggc ctt gag 355  
 Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr Leu Ser Gly Leu Glu  
                   70                                  75                                  80                                  85

aag ctt gag acc gtc gag gac ctc aag gag gct gcc cgc ctc att tat 403  
 Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala Ala Arg Leu Ile Tyr  
                                   90                                  95                                  100

gag caa ggc ccc cag tac gta gtc gtc aag ggt ggc atg gac ttc ccc 451  
 Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly Gly Met Asp Phe Pro  
                                   105                                  110                                  115

ggc gag aac gcc gtg gat gtg ctt ttc gac gga tcc tcc tac cac gtc 499  
 Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly Ser Ser Tyr His Val  
                   120                                  125                                  130

ttc tct gag cca aag att ggt gaa gag cgc gtt tcc ggc gca gtc tgc 547  
 Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val Ser Gly Ala Val Cys  
                   135                                  140                                  145

acc ttc gca gct gtt atc acc gca gag cta gca aag ggt gct gag gtt 595  
 Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Ala Glu Val  
                   150                                  155                                  160                                  165

gta gac cca gtg gca acc gca aag cgt gtg gtc acc cgt gcg gtt caa 643  
 Val Asp Pro Val Ala Thr Ala Lys Arg Val Val Thr Arg Ala Val Gln  
                                   170                                  175                                  180

gat gct gtt gca tcc aac gca cct ttt acc tcc gta tgg ctt gct gag 691  
 Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu  
                                   185                                  190                                  195

gac aac aag tagagtttta aaataccgat caa 723  
 Asp Asn Lys  
                   200

<210> 544  
 <211> 200  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 544  
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           1                                  5                                  10                                  15  
 Gln Gln Asp Gly Tyr Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu  
                   20                                  25                                  30

Gln His Leu Arg Asn Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg  
           35                                  40                                  45  
 Trp Cys Glu Leu Tyr Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu  
           50                                  55                                  60  
 Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr  
           65                                  70                                  75                                  80  
 Leu Ser Gly Leu Glu Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala  
                                   85                                  90                                  95  
 Ala Arg Leu Ile Tyr Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly  
                                   100                                  105                                  110  
 Gly Met Asp Phe Pro Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly  
                                   115                                  120                                  125  
 Ser Ser Tyr His Val Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val  
           130                                  135                                  140  
 Ser Gly Ala Val Cys Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala  
   145                                  150                                  155                                  160  
 Lys Gly Ala Glu Val Val Asp Pro Val Ala Thr Ala Lys Arg Val Val  
                                   165                                  170                                  175  
 Thr Arg Ala Val Gln Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser  
                                   180                                  185                                  190  
 Val Trp Leu Ala Glu Asp Asn Lys  
           195                                  200

<210> 545  
 <211> 795  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(772)  
 <223> RXN01617

<400> 545  
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 tgtttatggc attgggtcca tcacatgctt ggggtggcctt ttg atc cta aag aca 115  
   Leu Ile Leu Lys Thr  
   1                                  5  
 act gga atc acc gtt ttg tcc cgg ttt gat gcg cag gtt atc gct aat 163  
 Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn  
                                   10                                  15                                  20  
 cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg aag atc 211  
 Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val Lys Ile  
                                   25                                  30                                  35  
 ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc gct ttg 259  
 Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu

40	45	50	
gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg atc tgc			307
Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys			
55	60	65	
aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc ctt cgc			355
Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg			
70	75	80	85
gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag			403
Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu			
90	95	100	
gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg			451
Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu			
105	110	115	
aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt			499
Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val			
120	125	130	
gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt			547
Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu			
135	140	145	
ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac			595
Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp			
150	155	160	165
gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca			643
Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala			
170	175	180	
gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag			691
Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys			
185	190	195	
cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg			739
Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro			
200	205	210	
ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatcctt aaacaagctc			792
Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys			
215	220		
cct			795
<210> 546			
<211> 224			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 546			
Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala			
1	5	10	15
Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu			
20	25	30	

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr  
 35 40 45  
 Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp  
 50 55 60  
 Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr  
 65 70 75 80  
 Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr  
 85 90 95  
 Pro Asn Asn Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu  
 100 105 110  
 Thr Ile Asp Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly  
 115 120 125  
 Pro Gln Tyr Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn  
 130 135 140  
 Ala Val Asp Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu  
 145 150 155 160  
 Pro Lys Ile Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala  
 165 170 175  
 Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala  
 180 185 190  
 Val Thr Thr Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val  
 195 200 205  
 Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
 210 215 220

<210> 547  
 <211> 638  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(615)  
 <223> FRXA01617

<400> 547  
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 Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val  
 1 5 10 15  
 aag atc ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc 96  
 Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr  
 20 25 30  
 gct ttg gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg 144  
 Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu

35	40	45	
atc tgc aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc			192
Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala			
50	55	60	
ctt cgc gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac			240
Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn			
65	70	75	80
ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac			288
Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp			
	85	90	95
gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac			336
Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr			
	100	105	110
gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac			384
Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp			
	115	120	125
gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc			432
Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile			
	130	135	140
ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc			480
Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile			
145	150	155	160
acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc			528
Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr			
	165	170	175
gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac			576
Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn			
	180	185	190
gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt			625
Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys			
	195	200	205
aaacaagctc cct			638
<210> 548			
<211> 205			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 548			
Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val			
1	5	10	15
Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr			
	20	25	30
Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu			
35	40	45	
Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala			

50	55	60
Leu Arg Ala Lys Val	Leu Pro Gln Ala Thr Val	Val Thr Pro Asn Asn
65	70	75 80
Phe Glu Ala Thr Thr	Leu Ser Gly Leu Asp Lys	Leu Glu Thr Ile Asp
	85	90 95
Asp Leu Lys Glu Ala Ala	Arg Leu Ile His Glu Gln Gly	Pro Gln Tyr
	100	105 110
Val Val Val Lys Gly Gly	Ile Asp Phe Pro Gly Asp	Asn Ala Val Asp
	115	120 125
Val Leu Phe Asp Gly Thr	Asp Tyr His Val Phe Ser	Glu Pro Lys Ile
	130	135 140
Gly Asp Glu Arg Val Ser	Gly Ala Gly Cys Thr Phe	Ala Ala Val Ile
	145	150 155 160
Thr Ala Glu Leu Ala Lys	Gly Asn Ser Ala Val Asp	Ala Val Thr Thr
	165	170 175
Ala Lys Arg Val Val Thr	Arg Ala Val Lys Asp	Ala Val Ala Ser Asn
	180	185 190
Ala Pro Phe Thr Ser Val	Trp Leu Ala Glu Asp	Asn Lys
	195	200 205

<210> 549  
 <211> 915  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(892)  
 <223> RXS01807

<400> 549  
 gctcaccgag ctggacacca agctccgcgc agtgcaggaa gaacacggcg agctggaaat 60  
 gcagtggctg gaactcggcg aggaaatcga gggctagtctc atg ccg tcg gca ggc 115  
 Met Pro Ser Ala Gly  
 1 5  
 gag gag att tta gag cag cgc gca cag ctg gag ttt gat cag cgc cgc 163  
 Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu Phe Asp Gln Arg Arg  
 10 15 20  
 gcc gat gtg gtg atg atc ggc agc cag gtg gtt tat ggt tcc gtg ggg 211  
 Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly  
 25 30 35  
 ctc agt gct gcc att ccg gtg atg cac aac gaa ggc ctc cgc gtg gtc 259  
 Leu Ser Ala Ala Ile Pro Val Met His Asn Glu Gly Leu Arg Val Val  
 40 45 50  
 gct gtc ccc acc gtg gtg tta agt tcc atg ccg cgt tat gca agt tct 307  
 Ala Val Pro Thr Val Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser

55	60	65	
cac cgc cag ccg atg tcg gac caa tgg ctc gcc gac gcg ctg caa gac His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp 70 75 80 85			355
ctg gtg gat ctg ggg att atc gat gag gtt tcc acc att tcc acc ggc Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser Thr Ile Ser Thr Gly 90 95 100			403
tat ttt acc tcc gct tct cag gtg cgt gtg gtc gct gcg tgg ctg cag Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln 105 110 115			451
aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile 120 125 130			499
atg ggg gac agt gac gtg gga att tat gtc gcc gac gag atc gca acc Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr 135 140 145			547
gcc atc tgc cag gac tta tgc cct ctg gct acc gga atc att ccc aat Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn 150 155 160 165			595
gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu 170 175 180			643
ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr Ser Ala Thr Glu Thr 185 190 195			691
gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu 200 205 210			739
atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val 215 220 225			787
tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile 230 235 240 245			835
gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr 250 255 260			883
aaa gcg ctt taggttttcgt ccgtctctga cag Lys Ala Leu			915

&lt;210&gt; 550

&lt;211&gt; 264

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 550

Met Pro Ser Ala Gly Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu  
 1 5 10 15  
 Phe Asp Gln Arg Arg Ala Asp Val Val Met Ile Gly Ser Gln Val Val  
 20 25 30  
 Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu  
 35 40 45  
 Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro  
 50 55 60  
 Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala  
 65 70 75 80  
 Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser  
 85 90 95  
 Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val  
 100 105 110  
 Ala Ala Trp Leu Gln Lys Ile Arg Glu Thr His Pro His Val Arg Ile  
 115 120 125  
 Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala  
 130 135 140  
 Asp Glu Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr  
 145 150 155 160  
 Gly Ile Ile Pro Asn Ala Phe Glu Leu Ser His Met Val Gly Ser Gly  
 165 170 175  
 Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr  
 180 185 190  
 Ser Ala Thr Glu Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg  
 195 200 205  
 Asp Ser Val Gln Glu Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys  
 210 215 220  
 Gly Ala Gly Asp Val Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys  
 225 230 235 240  
 Asp Phe Ser Leu Ile Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys  
 245 250 255  
 Ala Gly Leu Gln Thr Lys Ala Leu  
 260

<210> 551  
 <211> 622  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(622)  
 <223> RXC01021



&lt;400&gt; 551

cgagaggctt ttttggctct aagcctttta gtcgtgcgaa cgaaatctta agcagcctcg 60

gtgccaccga gatcgattgg tcgctgtaag gtatctgatt atg tcc agt tcc gaa 115  
 Met Ser Ser Ser Glu  
 1 5

agc tcg cgt tcc gaa ggc tcg cag cca gca ccg tct gta cag cct gaa 163  
 Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro Ser Val Gln Pro Glu  
 10 15 20

cgc cgt gct gat tca acg ggg gct cct gcg gca gct tcc aag gaa gct 211  
 Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ala Ser Lys Glu Ala  
 25 30 35

tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct 259  
 Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu Trp Ala Arg Thr Ala  
 40 45 50

gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc 307  
 Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile Asn Ala Leu Asn Val  
 55 60 65

ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg 355  
 Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met  
 70 75 80 85

aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg ggt gat gtc 403  
 Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly Glu Leu Gly Asp Val  
 90 95 100

gca agg att act gag gct ttg gct gtt ggt tct gtg cgt gga gcc cga 451  
 Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg  
 105 110 115

gga aat tct gga gta gtc ctt agt cag gtc ctt cgc gct att gct cag 499  
 Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu Arg Ala Ile Ala Gln  
 120 125 130

gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta 547  
 Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Glu Ala Leu  
 135 140 145

tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtg gag 595  
 Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Glu  
 150 155 160 165

ggc act gtt gtc act gtg ttg cgt tct 622  
 Gly Thr Val Val Thr Val Leu Arg Ser  
 170

&lt;210&gt; 552

&lt;211&gt; 174

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 552

Met Ser Ser Ser Glu Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro  
 1 5 10 15

Ser Val Gln Pro Glu Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala  
20 25 30

Ala Ser Lys Glu Ala Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu  
35 40 45

Trp Ala Arg Thr Ala Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile  
50 55 60

Asn Ala Leu Asn Val Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn  
65 70 75 80

Met Thr Tyr Thr Met Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly  
85 90 95

Glu Leu Gly Asp Val Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser  
100 105 110

Val Arg Gly Ala Arg Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu  
115 120 125

Arg Ala Ile Ala Gln Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr  
130 135 140

Ile Gln Glu Ala Leu Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile  
145 150 155 160

Thr Asp Pro Val Glu Gly Thr Val Val Thr Val Leu Arg Ser  
165 170

<210> 553

<211> 1107

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1084)

<223> RXN02246

<400> 553

tgccgacgct ggcgtggatg ccttcgttgc aggttccgct gtgtacggcg ctgaggatcc 60

caacaaggcg atccaggagt tgcgagcact cgcgacagtaa atg gat gtt gcg cac 115  
Met Asp Val Ala His  
1 5

gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc 163  
Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr  
10 15 20

agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag 211  
Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu Asp Ala Asp Gly Glu  
25 30 35

gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa 259  
Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Gly Pro His Ala Glu  
40 45 50

gtg	gtg	gcg	ctt	gca	gct	gcc	gga	gtg	cgt	gcc	aac	ggg	ggc	acg	gcg	307
Val	Val	Ala	Leu	Ala	Ala	Ala	Gly	Val	Arg	Ala	Asn	Gly	Gly	Thr	Ala	
	55					60					65					
gtg	gtc	acc	ctc	gag	ccg	tgc	aac	cat	tac	ggc	cgc	acg	ggt	cca	tgt	355
Val	Val	Thr	Leu	Glu	Pro	Cys	Asn	His	Tyr	Gly	Arg	Thr	Gly	Pro	Cys	
	70				75					80					85	
tcc	aag	gcg	ctt	ctc	gac	gcc	ggg	atc	gca	cac	gtg	ttt	tac	gcc	aat	403
Ser	Lys	Ala	Leu	Leu	Asp	Ala	Gly	Ile	Ala	His	Val	Phe	Tyr	Ala	Asn	
				90					95					100		
gcg	gat	ccc	ttc	ccg	tca	gcc	gct	ggg	ggc	ggt	gcc	ttt	ttg	gcg	gag	451
Ala	Asp	Pro	Phe	Pro	Ser	Ala	Ala	Gly	Gly	Gly	Ala	Phe	Leu	Ala	Glu	
			105					110					115			
gcg	ggc	gtc	gat	acg	cat	ttt	tta	gat	gag	cgg	atc	agg	gca	ctg	gag	499
Ala	Gly	Val	Asp	Thr	His	Phe	Leu	Asp	Glu	Arg	Ile	Arg	Ala	Leu	Glu	
		120					125					130				
ccc	tgg	ctg	gtt	gcg	acg	cgt	ctg	ggc	agg	ccc	cat	gtc	acg	ttg	aag	547
Pro	Trp	Leu	Val	Ala	Thr	Arg	Leu	Gly	Arg	Pro	His	Val	Thr	Leu	Lys	
	135					140					145					
ttt	gcg	tcc	acc	gtg	gac	ggc	ttt	gct	ggc	gcc	acc	gat	ggc	acc	agc	595
Phe	Ala	Ser	Thr	Val	Asp	Gly	Phe	Ala	Gly	Ala	Thr	Asp	Gly	Thr	Ser	
150					155					160					165	
cag	tgg	att	acc	ggg	ccg	gat	gcg	cgg	gcg	ttt	gtg	cac	gaa	gat	cga	643
Gln	Trp	Ile	Thr	Gly	Pro	Asp	Ala	Arg	Ala	Phe	Val	His	Glu	Asp	Arg	
				170				175						180		
agt	aaa	aga	gat	gcg	atc	atc	gtg	ggt	acc	ggc	act	gcg	ttg	act	gat	691
Ser	Lys	Arg	Asp	Ala	Ile	Ile	Val	Gly	Thr	Gly	Thr	Ala	Leu	Thr	Asp	
			185				190						195			
aat	ccc	tcc	ttg	acg	gcg	cgg	acc	gat	acg	ggc	ctt	tat	gaa	aat	caa	739
Asn	Pro	Ser	Leu	Thr	Ala	Arg	Thr	Asp	Thr	Gly	Leu	Tyr	Glu	Asn	Gln	
		200					205					210				
ccc	agg	cgc	gtt	gtt	att	ggc	tcc	cgc	gag	gtt	cca	gca	gat	tcc	aac	787
Pro	Arg	Arg	Val	Val	Ile	Gly	Ser	Arg	Glu	Val	Pro	Ala	Asp	Ser	Asn	
	215					220					225					
ttg	gct	cgc	ttg	gga	tat	gag	cag	tac	gcg	gga	ata	cca	gag	gct	tta	835
Leu	Ala	Arg	Leu	Gly	Tyr	Glu	Gln	Tyr	Ala	Gly	Ile	Pro	Glu	Ala	Leu	
230				235						240					245	
tca	gcg	ctg	tgg	gat	aaa	ggg	tgc	cga	gac	att	tta	atc	gaa	ggt	ggc	883
Ser	Ala	Leu	Trp	Asp	Lys	Gly	Cys	Arg	Asp	Ile	Leu	Ile	Glu	Gly	Gly	
			250					255						260		
cca	acg	tta	gct	ggg	gca	gcg	ctg	cgc	tta	ggc	att	gtt	gat	cag	gtg	931
Pro	Thr	Leu	Ala	Gly	Ala	Ala	Leu	Arg	Leu	Gly	Ile	Val	Asp	Gln	Val	
			265				270						275			
cag	gcc	tat	gtt	gcc	ccc	gct	ttg	ttg	ggc	gct	gga	cga	tca	gtg	att	979
Gln	Ala	Tyr	Val	Ala	Pro	Ala	Leu	Leu	Gly	Ala	Gly	Arg	Ser	Val	Ile	
	280					285						290				

aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc  
1027

Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr  
295 300 305

acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga  
1075

Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg  
310 315 320 325

aag gaa cac taaatgttca caggtattgt cga  
1107

Lys Glu His

<210> 554

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 554

Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln  
1 5 10 15

Val Arg Gly Thr Thr Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu  
20 25 30

Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly  
35 40 45

Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala  
50 55 60

Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly  
65 70 75 80

Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His  
85 90 95

Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly  
100 105 110

Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg  
115 120 125

Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro  
130 135 140

His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala  
145 150 155 160

Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe  
165 170 175

Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly  
180 185 190

Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly  
195 200 205

Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val  
210 215 220

Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly  
225 230 235 240

Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile  
245 250 255

Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly  
260 265 270

Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala  
275 280 285

Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile  
290 295 300

Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu  
305 310 315 320

Ile Glu Met Met Arg Lys Glu His  
325

<210> 555

<211> 1107

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1084)

<223> FRXA02246

<400> 555

tgccgacgct ggcgtggatg ccttcgttgc aggttccgct gtgtacggcg ctgaggatcc 60  
caacaaggcg atccaggagt tgcgagcact cgcgacagtaa atg gat gtt gcg cac 115  
Met Asp Val Ala His  
1 5  
gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc 163  
Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr  
10 15 20  
agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag 211  
Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu Asp Ala Asp Gly Glu  
25 30 35  
gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa 259  
Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Gly Pro His Ala Glu  
40 45 50  
gtg gtg gcg ctt gca gct gcc gga gtg cgt gcc aac ggg ggc acg gcg 307  
Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala Asn Gly Gly Thr Ala  
55 60 65  
gtg gtc acc ctc gag ccg tgc aac cat tac ggc cgc acg ggt cca tgt 355  
Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly Arg Thr Gly Pro Cys  
70 75 80 85

tcc aag gcg ctt ctc gac gcc ggg atc gca cac gtg ttt tac gcc aat 403  
 Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His Val Phe Tyr Ala Asn  
                     90                                    95                                    100

gcg gat ccc ttc ccg tca gcc gct ggg ggc ggt gcc ttt ttg gcg gag 451  
 Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly Ala Phe Leu Ala Glu  
                     105                                    110                                    115

gcg ggc gtc gat acg cat ttt tta gat gag cgg atc agg gca ctg gag 499  
 Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg Ile Arg Ala Leu Glu  
                     120                                    125                                    130

ccc tgg ctg gtt gcg acg cgt ctg ggc agg ccc cat gtc acg ttg aag 547  
 Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro His Val Thr Leu Lys  
                     135                                    140                                    145

ttt gcg tcc acc gtg gac ggt ttt gct ggt gcc acc gat ggc acc agc 595  
 Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala Thr Asp Gly Thr Ser  
 150                                    155                                    160                                    165

cag tgg att acc ggg ccg gat gcg cgg gcg ttt gtg cac gaa gat cga 643  
 Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe Val His Glu Asp Arg  
                     170                                    175                                    180

agt aaa aga gat gcg atc atc gtg ggt acc ggt act gcg ttg act gat 691  
 Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly Thr Ala Leu Thr Asp  
                     185                                    190                                    195

aat ccc tcc ttg acg gcg cgg acc gat acg ggt ctt tat gaa aat caa 739  
 Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly Leu Tyr Glu Asn Gln  
                     200                                    205                                    210

ccc agg cgc gtt gtt att ggc tcc cgc gag gtt cca gca gat tcc aac 787  
 Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val Pro Ala Asp Ser Asn  
                     215                                    220                                    225

ttg gct cgc ttg gga tat gag cag tac gcg gga ata cca gag gct tta 835  
 Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly Ile Pro Glu Ala Leu  
 230                                    235                                    240                                    245

tca gcg ctg tgg gat aaa ggg tgc cga gac att tta atc gaa ggt ggc 883  
 Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile Leu Ile Glu Gly Gly  
                     250                                    255                                    260

cca acg tta gct ggg gca gcg ctg cgc tta ggc att gtt gat cag gtg 931  
 Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly Ile Val Asp Gln Val  
                     265                                    270                                    275

cag gcc tat gtt gcc ccc gct ttg ttg ggc gct gga cga tca gtg att 979  
 Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala Gly Arg Ser Val Ile  
                     280                                    285                                    290

aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc  
 1027  
 Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr  
                     295                                    300                                    305

acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga  
 1075  
 Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg

310

315

320

325

aag gaa cac taaatgttca caggtattgt cga  
 1107  
 Lys Glu His

&lt;210&gt; 556

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 556

Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln  
 1 5 10 15

Val Arg Gly Thr Thr Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu  
 20 25 30

Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly  
 35 40 45

Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala  
 50 55 60

Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly  
 65 70 75 80

Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His  
 85 90 95

Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly  
 100 105 110

Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg  
 115 120 125

Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro  
 130 135 140

His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala  
 145 150 155 160

Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe  
 165 170 175

Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly  
 180 185 190

Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly  
 195 200 205

Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val  
 210 215 220

Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly  
 225 230 235 240

Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile  
 245 250 255

Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly  
260 265 270

Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala  
275 280 285

Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile  
290 295 300

Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu  
305 310 315 320

Ile Glu Met Met Arg Lys Glu His  
325

<210> 557

<211> 756

**<212> DNA**

<213> *Corynebacterium glutamicum*

**<220>**

<221> CDS

**<222> (101) . . (733)**

<223> RXA02247

**<400> 557**

acaagaaacc acgatggatc agattatgcg ttttgacacc acgtccgtga gacagttggg 60

ttcagatgta ttgatagaaa tgatgagaaa ggaacactaa atg ttc aca ggt att 115  
Met Phe Thr Gly Ile  
1 5

gtc gag gag ctt ggc tcc gtt gca ggc gtg gaa cat ctg gga gat tcc 163  
Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu His Leu Gly Asp Ser  
10 15 20

atc cgg atg cag att tcc gcg tcc acc gtt tta gag ggt gtg cat ttg 211  
Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu Glu Gly Val His Leu  
25 30 35

ggg gat tcc att tct gtc aat ggt gtg tgc ttg aca gtg gcg tcc ttt 259  
 Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu Thr Val Ala Ser Phe  
 40 45 50

ggc gag gga cat ttc act gca gac ctc atg cag gaa acc tta gat cgc 307  
Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln Glu Thr Leu Asp Arg  
55 60 65

agc tcc ctg ggc gca tta tcc acc ggt agc aaa gtc aac ctt gag cgc 355  
Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys Val Asn Leu Glu Arg  
70 75 80 85

gcc atg gca gcc gat ggc cgt ctg ggt gga cac atc atg caa ggc cat 403  
Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His Ile Met Gln Gly His  
90 95 100

gtt gat gcc acc acc tcg ctg atc aag cgc acc agc tca gag aac tgg 451  
Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr Ser Ser Glu Asn Trp  
105 110 115



gat gtt ctg cgt ttt gag ctg cca gct gat ttg gct cgc tat gtg gtg 499  
Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu Ala Arg Tyr Val Val  
120 125 130

gaa aaa ggc tcc atc gca ctc aat ggc aca tcc ttg act gta tcg tct 547  
Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser Leu Thr Val Ser Ser  
135 140 145

ttg ggt gat gat tgg ttt gag gtt tcc ctg att ccc acc acc ttg cgc 595  
Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile Pro Thr Thr Leu Arg  
150 155 160 165

gac acc acc cac ggc gaa ctg gcg gta ggg gat atc gta aac att gag 643  
Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp Ile Val Asn Ile Glu  
170 175 180

gtt gat gtg atc gct aag tac gtc gaa cgc atg atg acg cgc ggc gtg 691  
Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met Met Thr Arg Gly Val  
185 190 195

gct gga aac act ccc aat gac tac acc gat ttc acg aga gac 733  
Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe Thr Arg Asp  
200 205 210

taggttagac aacgtgagtg aac 756

&lt;210&gt; 558

&lt;211&gt; 211

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 558

Met Phe Thr Gly Ile Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu  
1 5 10 15

His Leu Gly Asp Ser Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu  
20 25 30

Glu Gly Val His Leu Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu  
35 40 45

Thr Val Ala Ser Phe Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln  
50 55 60

Glu Thr Leu Asp Arg Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys  
65 70 75 80

Val Asn Leu Glu Arg Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His  
85 90 95

Ile Met Gln Gly His Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr  
100 105 110

Ser Ser Glu Asn Trp Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu  
115 120 125

Ala Arg Tyr Val Val Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser  
130 135 140

Leu Thr Val Ser Ser Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile  
 145 150 155 160

Pro Thr Thr Leu Arg Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp  
 165 170 175

Ile Val Asn Ile Glu Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met  
 180 185 190

Met Thr Arg Gly Val Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe  
 195 200 205

Thr Arg Asp  
 210

<210> 559

<211> 1389

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1366)

<223> RXN02248

<400> 559

gatgtgatcg ctaagtacgt cgaacgcatg atgacgcgcg gcgtggctgg aaacactccc 60

aatgactaca ccgatttcac gagagactag gttagacaac gtg agt gaa cat gag 115  
 Val Ser Glu His Glu  
 1 5

cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163  
 Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile  
 10 15 20

gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211  
 Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn  
 25 30 35

gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259  
 Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val  
 40 45 50

gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307  
 Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr  
 55 60 65

gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat 355  
 Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn  
 70 75 80 85

cag gat gcc cgc ggc acc gct tac acc gtg acc gtt gat gcc aac acc 403  
 Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr  
 90 95 100

ggc acc aca ggc att tct gca aca gac cgc gcc cac act ttg cgc ttg 451  
 Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu  
 105 110 115

ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac 499  
 Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His  
 120 125 130

gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga 547  
 Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly  
 135 140 145

cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca 595  
 His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro  
 150 155 160 165

gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg 643  
 Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met  
 170 175 180

gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag 691  
 Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys  
 185 190 195

ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att 739  
 Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg Arg Lys Asn Glu Ile  
 200 205 210

ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg 787  
 Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr  
 215 220 225

ttc aag gct gtt ggt tac cgt tcc atc atc gat ggc acc gag ctt gtt 835  
 Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val  
 230 235 240 245

gcc att gtt gcc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg 883  
 Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu  
 250 255 260

gtt cga gtc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg 931  
 Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg  
 265 270 275

cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag 979  
 Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln  
 280 285 290

gaa gct ggt cgg gga gta gtg gtg tac atg cgt ggg cat gag gga cga  
 1027  
 Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg  
 295 300 305

ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa  
 1075  
 Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu  
 310 315 320 325

ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat  
 1123  
 Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp  
 330 335 340

gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg  
 1171

Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val  
 345 350 355

cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt  
 1219

Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu  
 360 365 370

gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct  
 1267

Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala  
 375 380 385

gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg  
 1315

Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met  
 390 395 400 405

gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa  
 1363

Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu  
 410 415 420

aac taaggagcac aacaatggct aaa  
 1389

Asn

<210> 560

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 560

Val Ser Glu His Glu Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu  
 1 5 10 15

Ala Ile Ala Asp Ile Ala Ala Gly Lys Ala Val Val Val Val Asp Asp  
 20 25 30

Glu Asp Arg Glu Asn Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala  
 35 40 45

Thr Pro Glu Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile  
 50 55 60

Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro  
 65 70 75 80

Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr  
 85 90 95

Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala  
 100 105 110

His Thr Leu Arg Leu Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe  
 115 120 125

Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val  
 130 135 140

Leu Val Arg Ala Gly His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala  
 145 150 155 160  
 Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu  
 165 170 175  
 Asp Pro Thr Gly Met Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp  
 180 185 190  
 Glu His Asp Leu Lys Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg  
 195 200 205  
 Arg Lys Asn Glu Ile Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro  
 210 215 220  
 Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp  
 225 230 235 240  
 Gly Thr Glu Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly  
 245 250 255  
 Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp  
 260 265 270  
 Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser  
 275 280 285  
 Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg  
 290 295 300  
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr  
 305 310 315 320  
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu  
 325 330 335  
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu  
 340 345 350  
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala  
 355 360 365  
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr  
 370 375 380  
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr  
 385 390 395 400  
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu  
 405 410 415  
 Gln Glu His Pro Glu Asn  
 420

&lt;210&gt; 561

&lt;211&gt; 1389

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1366)  
 <223> FRXA02248

<400> 561

gatgtgatcg ctaagtacgt cgaacgcatg atgacgcgcg gcgtggctgg aaacactccc 60

aatgactaca ccgatttcac gagagactag gttagacaac gtg agt gaa cat gag 115  
 Val Ser Glu His Glu  
 1 5

cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163  
 Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile  
 10 15 20

gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211  
 Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn  
 25 30 35

gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259  
 Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val  
 40 45 50

gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307  
 Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr  
 55 60 65

gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat 355  
 Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn  
 70 75 80 85

cag gat gcc cgc ggc acc gct tac acc gtg acc gtt gat gcc aac acc 403  
 Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr  
 90 95 100

ggc acc aca ggc att tct gca aca gac cgc gcc cac act ttg cgc ttg 451  
 Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu  
 105 110 115

ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac 499  
 Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His  
 120 125 130

gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga 547  
 Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly  
 135 140 145

cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca 595  
 His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro  
 150 155 160 165

gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg 643  
 Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met  
 170 175 180

gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag 691  
 Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys  
 185 190 195

ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att 739

Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg Arg Lys Asn Glu Ile	
200 205 210	
ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg	787
Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr	
215 220 225	
ttc aag gct gtt ggt tac cgt tcc atc atc gat ggc acc gag ctt gtt	835
Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val	
230 235 240 245	
gcc att gtt gcc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg	883
Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu	
250 255 260	
gtt cga gtc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg	931
Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg	
265 270 275	
cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag	979
Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln	
280 285 290	
gaa gct ggt cgg gga gta gtg gtg tac atg cgt ggg cat gag gga cga	
1027	
Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg	
295 300 305	
ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa	
1075	
Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu	
310 315 320 325	
ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat	
1123	
Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp	
330 335 340	
gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg	
1171	
Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val	
345 350 355	
cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt	
1219	
Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu	
360 365 370	
gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct	
1267	
Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala	
375 380 385	
gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg	
1315	
Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met	
390 395 400 405	
gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa	
1363	
Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu	

410

415

420

aac taaggagcac aacaatggct aaa  
1389  
Asn

&lt;210&gt; 562

&lt;211&gt; 422

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 562

Val Ser Glu His Glu Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu  
1 5 10 15

Ala Ile Ala Asp Ile Ala Ala Gly Lys Ala Val Val Val Val Asp Asp  
20 25 30

Glu Asp Arg Glu Asn Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala  
35 40 45

Thr Pro Glu Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile  
50 55 60

Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro  
65 70 75 80

Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr  
85 90 95

Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala  
100 105 110

His Thr Leu Arg Leu Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe  
115 120 125

Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val  
130 135 140

Leu Val Arg Ala Gly His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala  
145 150 155 160

Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu  
165 170 175

Asp Pro Thr Gly Met Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp  
180 185 190

Glu His Asp Leu Lys Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg  
195 200 205

Arg Lys Asn Glu Ile Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro  
210 215 220

Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp  
225 230 235 240

Gly Thr Glu Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly  
245 250 255



Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp  
 260 265 270

Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser  
 275 280 285

Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg  
 290 295 300

Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr  
 305 310 315 320

Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu  
 325 330 335

Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu  
 340 345 350

Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala  
 355 360 365

Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr  
 370 375 380

Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr  
 385 390 395 400

Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu  
 405 410 415

Gln Glu His Pro Glu Asn  
 420

<210> 563

<211> 600

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(577)

<223> RXN02249

<400> 563

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tgtgggaaca agagcaccca gaaaactaag gagcacaaca atg gct aaa gaa gga 115  
 Met Ala Lys Glu Gly  
 1 5

ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163  
 Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val  
 10 15 20

gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211  
 Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His  
 25 30 35

gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259

Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg  
40 45 50

gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307  
Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg  
55 60 65

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355  
Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr  
70 75 80 85

cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403  
Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg  
90 95 100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451  
Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr  
105 110 115

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499  
Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val  
120 125 130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547  
Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu  
135 140 145

gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaaggt 597  
Val Leu Ser Gln Ile Arg Ala Thr Glu Gly  
150 155

ttg 600

<210> 564  
<211> 159  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 564  
Met Ala Lys Glu Gly Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly  
1 5 10 15  
Leu Lys Val Ala Val Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp  
20 25 30  
Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr  
35 40 45  
Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val  
50 55 60  
Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val  
65 70 75 80  
Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr  
85 90 95  
Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn  
100 105 110

Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly  
 115 120 125

Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala  
 130 135 140

Leu Asp Thr Ala Leu Val Leu Ser Gln Ile Arg Ala Thr Glu Gly  
 145 150 155

<210> 565

<211> 600

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(577)

<223> FRXA02249

<400> 565

atgttcgata cctgaaaacc aagcgtgacc gcatgggaca tgacctccca gatgtcgcac 60

tgtgggaaca agagcaccca gaaaactaag gagcacaaca atg gct aaa gaa gga 115  
 Met Ala Lys Glu Gly  
 1 5

ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163  
 Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val  
 10 15 20

gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211  
 Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His  
 25 30 35

gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259  
 Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg  
 40 45 50

gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307  
 Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg  
 55 60 65

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355  
 Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr  
 70 75 80 85

cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403  
 Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg  
 90 95 100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451  
 Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr  
 105 110 115

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499  
 Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val  
 120 125 130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547  
 Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu

135 140 145

gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaaggt 597  
 Val Leu Ser Gln Ile Arg Ala Thr Glu Gly  
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 Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val  
 50 55 60  
 Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val  
 65 70 75 80  
 Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr  
 85 90 95  
 Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn  
 100 105 110  
 Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly  
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 Val Thr Thr Asn Ala

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ccc gac gga gca acg aac aac atc aac aac gca cat tcg ggc gct gtc																163	
Pro Asp Gly Ala Thr Asn Asn Ile Asn Asn Ala His Ser Gly Ala Val																	
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ggg aag cca aag gta cag ctc agc gat gcg gaa att cag gaa tac acc																211	
Gly Lys Pro Lys Val Gln Leu Ser Asp Ala Glu Ile Gln Glu Tyr Thr																	
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Ala Ala Phe Ala Gly Thr Thr Thr Thr Lys Pro Trp Glu Leu Glu Val																	
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Thr Thr Lys Phe Leu Lys Lys Ile Ala Trp Val Ala Val Val Val Ile																	
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Met Ala Val His Ile Phe Met Gly Ala Val Val Asp Val Asp Phe Thr																	
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Gly Ala Ala Val Thr Phe Val Asp Thr Leu Ala Phe Pro Ala Leu Gly																	
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Ile Ile Phe Ser Val Leu Val Phe Leu Gly Leu Thr Arg Pro Arg Val																	
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cgt gcc aac gaa gac ggc gtt gag gtg cgt aac ttc atc gga act cgt																499	
Arg Ala Asn Glu Asp Gly Val Glu Val Arg Asn Phe Ile Gly Thr Arg																	
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Phe Tyr Pro Trp Val Val Ile Tyr Gly Met Ser Phe Pro Lys Gly Ser																	
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Ser Val Ala Arg Leu Glu Leu Pro Asp Phe Glu Phe Val Pro Met Trp																	
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Ala Phe Gln Ser Arg Asp Gly Glu Asp Val Val Arg Ala Val Ala Thr																	
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ttc cgc gac ctc gaa aac aag tac atg cca gag gac taattaagct																689	
Phe Arg Asp Leu Glu Asn Lys Tyr Met Pro Glu Asp																	
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&lt;210&gt; 568

&lt;211&gt; 193

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 568

Val Thr Thr Asn Ala Pro Asp Gly Ala Thr Asn Asn Ile Asn Asn Ala

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5

10

15

His	Ser	Gly	Ala	Val	Gly	Lys	Pro	Lys	Val	Gln	Leu	Ser	Asp	Ala	Glu	
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Ile	Gln	Glu	Tyr	Thr	Ala	Ala	Phe	Ala	Gly	Thr	Thr	Thr	Thr	Lys	Pro	
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Trp	Glu	Leu	Glu	Val	Thr	Thr	Lys	Phe	Leu	Lys	Lys	Ile	Ala	Trp	Val	
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Ala	Val	Val	Val	Ile	Met	Ala	Val	His	Ile	Phe	Met	Gly	Ala	Val	Val	
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Asp	Val	Asp	Phe	Thr	Gly	Ala	Ala	Val	Thr	Phe	Val	Asp	Thr	Leu	Ala	
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Phe	Pro	Ala	Leu	Gly	Ile	Ile	Phe	Ser	Val	Leu	Val	Phe	Leu	Gly	Leu	
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Thr	Arg	Pro	Arg	Val	Arg	Ala	Asn	Glu	Asp	Gly	Val	Glu	Val	Arg	Asn	
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Phe	Pro	Lys	Gly	Ser	Ser	Val	Ala	Arg	Leu	Glu	Leu	Pro	Asp	Phe	Glu	
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Phe	Val	Pro	Met	Trp	Ala	Phe	Gln	Ser	Arg	Asp	Gly	Glu	Asp	Val	Val	
				165					170					175		
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                                         Val Asp Ile Trp Ser
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gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att 163
Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile
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ggg gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag 211
Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu

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Phe	Asp	Pro	His	Pro	Ile	Ala	Val	Phe	Leu	Pro	Gly	Lys	Glu	Pro	Thr	
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Arg	Leu	Ala	Pro	Leu	Asp	Tyr	Arg	Leu	Asn	Leu	Ala	Ala	Glu	Cys	Gly	
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Val	Asp	Ala	Ala	Leu	Val	Ile	Asp	Phe	Thr	Lys	Glu	Leu	Ala	Gly	Leu	
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Ser	Ala	Glu	Glu	Tyr	Phe	Thr	Thr	Met	Ile	Val	Asp	Thr	Leu	His	Ala	
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cgt	tca	gtt	gtg	gtg	ggg	gag	aac	ttc	acc	ttc	ggt	gtc	aat	ggc	gct	499
Arg	Ser	Val	Val	Val	Gly	Glu	Asn	Phe	Thr	Phe	Gly	Val	Asn	Gly	Ala	
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Gly	Thr	Glu	Ser	Thr	Met	Arg	Glu	Leu	Gly	Gln	Lys	Phe	Gly	Val	Asn	
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gtc	acg	att	gct	ccg	ctg	ctg	cat	gat	gat	gac	cag	cgt	att	tgc	tcc	595
Val	Thr	Ile	Ala	Pro	Leu	Leu	His	Asp	Asp	Asp	Gln	Arg	Ile	Cys	Ser	
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Thr	Leu	Val	Arg	Asp	Tyr	Leu	Asp	Gln	Gly	Glu	Val	Glu	Arg	Ala	Asn	
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Trp	Ala	Leu	Gly	Arg	Arg	Tyr	Ala	Val	Arg	Gly	Glu	Val	Val	Arg	Gly	
185				190				195								
gct	ggc	cgt	ggc	ggc	aaa	gaa	ttg	ggc	tat	ccc	acc	gcg	aat	ctc	tac	739
Ala	Gly	Arg	Gly	Gly	Lys	Glu	Leu	Gly	Tyr	Pro	Thr	Ala	Asn	Leu	Tyr	
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ctg	ccg	acc	tct	gtg	gcg	ctg	ccc	gcc	gat	ggc	gtg	tat	gca	ggc	tgg	787
Leu	Pro	Thr	Ser	Val	Ala	Leu	Pro	Ala	Asp	Gly	Val	Tyr	Ala	Gly	Trp	
215				220				225								
ttc	acc	atc	acc	gat	gac	cgc	gaa	atc	gac	aag	gaa	atc	tcc	cgc	gat	835
Phe	Thr	Ile	Thr	Asp	Asp	Arg	Glu	Ile	Asp	Lys	Glu	Ile	Ser	Arg	Asp	
230				235				240				245				
atc	gac	ggc	acc	atg	gtt	cca	ggc	gtg	cgt	tac	caa	act	gcc	att	tcc	883
Ile	Asp	Gly	Thr	Met	Val	Pro	Gly	Val	Arg	Tyr	Gln	Thr	Ala	Ile	Ser	
250				255				260								
gtg	ggc	acc	aat	ccc	acc	ttc	ggc	gat	gag	cga	cgc	agc	gtc	gag	gca	931
Val	Gly	Thr	Asn	Pro	Thr	Phe	Gly	Asp	Glu	Arg	Arg	Ser	Val	Glu	Ala	
265				270				275								

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 Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly His His Val Met Val  
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gaa ttc gtg gga cac ttg cgc gac atg gtc aaa ttc aac ggc gtc gac  
 1027  
 Glu Phe Val Gly His Leu Arg Asp Met Val Lys Phe Asn Gly Val Asp  
           295                                  300                                  305

gag cta cta gac gcc atg gcc cga gat gtc acc aac gcc cgc gac atc  
 1075  
 Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr Asn Ala Arg Asp Ile  
 310                                  315                                  320                                  325

ctt gcc aaa gac aaa ttg ctt ctc gac gcc gac acc cag ccc agc gct  
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 Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp Thr Gln Pro Ser Ala  
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 1146

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 <213> Corynebacterium glutamicum

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 Ser Leu Ile Gly Glu Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro  
                                   35                                  40                                  45  
 Cys Val Met Val Thr Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro  
                                   50                                  55                                  60  
 Gly Lys Glu Pro Thr Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu  
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 Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys  
                                   85                                  90                                  95  
 Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val  
                                   100                                  105                                  110  
 Asp Thr Leu His Ala Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe  
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 Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln  
                                   130                                  135                                  140  
 Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp  
   145                                  150                                  155                                  160  
 Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu



165 170 175  
 Val Glu Arg Ala Asn Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly  
 180 185 190  
 Glu Val Val Arg Gly Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro  
 195 200 205  
 Thr Ala Asn Leu Tyr Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly  
 210 215 220  
 Val Tyr Ala Gly Trp Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys  
 225 230 235 240  
 Glu Ile Ser Arg Asp Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr  
 245 250 255  
 Gln Thr Ala Ile Ser Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg  
 260 265 270  
 Arg Ser Val Glu Ala Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly  
 275 280 285  
 His His Val Met Val Glu Phe Val Gly His Leu Arg Asp Met Val Lys  
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 Phe Asn Gly Val Asp Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr  
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 Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys Ile Leu Ala Gln Thr  
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 aag gat ttc cat gac tcc ctc acc aag cca ccc gga tct ttg ggc aag 211  
 Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro Gly Ser Leu Gly Lys  
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ttg gag cag atc ggc tgt ttc att tcc gca tgc cag ggc cag att ccg	259
Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys Gln Gly Gln Ile Pro	
40 45 50	
cca cgt cca ctc aac aac tca aag atc gtt gtt ttc gct ggc gat cac	307
Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val Phe Ala Gly Asp His	
55 60 65	
ggc gtt gca act aaa ggc gtg tcc gcg tac cca tcc tca gta agc ttg	355
Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro Ser Ser Val Ser Leu	
70 75 80 85	
cag atg gct gaa aac att aca aac ggt ggc gcc gcc atc aac gtg att	403
Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala Ala Ile Asn Val Ile	
90 95 100	
gca cgc acc acc ggc acg tcc gtc cga ctt att gat acc tcc ctc gac	451
Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile Asp Thr Ser Leu Asp	
105 110 115	
cac gaa gca tgg ggc gac gag cgc gta tct agg tcc tgc gga tcc atc	499
His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg Ser Cys Gly Ser Ile	
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Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val Glu Arg Ala Leu Lys	
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Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp Ala Gly Ala Asp Ile	
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Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr Thr Thr Ala Ala Ala	
170 175 180	
ctc gtt gga acg ttc acc ctc gca gag cct gtt gtt gtc gta ggc cgc	691
Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val Val Val Val Gly Arg	
185 190 195	
ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc	739
Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu Lys Val Ser Ala Ile	
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cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc	787
Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala	
215 220 225	
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Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Ala Met Ala Ala Phe	
230 235 240 245	
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Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val	
250 255 260	
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Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala	
265 270 275	
agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc	979

Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser  
 280 285 290

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Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met  
 295 300 305

tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag  
 1075

Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys  
 310 315 320 325

att gcc gtt gac ctg atg aac gac atg tcg aca ttt tct tcc gcc ggc  
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Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly  
 330 335 340

gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg  
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<211> 358

<212> PRT

<213> Corynebacterium glutamicum

<400> 572

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Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val  
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Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro  
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Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala  
 85 90 95

Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile  
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Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg  
 115 120 125

Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val  
 130 135 140

Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp  
 145 150 155 160  
 Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr  
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 Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val  
 180 185 190  
 Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu  
 195 200 205  
 Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg  
 210 215 220  
 Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala  
 225 230 235 240  
 Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val  
 245 250 255  
 Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys  
 260 265 270  
 Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr  
 275 280 285  
 Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile  
 290 295 300  
 Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala  
 305 310 315 320  
 Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr  
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 Pro Glu Gln Asn Thr Glu  
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 Val Asp Ile Trp Ser  
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gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att 163  
 Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile  
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ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag 211  
 Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu  
 25 30 35

gcc aag aag cag gcc gag gag ctg ggt gtg cct tgt gtc atg gtg acc 259  
 Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro Cys Val Met Val Thr  
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ttt gac ccg cat ccg atc gct gtg ttt ttg cca ggt aaa gag cca acc 307  
 Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro Gly Lys Glu Pro Thr  
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cgt ttg gct cct ttg gat tat cgc ctt aat ttg gct gcg gaa tgt ggc 355  
 Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu Ala Ala Glu Cys Gly  
 70 75 80 85

gtc gat gct gcg ttg gtt att gat ttc act aaa gaa ctc gca ggt ctg 403  
 Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys Glu Leu Ala Gly Leu  
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agc gct gaa gag tat ttc aca acc atg atc gtg gat acg ctg cat gcg 451  
 Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val Asp Thr Leu His Ala  
 105 110 115

cgt tca gtt gtg gtg ggg gag aac ttc acc ttc ggt gtc aat ggc gct 499  
 Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe Gly Val Asn Gly Ala  
 120 125 130

ggc act gag tcc acg atg cgg gaa ttg gga caa aag ttt ggc gtg aat 547  
 Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln Lys Phe Gly Val Asn  
 135 140 145

gtc acg att gct ccg ctg ctg cat gat gat gac cag cgt att tgc tcc 595  
 Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp Gln Arg Ile Cys Ser  
 150 155 160 165

acc ttg gtg cgc gat tac ttg gat cag ggc gag gtt gag cgc gcg aac 643  
 Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu Val Glu Arg Ala Asn  
 170 175 180

tgg gcg ctt ggt cga cgc tat gcc gtg cgc ggc gaa gtt gtc cgt ggt 691  
 Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly Glu Val Val Arg Gly  
 185 190 195

gct ggc cgt ggc ggc aaa gaa ttg ggc tat ccc acc gcg aat ctc tac 739  
 Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro Thr Ala Asn Leu Tyr  
 200 205 210

ctg ccg acc tct gtg gcg ctg ccc gcc gat ggc gtg tat gca ggc tgg 787  
 Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly Val Tyr Ala Gly Trp  
 215 220 225

ttc acc atc acc gat gac cgc gaa atc gac aag gaa atc tcc cgc gat 835  
 Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys Glu Ile Ser Arg Asp  
 230 235 240 245

atc gac ggc acc atg gtt cca ggc gtg cgt tac caa act gcc att tcc 883

Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr Gln Thr Ala Ile Ser  
250 255 260

gtg ggc acc aat ccc acc ttc ggc gat gag cga cgc agc gtc gag gca 931  
Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg Arg Ser Val Glu Ala  
265 270 275

ttc	atc	ctc	gac	cag	gaa	gcc	gac	ctg	tac	ggt	cac	cat	gtc	atg	gtg	979
Phe	Ile	Leu	Asp	Gln	Glu	Ala	Asp	Leu	Tyr	Gly	His	His	Val	Met	Val	
		280					285					290				

gaa ttc gtg gga cac ttg cgc gac atg gtc aaa ttc aac ggc gtc gac  
1027  
Glu Phe Val Gly His Leu Arg Asp Met Val Lys Phe Asn Gly Val Asp  
295 300 305

gag cta cta gac gcc atg gcc cga gat gtc acc aac gcc cgc gac atc  
1075  
Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr Asn Ala Arg Asp Ile  
310 315 320 325

ctt gcc aaa gac aaa ttg ctt ctc gac gcc gac acc cag ccc agc gct  
1123  
Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp Thr Gln Pro Ser Ala  
330 335 340

taaggccggt caccggccat caa  
1146

<210> 574

**<211> 341**

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 574

Val Asp Ile Trp Ser Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly  
1 5 10 15

Ser Val Val Thr Ile Gly Val Phe Asp Gly Leu His Arg Gly His Gln  
20 25 30

Ser Leu Ile Gly Glu Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro  
35 40 45

Cys Val Met Val Thr Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro  
50 55 60

Gly Lys Glu Pro Thr Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu  
65 70 75 80

Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys  
85 90 95

Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val  
100 105 110

Asp Thr Leu His Ala Arg S r Val Val Val Gly Glu Asn Phe Thr Phe  
115 120 125

Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln

130                      135                      140  
 Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp  
 145                      150                      155                      160  
 Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu  
                     165                      170                      175  
 Val Glu Arg Ala Asn Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly  
                     180                      185                      190  
 Glu Val Val Arg Gly Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro  
                     195                      200                      205  
 Thr Ala Asn Leu Tyr Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly  
                     210                      215                      220  
 Val Tyr Ala Gly Trp Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys  
 225                      230                      235                      240  
 Glu Ile Ser Arg Asp Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr  
                     245                      250                      255  
 Gln Thr Ala Ile Ser Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg  
                     260                      265                      270  
 Arg Ser Val Glu Ala Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly  
                     275                      280                      285  
 His His Val Met Val Glu Phe Val Gly His Leu Arg Asp Met Val Lys  
                     290                      295                      300  
 Phe Asn Gly Val Asp Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr  
 305                      310                      315                      320  
 Asn Ala Arg Asp Ile Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp  
                     325                      330                      335  
 Thr Gln Pro Ser Ala  
                     340

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (87)..(782)  
 <223> RXN01712

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                     Met Val Asp Ile Leu Glu Leu Ile Gly  
                     1                      5  
 ccc cta cct ttt gtg tct acg cca gag tta agg gca att gtc gtg act 161  
 Pro Leu Pro Phe Val Ser Thr Pro Glu Leu Arg Ala Ile Val Val Thr

10	15	20	25	
gcc att aat ggt tcc acc act att aat ggc acg tct ggt cag ctt gga				209
Ala Ile Asn Gly Ser Thr Thr Ile Asn Gly Thr Ser Gly Gln Leu Gly				
	30	35	40	
aat tcc acg gat acg gaa ctt ctg ttg gcg ctt cgc agg tgg tcg gac				257
Asn Ser Thr Asp Thr Glu Leu Leu Leu Ala Leu Arg Arg Trp Ser Asp				
	45	50	55	
gtg gtg ttg gtt ggg tcg agc acg gtg aag gct gaa aat tat ggt ggc				305
Val Val Leu Val Gly Ser Ser Thr Val Lys Ala Glu Asn Tyr Gly Gly				
	60	65	70	
gtg gag gtt tcg cct gaa atc cag aag caa cgc cag gag ttg ggt cag				353
Val Glu Val Ser Pro Glu Ile Gln Lys Gln Arg Gln Glu Leu Gly Gln				
	75	80	85	
gaa gcg att ccg ccg att gcg gtg atg tca ggg tcg ttg aat ttt gat				401
Glu Ala Ile Pro Pro Ile Ala Val Met Ser Gly Ser Leu Asn Phe Asp				
	90	95	100	105
gtg gat act cgc ttt ttc ctt gag gcc gaa gtg ccg ccg atc atc atc				449
Val Asp Thr Arg Phe Phe Leu Glu Ala Glu Val Pro Pro Ile Ile Ile				
	110	115	120	
acg gat aat tcc gat caa gca aag cag cag ccg ctt gtg gat gct ggg				497
Thr Asp Asn Ser Asp Gln Ala Lys Gln Gln Arg Leu Val Asp Ala Gly				
	125	130	135	
gct cag gtt att gag gtg gag acg ttg acg gcg gag gtt ggc gtc gaa				545
Ala Gln Val Ile Glu Val Glu Thr Leu Thr Ala Glu Val Gly Val Glu				
	140	145	150	
aag ctt agg tct ttg ggt tac gcc cgc att gat tgt gag ggc ggt gca				593
Lys Leu Arg Ser Leu Gly Tyr Ala Arg Ile Asp Cys Glu Gly Gly Ala				
	155	160	165	
acg ttg tat ggg cag atg ttg gcc gcc gat ctt gtt gat gtg tgg cat				641
Thr Leu Tyr Gly Gln Met Leu Ala Ala Asp Leu Val Asp Val Trp His				
	170	175	180	185
cac acg att gat ccg acg ttg tcg ggc agc gtg gag cgc ccc acg gtg				689
His Thr Ile Asp Pro Thr Leu Ser Gly Ser Val Glu Arg Pro Thr Val				
	190	195	200	
aag ggc ggc gat gat gcg ccg cgc cga ttc gcg ttg gag cac gtc ttt				737
Lys Gly Gly Asp Asp Ala Pro Arg Arg Phe Ala Leu Glu His Val Phe				
	205	210	215	
gtc gat gat gac agc acc cta ttc ttg cgg tat aag cgc gcc aag				782
Val Asp Asp Asp Ser Thr Leu Phe Leu Arg Tyr Lys Arg Ala Lys				
	220	225	230	
tgagtgttgg actctccgga tct				805

&lt;210&gt; 576

&lt;211&gt; 232

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



&lt;400&gt; 576

Met Val Asp Ile Leu Glu Leu Ile Gly Pro Leu Pro Phe Val Ser Thr  
 1 5 10 15

Pro Glu Leu Arg Ala Ile Val Val Thr Ala Ile Asn Gly Ser Thr Thr  
 20 25 30

Ile Asn Gly Thr Ser Gly Gln Leu Gly Asn Ser Thr Asp Thr Glu Leu  
 35 40 45

Leu Leu Ala Leu Arg Arg Trp Ser Asp Val Val Leu Val Gly Ser Ser  
 50 55 60

Thr Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile  
 65 70 75 80

Gln Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala  
 85 90 95

Val Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu  
 100 105 110

Glu Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala  
 115 120 125

Lys Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu  
 130 135 140

Thr Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr  
 145 150 155 160

Ala Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu  
 165 170 175

Ala Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu  
 180 185 190

Ser Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro  
 195 200 205

Arg Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu  
 210 215 220

Phe Leu Arg Tyr Lys Arg Ala Lys  
 225 230

&lt;210&gt; 577

&lt;211&gt; 578

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (55) .. (555)

&lt;223&gt; FRXA01712

&lt;400&gt; 577

cttctgttgg cgcttcgcag gtggtcggac gtgggtgttgg ttgggtcgag caccgtg 57  
 Val

1

aag gct gaa aat tat ggt ggc gtg gag gtt tcg cct gaa atc cag aag 105  
Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln Lys  
5 10 15

caa cgc cag gag ttg ggt cag gaa gcg att ccg ccg att gcg gtg atg 153  
Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val Met  
20 25 30

tca ggg tcg ttg aat ttt gat gtg gat act cgc ttt ttc ctt gag gcc 201  
Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu Ala  
35 40 45

gaa gtg ccg ccg atc atc atc acg gat aat tcc gat caa gca aag cag 249  
Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys Gln  
50 55 60 65

cag cgg ctt gtg gat gct ggg gct cag gtt att gag gtg gag acg ttg 297  
Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr Leu  
70 75 80

acg gcg gag gtt ggc gtc gaa aag ctt agg tct ttg ggt tac gcc cgc 345  
Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala Arg  
85 90 95

att gat tgt gag ggc ggt gca acg ttg tat ggg cag atg ttg gcc gcc 393  
Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala Ala  
100 105 110

gat ctt gtt gat gtg tgg cat cac acg att gat ccg acg ttg tcg ggc 441  
Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser Gly  
115 120 125

agc gtg gag cgc ccc acg gtg aag ggc ggc gat gat gcg ccg cgc cga 489  
Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg Arg  
130 135 140 145

ttc gcg ttg gag cac gtc ttt gtc gat gat gac agc acc cta ttc ttg 537  
Phe Ala Leu Glu His Val Phe Val Asp Asp Ser Thr Leu Phe Leu  
150 155 160

cgg tat aag cgc gcc aag tgagtgttgg actctccgga tct 578  
Arg Tyr Lys Arg Ala Lys  
165

&lt;210&gt; 578

&lt;211&gt; 167

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 578

Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln  
1 5 10 15

Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val  
20 25 30

Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu  
35 40 45

Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys  
50 55 60

Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr  
65 70 75 80

Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala  
85 90 95

Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala  
100 105 110

Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser  
115 120 125

Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg  
130 135 140

Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu Phe  
145 150 155 160

Leu Arg Tyr Lys Arg Ala Lys  
165

<210> 579

<211> 831

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(808)

<223> RXN02384

<400> 579

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aatacgagcc tggctacgag gacgattaag aggtagtcct gtg act cgt cgc ctg 115  
Val Thr Arg Arg Leu  
1 5

att ctg ctc cga cac ggg cag act gaa tac aac gcc acg tcc cga atg 163  
Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn Ala Thr Ser Arg Met  
10 15 20

cag gga caa ttg gac aca gag ctg tct gac ctg ggc ttt caa cag gcg 211  
Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu Gly Phe Gln Gln Ala  
25 30 35

gcc agc gca gcc tca gtg ctg gtt caa aaa aac atc acc cat gtg ttc 259  
Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn Ile Thr His Val Phe  
40 45 50

agc tcg gat ctt tcc cgc gcc ttc aac acc gca agc gcg gtt gcg gcg 307  
Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala Ser Ala Val Ala Ala  
55 60 65

ctg att gac gcg gag gtg cgc gtc gat aag cgt ctt cgg gaa acg cat 355  
Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg Leu Arg Glu Thr His

70	75	80	85	
ttg ggt gag tgg cag gcc aaa acc cac act gag gtg gat tcc gaa tat				403
Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu Val Asp Ser Glu Tyr				
	90	95	100	
cca ggt gcg cgc gct caa tgg cgc cac gat ccg cag tgg gca cca ccc				451
Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro Gln Trp Ala Pro Pro				
	105	110	115	
ggc ggc gaa tcg cgc gtg gat gtt gcg cgc cgg gca cgc caa gtt gtc				499
Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg Ala Arg Gln Val Val				
	120	125	130	
gac gag ttg atg gtg tcg ctt gat gat tgg gat gaa ggc acc gtg ctc				547
Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp Glu Gly Thr Val Leu				
	135	140	145	
atc gtg gct cac ggt ggc acg att aat gcg ctg acc tcg aat ctt ttg				595
Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu Thr Ser Asn Leu Leu				
	150	155	160	165
gac ctg gcg tat gat cag tac ccc atg ttc tct gga ctt gga aat acc				643
Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser Gly Leu Gly Asn Thr				
	170	175	180	
tgt tgg gca caa ttg acc gcc cga cct cgc tat tat gca ggt agt gag				691
Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr Tyr Ala Gly Ser Glu				
	185	190	195	
aac cca gaa gat gac ctc aag att tct tcg gcg gtt tcc aac agc cct				739
Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala Val Ser Asn Ser Pro				
	200	205	210	
cat ttt gag ggc aac aat gtg gaa aac gcc cag tgg tat ctt gac ggc				787
His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln Trp Tyr Leu Asp Gly				
	215	220	225	
tgg aac atg ggt gtt acg cag taaagaagat ggcaataaaa atg				831
Trp Asn Met Gly Val Thr Gln				
	230	235		
<210> 580				
<211> 236				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 580				
Val Thr Arg Arg Leu Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn				
1	5	10	15	
Ala Thr Ser Arg Met Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu				
	20	25	30	
Gly Phe Gln Gln Ala Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn				
	35	40	45	
Ile Thr His Val Phe Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala				
	50	55	60	

Ser Ala Val Ala Ala Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg  
 65 70 75 80  
 Leu Arg Glu Thr His Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu  
 85 90 95  
 Val Asp Ser Glu Tyr Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro  
 100 105 110  
 Gln Trp Ala Pro Pro Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg  
 115 120 125  
 Ala Arg Gln Val Val Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp  
 130 135 140  
 Glu Gly Thr Val Leu Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu  
 145 150 155 160  
 Thr Ser Asn Leu Leu Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser  
 165 170 175  
 Gly Leu Gly Asn Thr Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr  
 180 185 190  
 Tyr Ala Gly Ser Glu Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala  
 195 200 205  
 Val Ser Asn Ser Pro His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln  
 210 215 220  
 Trp Tyr Leu Asp Gly Trp Asn Met Gly Val Thr Gln  
 225 230 235

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 <212> DNA  
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<220>  
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 <223> RXN01560

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 Val Gly Val Ser Tyr  
 1 5  
 atc atc gcc ggc gat gag cag ctg gat atg gca gaa gcc gtt cgc aaa 163  
 Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala Glu Ala Val Arg Lys  
 10 15 20  
 att ggg gag acc ttt aaa act gag gaa att atc ctt ggt ggc gga gga 211  
 Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile Leu Gly Gly Gly Gly  
 25 30 35  
 acc ctg aac tgg tcc atg ctc cgc gac ggt ttg tgc gac gag gtt agc 259  
 Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu Cys Asp Glu Val Ser

40	45	50	
atc gtg atg atg cca atc gcc gat ggt gaa aag cac acc cac tct ttg			307
Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys His Thr His Ser Leu			
55	60	65	
ttc gaa gcc gat gaa aaa tac tca gca ccg ttg ccg atc ggt ttt tca			355
Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu Pro Ile Gly Phe Ser			
70	75	80	85
ctc gcc agc gtt gaa cca cta gaa gat gga agc gtt tgg atg cgt tac			403
Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser Val Trp Met Arg Tyr			
90	95	100	
ggg gtc aat ggc cca gtg gac gcg aac taggtagcaa atactcgctc			450
Gly Val Asn Gly Pro Val Asp Ala Asn			
105	110		
ttt			453
<210> 582			
<211> 110			
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<213> Corynebacterium glutamicum			
<400> 582			
Val Gly Val Ser Tyr Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala			
1	5	10	15
Glu Ala Val Arg Lys Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile			
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Leu Gly Gly Gly Gly Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu			
35	40	45	
Cys Asp Glu Val Ser Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys			
50	55	60	
His Thr His Ser Leu Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu			
65	70	75	80
Pro Ile Gly Phe Ser Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser			
85	90	95	
Val Trp Met Arg Tyr Gly Val Asn Gly Pro Val Asp Ala Asn			
100	105	110	
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<212> DNA			
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agcaccgaga	tctgtgctga	agaattcaat	gattggggttg	atg	att	gcg	ttg	aag	115							
				Met	Ile	Ala	Leu	Lys								
				1				5								
tcc	atg	tct	aac	agg	gta	gta	caa	aag	cca	aaa	atg	aaa	gcg	ccg	cta	163
Ser	Met	Ser	Asn	Arg	Val	Val	Gln	Lys	Pro	Lys	Met	Lys	Ala	Pro	Leu	
			10						15					20		
ccc	atc	cg	gac	ggc	ctc	aac	cct	tcc	cgt	gtg	cg	ttg	ccg	ctc	gac	211
Pro	Ile	Arg	Asp	Gly	Leu	Asn	Pro	Ser	Arg	Val	Arg	Leu	Pro	Leu	Asp	
			25					30					35			
gcg	gcg	ccg	atc	cg	gcc	atc	gat	ttt	gtt	gaa	tac	ctc	att	tcc	acg	259
Ala	Ala	Pro	Ile	Arg	Ala	Ile	Asp	Phe	Val	Glu	Tyr	Leu	Ile	Ser	Thr	
		40					45					50				
cag	cg	cac	cg	aat	ccg	gcc	gac	aac	gcc	gaa	gcg	ctt	caa	gcg	cgt	307
Gln	Arg	His	Arg	Asn	Pro	Ala	Asp	Asn	Ala	Glu	Ala	Leu	Gln	Ala	Arg	
	55					60					65					
ttc	gac	gcc	gac	ctt	gtt	gtc	aac	cac	tac	ggc	gag	ccc	tac	gcc	ccc	355
Phe	Asp	Ala	Asp	Leu	Val	Val	Asn	His	Tyr	Gly	Glu	Pro	Tyr	Ala	Pro	
70					75					80					85	
gac	acc	atg	gtt	cag	ccc	gac	gac	gac	att	tgg	ttc	tac	cg	atg	ccc	403
Asp	Thr	Met	Val	Gln	Pro	Asp	Asp	Asp	Ile	Trp	Phe	Tyr	Arg	Met	Pro	
				90					95					100		
gcc	gcc	gaa	cgg	ccg	atc	cct	tac	aaa	att	cat	gtc	att	cac	gaa	gac	451
Ala	Ala	Glu	Arg	Pro	Ile	Pro	Tyr	Lys	Ile	His	Val	Ile	His	Glu	Asp	
			105					110					115			
gat	gac	atc	ctc	gtc	att	gac	aag	cca	ccc	tac	cta	gca	acc	atg	cct	499
Asp	Asp	Ile	Leu	Val	Ile	Asp	Lys	Pro	Pro	Tyr	Leu	Ala	Thr	Met	Pro	
		120					125					130				
cgt	ggc	cg	cac	atc	acc	gaa	acc	gct	ctg	gtg	aaa	atg	cgt	gtg	ctg	547
Arg	Gly	Arg	His	Ile	Thr	Glu	Thr	Ala	Leu	Val	Lys	Met	Arg	Val	Leu	
	135					140					145					
act	gga	aac	aac	gat	ctc	acc	cca	gct	cac	cg	ctc	gat	cg	ctg	act	595
Thr	Gly	Asn	Asn	Asp	Leu	Thr	Pro	Ala	His	Arg	Leu	Asp	Arg	Leu	Thr	
150					155					160					165	
tcc	ggt	gtg	tta	gtc	atg	gtg	aaa	aaa	cca	gaa	ctc	cgt	ggc	gct	tac	643
Ser	Gly	Val	Leu	Val	Met	Val	Lys	Lys	Pro	Glu	Leu	Arg	Gly	Ala	Tyr	
				170					175					180		
caa	acc	ttg	ttt	gcc	cga	cgt	gag	gcg	tcc	aaa	acc	tat	gag	gca	atc	691
Gln	Thr	Leu	Phe	Ala	Arg	Arg	Glu	Ala	Ser	Lys	Thr	Tyr	Glu	Ala	Ile	
			185					190					195			
gca	gaa	ttc	gtt	cca	ggg	cta	ctt	gat	gat	ggt	ccc	gcg	att	tgg	gaa	739
Ala	Glu	Phe	Val	Pro	Gly	Leu	Leu	Asp	Asp	Gly	Pro	Ala	Ile	Trp		

ggc ccc gtc aac gca cgc act gaa ctg gtg tca gtc acc cca gtc gaa 835  
 Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser Val Thr Pro Val Glu  
 230 235 240 245

gac gcc gaa cag agc atc ctc gaa gaa atg cac ggg cca ctc ccc cgc 883  
 Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His Gly Pro Leu Pro Arg  
 250 255 260

caa gcg cgc tac gtt cta gcc ccc tca aca ggc aaa acc cac cag ctg 931  
 Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly Lys Thr His Gln Leu  
 265 270 275

cgc atc cac atg cgc gac ttc gca gcc ccc atc ctc ggc gac ccc ctc 979  
 Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile Leu Gly Asp Pro Leu  
 280 285 290

tac ccc gtc ctc cac gca gtc gac gat gag gac tac acc acc cca atg  
 1027  
 Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp Tyr Thr Thr Pro Met  
 295 300 305

cac ctc atc gcc cgc acg cta acc ttc gtg gat cct caa acc aac gag  
 1075  
 His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp Pro Gln Thr Asn Glu  
 310 315 320 325

gaa cgt acc ttt gtg agt aat cga cct acg gga agt ttg taggcctcgt  
 1124  
 Glu Arg Thr Phe Val Ser Asn Arg Pro Thr Gly Ser Leu  
 330 335

agacatcacc cag  
 1137

<210> 584

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 584

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Met Lys Ala Pro Leu Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val  
 20 25 30

Arg Leu Pro Leu Asp Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu  
 35 40 45

Tyr Leu Ile Ser Thr Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu  
 50 55 60

Ala Leu Gln Ala Arg Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly  
 65 70 75 80

Glu Pro Tyr Ala Pro Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp  
 85 90 95

Phe Tyr Arg Met Pro Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His  
 100 105 110



Val Ile His Glu Asp Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr  
 115 120 125  
 Leu Ala Thr Met Pro Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val  
 130 135 140  
 Lys Met Arg Val Leu Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg  
 145 150 155 160  
 Leu Asp Arg Leu Thr Ser Gly Val Leu Val Met Val Lys Lys Pro Glu  
 165 170 175  
 Leu Arg Gly Ala Tyr Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys  
 180 185 190  
 Thr Tyr Glu Ala Ile Ala Glu Phe Val Pro Gly Leu Leu Asp Asp Gly  
 195 200 205  
 Pro Ala Ile Trp Glu Ser Arg Ile Glu Lys Glu Arg Gly Ile Val Gln  
 210 215 220  
 Ala Phe Val Val Glu Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser  
 225 230 235 240  
 Val Thr Pro Val Glu Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His  
 245 250 255  
 Gly Pro Leu Pro Arg Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly  
 260 265 270  
 Lys Thr His Gln Leu Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile  
 275 280 285  
 Leu Gly Asp Pro Leu Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp  
 290 295 300  
 Tyr Thr Thr Pro Met His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp  
 305 310 315 320  
 Pro Gln Thr Asn Glu Glu Arg Thr Phe Val Ser Asn Arg Pro Thr Gly  
 325 330 335  
 Ser Leu

<210> 585  
 <211> 1281  
 <212> DNA  
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<220>  
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 <222> (101)..(1258)  
 <223> RXC01711

<400> 585  
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 gtgggatagc atcggcaacg cggttgcatg gccgttggcc atg ttg ttg atg gcg 115

												Met	Leu	Leu	Met	Ala	
												1				5	
cat	cgc	ttc	ttc	gtg	ctt	gcg	att	aac	ggc	gca	gtc	acc	gac	gat	ttc		163
His	Arg	Phe	Phe	Val	Leu	Ala	Ile	Asn	Gly	Ala	Val	Thr	Asp	Asp	Phe		
				10					15					20			
acg	acg	gtt	tat	agt	gct	tta	cga	cgt	ttc	gtt	gaa	ggc	att	ccg	gtc		211
Thr	Thr	Val	Tyr	Ser	Ala	Leu	Arg	Arg	Phe	Val	Glu	Gly	Ile	Pro	Val		
			25					30					35				
tac	aac	gag	gtc	tac	cac	ttc	gtc	gat	ccg	cac	tac	ctc	tat	aac	ccg		259
Tyr	Asn	Glu	Val	Tyr	His	Phe	Val	Asp	Pro	His	Tyr	Leu	Tyr	Asn	Pro		
		40					45					50					
ggc	gcc	acc	ctc	cta	ttg	gca	cca	ttg	gga	tat	atc	acc	cat	ttc	acg		307
Gly	Ala	Thr	Leu	Leu	Leu	Ala	Pro	Leu	Gly	Tyr	Ile	Thr	His	Phe	Thr		
	55					60					65						
ttg	gct	cgg	tgg	atg	ttc	atc	gcg	gtg	aac	ctc	ctt	gcc	att	gtt	tta		355
Leu	Ala	Arg	Trp	Met	Phe	Ile	Ala	Val	Asn	Leu	Leu	Ala	Ile	Val	Leu		
70					75					80					85		
gcg	ttc	ggg	ctg	ctg	acc	aga	ctc	tcc	ggc	tgg	gcg	ctg	cgc	agc	atg		403
Ala	Phe	Gly	Leu	Leu	Thr	Arg	Leu	Ser	Gly	Trp	Ala	Leu	Arg	Ser	Met		
				90					95					100			
gtg	tgg	ccg	att	gcg	atc	gcc	ttg	gcg	atg	ctg	aca	gaa	acc	gtg	caa		451
Val	Trp	Pro	Ile	Ala	Ile	Ala	Leu	Ala	Met	Leu	Thr	Glu	Thr	Val	Gln		
			105					110					115				
aac	acc	ctc	att	ttc	tcc	aac	atc	aac	ggc	atc	ctg	ctg	ctc	atg	ttg		499
Asn	Thr	Leu	Ile	Phe	Ser	Asn	Ile	Asn	Gly	Ile	Leu	Leu	Leu	Met	Leu		
		120					125					130					
gcg	att	ttc	ctg	tgg	tgc	gtg	gtg	cac	aaa	aaa	tcc	tgg	ttg	ggc	gga		547
Ala	Ile	Phe	Leu	Trp	Cys	Val	Val	His	Lys	Lys	Ser	Trp	Leu	Gly	Gly		
	135					140					145						
cta	gtc	att	ggc	ttg	gcc	att	ttg	atc	aaa	ccc	atg	ttc	ctg	cca	ctt		595
Leu	Val	Ile	Gly	Leu	Ala	Ile	Leu	Ile	Lys	Pro	Met	Phe	Leu	Pro	Leu		
150					155					160					165		
ctc	ttc	cta	cct	ttg	gtg	aaa	aag	caa	tgg	gga	tgc	ctc	atc	ctc	ggc		643
Leu	Phe	Leu	Pro	Leu	Val	Lys	Lys	Gln	Trp	Gly	Ser	Leu	Ile	Leu	Gly		
			170						175					180			
att	tta	acc	cca	gtg	att	ttc	aat	gca	gtg	gcc	tgg	ttc	tta	gtt	ccg		691
Ile	Leu	Thr	Pro	Val	Ile	Phe	Asn	Ala	Val	Ala	Trp	Phe	Leu	Val	Pro		
			185					190					195				
gga	gca	tct	gaa	tac	gtc	acc	cgc	acg	atg	ccc	tac	ctt	ggc	gaa	act		739
Gly	Ala	Ser	Glu	Tyr	Val	Thr	Arg	Thr	Met	Pro	Tyr	Leu	Gly	Glu	Thr		
		200					205					210					
cga	gat	ttt	gcc	aac	agc	tca	ctc	cca	ggc	ttg	gcc	atc	tat	ttc	gga		787
Arg	Asp	Phe	Ala	Asn	Ser	Ser	Leu	Pro	Gly	Leu	Ala	Ile	Tyr	Phe	Gly		
	215					220					225						
atg	ccc	acc	tgg	atg	gaa	atc	acc	tgg	ttc	ctc	atc	ttc	ggc	gca	atg		835
Met	Pro	Thr	Trp	Met	Glu	Ile	Thr	Trp	Phe	Leu	Ile	Phe	Gly	Ala	Met		

230	235	240	245	
gtc ggc ctc gca gtg ctg gca ctc ctg aga ttc cgt aac acc gag cca				883
Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe Arg Asn Thr Glu Pro	250	255	260	
tac ttc tgg gca gca acc acc acc ggt gta ctc ctg act ggc gta ttc				931
Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu Leu Thr Gly Val Phe	265	270	275	
ttc ctg tcc tca ctg gga cag atg tac tac tcc atg atg atc ttc cct				979
Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser Met Met Ile Phe Pro	280	285	290	
atg atc ttc acc ctg ctc gga agc cga tcc gta ttc cac aac tgg gtt				
1027				
Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val Phe His Asn Trp Val	295	300	305	
gcc tgg gtc gcc gcc tac ttc tta cta tcc cct gac act ttc acc tcc				
1075				
Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro Asp Thr Phe Thr Ser	310	315	320	325
cag cga cta ccc gat gta gcc cgc tgg atg gaa ttt ttc agc gcg acc				
1123				
Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu Phe Phe Ser Ala Thr	330	335	340	
gtt ggt tgg gga cta ttg ata gtg gtt aca ttt gtc tcg gcg cta atc				
1171				
Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile	345	350	355	
tgg ttt att ggt gat atc cga gcc aag gga act ccg agc tca ccc att				
1219				
Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr Pro Ser Ser Pro Ile	360	365	370	
acc act gat cca acg cac gac cat ctt gag agg aca gca tgacagactt				
1268				
Thr Thr Asp Pro Thr His Asp His Leu Glu Arg Thr Ala	375	380	385	
caaactcatc agc				
1281				
<210> 586				
<211> 386				
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<213> Corynebacterium glutamicum				
<400> 586				
Met Leu Leu Met Ala His Arg Phe Phe Val Leu Ala Ile Asn Gly Ala	1	5	10	15
Val Thr Asp Asp Phe Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val	20	25	30	
Glu Gly Ile Pro Val Tyr Asn Glu Val Tyr His Phe Val Asp Pro His				

35					40					45					
Tyr	Leu	Tyr	Asn	Pro	Gly	Ala	Thr	Leu	Leu	Leu	Ala	Pro	Leu	Gly	Tyr
50					55					60					
Ile	Thr	His	Phe	Thr	Leu	Ala	Arg	Trp	Met	Phe	Ile	Ala	Val	Asn	Leu
65					70					75				80	
Leu	Ala	Ile	Val	Leu	Ala	Phe	Gly	Leu	Leu	Thr	Arg	Leu	Ser	Gly	Trp
				85					90					95	
Ala	Leu	Arg	Ser	Met	Val	Trp	Pro	Ile	Ala	Ile	Ala	Leu	Ala	Met	Leu
			100					105					110		
Thr	Glu	Thr	Val	Gln	Asn	Thr	Leu	Ile	Phe	Ser	Asn	Ile	Asn	Gly	Ile
			115				120					125			
Leu	Leu	Leu	Met	Leu	Ala	Ile	Phe	Leu	Trp	Cys	Val	Val	His	Lys	Lys
130					135					140					
Ser	Trp	Leu	Gly	Gly	Leu	Val	Ile	Gly	Leu	Ala	Ile	Leu	Ile	Lys	Pro
145					150					155				160	
Met	Phe	Leu	Pro	Leu	Leu	Phe	Leu	Pro	Leu	Val	Lys	Lys	Gln	Trp	Gly
				165				170						175	
Ser	Leu	Ile	Leu	Gly	Ile	Leu	Thr	Pro	Val	Ile	Phe	Asn	Ala	Val	Ala
			180					185					190		
Trp	Phe	Leu	Val	Pro	Gly	Ala	Ser	Glu	Tyr	Val	Thr	Arg	Thr	Met	Pro
			195				200					205			
Tyr	Leu	Gly	Glu	Thr	Arg	Asp	Phe	Ala	Asn	Ser	Ser	Leu	Pro	Gly	Leu
210					215					220					
Ala	Ile	Tyr	Phe	Gly	Met	Pro	Thr	Trp	Met	Glu	Ile	Thr	Trp	Phe	Leu
225					230					235				240	
Ile	Phe	Gly	Ala	Met	Val	Gly	Leu	Ala	Val	Leu	Ala	Leu	Leu	Arg	Phe
				245					250					255	
Arg	Asn	Thr	Glu	Pro	Tyr	Phe	Trp	Ala	Ala	Thr	Thr	Thr	Gly	Val	Leu
			260					265					270		
Leu	Thr	Gly	Val	Phe	Phe	Leu	Ser	Ser	Leu	Gly	Gln	Met	Tyr	Tyr	Ser
			275				280					285			
Met	Met	Ile	Phe	Pro	Met	Ile	Phe	Thr	Leu	Leu	Gly	Ser	Arg	Ser	Val
290					295					300					
Phe	His	Asn	Trp	Val	Ala	Trp	Val	Ala	Ala	Tyr	Phe	Leu	Leu	Ser	Pro
305					310					315				320	
Asp	Thr	Phe	Thr	Ser	Gln	Arg	Leu	Pro	Asp	Val	Ala	Arg	Trp	Met	Glu
				325				330						335	
Phe	Phe	Ser	Ala	Thr	Val	Gly	Trp	Gly	Leu	Leu	Ile	Val	Val	Thr	Phe
			340					345					350		
Val	Ser	Ala	Leu	Ile	Trp	Phe	Ile	Gly	Asp	Ile	Arg	Ala	Lys	Gly	Thr
			355				360					365			

Pro Ser Ser Pro Ile Thr Thr Asp Pro Thr His Asp His Leu Glu Arg  
 370 375 380

Thr Ala  
 385

<210> 587

<211> 777

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(754)

<223> RXC02380

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tgctcagcaa ggtggtgtgc gaacactata ctgtccactc atg act aca acg gtg 115  
 Met Thr Thr Thr Val  
 1 5

aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttt gac ccc att 163  
 Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile  
 10 15 20

cat aat ggt cac ctt gtg gcg ggc tca gag gta gcg gat cga ttc gat 211  
 His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp  
 25 30 35

ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg 259  
 Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala  
 40 45 50

aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc 307  
 Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile  
 55 60 65

gcc act gcc tct aat cca cgg ttt atg gta tcg cgg gtt gat att gat 355  
 Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp  
 70 75 80 85

cgg gga ggg gat act tac acg atc gat acc ctg caa gat ttg agc aag 403  
 Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys  
 90 95 100

caa tac ccg gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg 451  
 Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu  
 105 110 115

gca cag atc gtg acg tgg cgc gat tgg gag aaa acc ttc gaa ctt gcc 499  
 Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys Thr Phe Glu Leu Ala  
 120 125 130

cac ttc gtt gga gtg act cga ccc ggt tat gaa ttg gat gga aac atc 547  
 His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile  
 135 140 145

att ccg gaa atg cac caa gat cga gtc tca ttg gtg gat atc ccc gcc 595  
 Ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala  
 150 155 160 165

atg gct att tcc tcc acg gac tgc aga gaa cgc tcc agc gaa gaa cgc 643  
 Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg  
 170 175 180

cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa 691  
 Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys  
 185 190 195

cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag 739  
 Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys  
 200 205 210

ggc caa aac caa gca taaatctagt caaaagtttc aac 777  
 Gly Gln Asn Gln Ala  
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<210> 588

<211> 218

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 588

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Thr Phe Asp Pro Ile His Asn Gly His Leu Val Ala Gly Ser Glu Val  
 20 25 30

Ala Asp Arg Phe Asp Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln  
 35 40 45

Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr  
 50 55 60

Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser  
 65 70 75 80

Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu  
 85 90 95

Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr  
 100 105 110

Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys  
 115 120 125

Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu  
 130 135 140

Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu  
 145 150 155 160

Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg  
 165 170 175

Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val

	180	185	190	
Gln Tyr Ile Ala Lys Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys				
	195	200	205	
Asp Met Asp Pro Lys Gly Gln Asn Gln Ala				
	210	215		
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<223> FRXA02380				
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tgctcagcaa ggtggtgtgc gaacactata ctgtccactc atg act aca acg gtg		115		
		Met Thr Thr Thr Val		
		1 5		
aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttt gac ccc att		163		
Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile				
	10 15 20			
cat aat ggt cac ctt gtg gcg ggc tca gag gta gcg gat cga ttc gat		211		
His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp				
	25 30 35			
ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg		259		
Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala				
	40 45 50			
aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc		307		
Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile				
	55 60 65			
gcc act gcc tct aat cca cgg ttt atg gta tcg cgg gtt gat att gat		355		
Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp				
	70 75 80 85			
cgg gga ggg gat act tac acg atc gat acc ctg caa gat ttg agc aag		403		
Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys				
	90 95 100			
caa tac ccg gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg		451		
Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu				
	105 110 115			
gca cag atc gtg acg tgg gcg gat tgg gag aaa acc ttc gaa ctt gcc		499		
Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys Thr Phe Glu Leu Ala				
	120 125 130			
cac ttc gtt gga gtg act cga ccc ggt tat gaa ttg gat gga aac atc		547		
His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile				
	135 140 145			

att ccg gaa atg cac caa gat cga gtc tca ttg gtg gat atc ccc gcc 595  
 Ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala  
 150 155 160 165  
  
 atg gct att tcc tcc acg gac tgc aga gaa cgc tcc agc gaa gaa cgc 643  
 Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg  
 170 175 180  
  
 cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa 691  
 Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys  
 185 190 195  
  
 cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag 739  
 Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys  
 200 205 210  
  
 ggc caa aac caa gca taaatctagt caaaagtttc aac 777  
 Gly Gln Asn Gln Ala  
 215

&lt;210&gt; 590

&lt;211&gt; 218

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 590

Met Thr Thr Thr Val Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly  
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 Thr Phe Asp Pro Ile His Asn Gly His Leu Val Ala Gly Ser Glu Val  
 20 25 30  
  
 Ala Asp Arg Phe Asp Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln  
 35 40 45  
  
 Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr  
 50 55 60  
  
 Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser  
 65 70 75 80  
  
 Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu  
 85 90 95  
  
 Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr  
 100 105 110  
  
 Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys  
 115 120 125  
  
 Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu  
 130 135 140  
  
 Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu  
 145 150 155 160  
  
 Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg  
 165 170 175



Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val  
 180 185 190

Gln Tyr Ile Ala Lys Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys  
 195 200 205

Asp Met Asp Pro Lys Gly Gln Asn Gln Ala  
 210 215

<210> 591

<211> 594

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(571)

<223> RXC02921

<400> 591

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 aaaagggtga ggaaccacat gagctgtttt aaggaatttt gtg tct gca ctt gaa 115  
 Val Ser Ala Leu Glu  
 1 5  
 gag tcg atc cgc atc gcg acc atc gcg gcg aaa gca gcg gat gaa aag 163  
 Glu Ser Ile Arg Ile Ala Thr Ile Ala Ala Lys Ala Ala Asp Glu Lys  
 10 15 20  
 aag gcc gat gac atc gct gtc atc gat gtc tct gac atg atc gca atc 211  
 Lys Ala Asp Asp Ile Ala Val Ile Asp Val Ser Asp Met Ile Ala Ile  
 25 30 35  
 acc gat tgc ttt gtt gtt gca tct gct gac aat gag cgc cag gtg ggc 259  
 Thr Asp Cys Phe Val Val Ala Ser Ala Asp Asn Glu Arg Gln Val Gly  
 40 45 50  
 gcc att gtt gag gag atc gaa gat gag atg acc aag gct ggt ttc gag 307  
 Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr Lys Ala Gly Phe Glu  
 55 60 65  
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 Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg Trp Val Leu Leu Asp  
 70 75 80 85  
 tac gga ttg gtt gtt atc cac gtt cag cga cag gca gag cgc gag ttc 403  
 Tyr Gly Leu Val Val Ile His Val Gln Arg Gln Ala Glu Arg Glu Phe  
 90 95 100  
 tac gga ctg gat cgt ctg tac cgc gac tgc cca ctc att gaa att gaa 451  
 Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro Leu Ile Glu Ile Glu  
 105 110 115  
 gga ctt gaa acc ttc aag cgt gaa tcc tcc tgg tct gat gag gcg gat 499  
 Gly Leu Glu Thr Phe Lys Arg Glu Ser S r Trp Ser Asp Glu Ala Asp  
 120 125 130  
 atc cgc aac atc gac agc att gat gaa ctc cca cct ttg cca gct gaa 547  
 Ile Arg Asn Ile Asp Ser Ile Asp Glu Leu Pro Pro Leu Pro Ala Glu

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 Tyr Glu Pro Gly Tyr Glu Asp Asp  
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 Glu Arg Gln Val Gly Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr  
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 Trp Val Leu Leu Asp Tyr Gly Leu Val Val Ile His Val Gln Arg Gln  
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 Ala Glu Arg Glu Phe Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro  
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 Leu Ile Glu Ile Glu Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp  
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 Val Leu Gly Ala Val  
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ctg	aca	tcg	ctg	gtt	att	ccg	gtc	ctt	acc	cgc	gcg	gaa	aaa	gaa	gac	163
Leu	Thr	Ser	Leu	Val	Ile	Pro	Val	Leu	Thr	Arg	Ala	Glu	Lys	Glu	Asp	
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gcc	gac	ggc	ggg	tcc	ggg	ttc	ttc	agg	cgg	ctg	ctc	acc	ctg	tcg	gtg	211
Ala	Asp	Gly	Gly	Ser	Gly	Phe	Phe	Arg	Arg	Leu	Leu	Thr	Leu	Ser	Val	
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acg	ctg	ctg	ggg	ggg	gtc	acc	atc	ctg	tcg	att	atc	ggc	gcg	ccg	ctg	259
Thr	Leu	Leu	Gly	Gly	Val	Thr	Ile	Leu	Ser	Ile	Ile	Gly	Ala	Pro	Leu	
		40					45					50				
ctg	aca	cgg	atg	atg	ctg	tcc	tct	gag	gga	caa	gtc	aac	gtg	gtc	atg	307
Leu	Thr	Arg	Met	Met	Leu	Ser	Ser	Glu	Gly	Gln	Val	Asn	Val	Val	Met	
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Ser	Thr	Ala	Phe	Ala	Tyr	Trp	Leu	Leu	Pro	Gln	Ile	Phe	Phe	Tyr	Gly	
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Leu	Phe	Ala	Leu	Phe	Met	Ala	Val	Leu	Asn	Thr	Arg	Glu	Val	Phe	Lys	
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ccc	ggc	gcg	tgg	gca	cct	gtt	gtc	aac	aat	gtg	atc	acc	ttg	acc	gtg	451
Pro	Gly	Ala	Trp	Ala	Pro	Val	Val	Asn	Asn	Val	Ile	Thr	Leu	Thr	Val	
			105					110					115			
ctg	ggc	gtg	tac	atg	gtg	ctg	cct	gcg	cgt	ttg	cac	ccg	cat	gag	cag	499
Leu	Gly	Val	Tyr	Met	Val	Leu	Pro	Ala	Arg	Leu	His	Pro	His	Glu	Gln	
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gtg	ggc	att	ttt	gat	ccg	cag	atc	att	ttc	ctc	ggc	gtg	ggc	acc	acc	547
Val	Gly	Ile	Phe	Asp	Pro	Gln	Ile	Ile	Phe	Leu	Gly	Val	Gly	Thr	Thr	
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ctt	ggg	gtg	gtt	gca	cag	tgt	cta	atc	atg	att	ccg	tac	ctg	cgt	cgc	595
Leu	Gly	Val	Val	Ala	Gln	Cys	Leu	Ile	Met	Ile	Pro	Tyr	Leu	Arg	Arg	
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gcg	ggc	att	gat	atg	cgc	cct	ctg	tgg	ggg	atc	gat	gcg	cgt	ttg	aag	643
Ala	Gly	Ile	Asp	Met	Arg	Pro	Leu	Trp	Gly	Ile	Asp	Ala	Arg	Leu	Lys	
				170					175					180		
caa	ttc	ggg	ggc	atg	gcg	atg	gcg	atc	atc	gtg	tac	gtg	gca	atc	tcc	691
Gln	Phe	Gly	Gly	Met	Ala	Met	Ala	Ile	Ile	Val	Tyr	Val	Ala	Ile	Ser	
			185					190					195			
cag	ttc	ggg	tac	atc	atc	acc	act	cgc	att	gcg	tcg	att	gca	gac	gat	739
Gln	Phe	Gly	Tyr	Ile	Ile	Thr	Thr	Arg	Ile	Ala	Ser	Ile	Ala	Asp	Asp	
		200					205					210				
gct	gcg	ccg	ttt	att	tat	cag	cag	cac	tgg	atg	ttg	ctg	caa	gtt	cct	787
Ala	Ala	Pro	Phe	Ile	Tyr	Gln	Gln	His	Trp	Met	Leu	Leu	Gln	Val	Pro	
	215					220					225					
tat	ggc	atc	atc	ggc	gtc	acc	ttg	ctc	acc	gcg	att	atg	ccg	cga	ctg	835
Tyr	Gly	Ile	Ile	Gly	Val	Thr	Leu	Leu	Thr	Ala	Ile	Met	Pro	Arg	Leu	
230					235					240					245	
tcc	cgc	aac	gcg	gca	gac	ggc	gat	gat	agg	gca	gta	gtc	tct	gac	ctt	883

Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu  
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cag ttg ggt tcc aag cta acc ttc atc gca ctg atc ccc atc gtg gtg 931  
 Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val  
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ttc ttc acc gcc ttc ggt gtc cct att gcc aat ggc ctt ttt gcc tac 979  
 Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr  
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ggc caa ttc gat gcc aac gcc gcc aac atc ctt ggt tgg act ctg agc  
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 Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser  
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ttc tct gct ttc acg ctg att cct tac gct ttg gtg ctg cta cat ctg  
 1075  
 Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu  
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cgt gtg ttt tat gcg cgt gaa gag gtc tgg acc cca acc ttc atc atc  
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 Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr Pro Thr Phe Ile Ile  
 330 335 340

gcc ggc atc acc gcc acc aag gtc gtg ctt tcc ctg ttg gca ccg ctg  
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 Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu  
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 1219  
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ggt ttc agt ttc atc acc ggc gcg gtc atc ggc gcg tat ctg ttg cgc  
 1267  
 Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg  
 375 380 385

aac aaa ctc ggc ctg ttg ggt atg cgc tct ttg gct aaa acc tcc ctg  
 1315  
 Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu  
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 1363  
 Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Ala Trp Ala Leu  
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 Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu  
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agc tcc gta ggc tac ttg ttg aac ctg gct gtg ttg ggt gtc ttc ttc  
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 Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe  
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atc ttc gtc acc ggc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc  
 1507  
 Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val  
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 1555  
 Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe  
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att cgc ccg aat acc aag atc tct ttg gat gtc ggc gaa gtc tcc gag  
 1603  
 Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu  
 490 495 500

cag gat ttc tcc acc cag ctg gtc gcg cca agc gag ttc gca gca acc  
 1651  
 Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr  
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cct gtg ccg cca ccg atg tcc gcc ggt att gtc cgc gga cct cgc ctg  
 1699  
 Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu  
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gtt ccc ggc gcc cca gtc ggc gac ggt cgt ttc cgt ctg ctc gcc gat  
 1747  
 Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp  
 535 540 545

cac ggc ggc gtc caa ggc gcg cgt ttc tgg cag gcc cgc gag atc gcc  
 1795  
 His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala  
 550 555 560 565

acc ggc aag gaa gtc gcg ctg atc ttt gtg gat act tcc ggc aac gcc  
 1843  
 Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala  
 570 575 580

cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag  
 1891  
 Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu  
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 1939  
 Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val  
 600 605 610

gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg  
 1987  
 Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val  
 615 620 625

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 2035  
 Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala Val Ala Glu Ser Gly  
 630 635 640 645

gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc  
2083

Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr  
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2131

Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys  
665 670 675

tgc cga att cgt atc aac acc gac ggc cat gcc gtc ctc gcc ttg ccg  
2179

Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro  
680 685 690

gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc  
2227

Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala  
695 700 705

tcg gcc gcc gag atg ctt atc gac gcg acc ctc gct ccc agc gac gtc  
2275

Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val  
710 715 720 725

aag gca atg gtc act gaa gcc cag ggg cta gct aca gaa gac aat ccc  
2323

Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro  
730 735 740

gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc  
2371

Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr  
745 750 755

gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct  
2419

Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro  
760 765 770

gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg  
2467

Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met  
775 780 785

gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc  
2515

Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala  
790 795 800 805

ggt acc gcg ttc ctc acc agc ttc ttc ggc agc agc acc aac gaa caa  
2563

Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln  
810 815 820

tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct  
2611

Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro  
825 830 835

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2659

Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp  
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2707

Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser  
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2755

Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser  
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acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc  
2803

Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser  
890 895 900

gac agc aac gtg acc tcg acc gtg aag atc tac gca ttc aac gac gcc  
2851

Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala  
905 910 915

tca cca cac tcc ctg tcg gaa ggc atc gag atc ggc acc gtg gat tat  
2899

Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr  
920 925 930

tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg  
2947

Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro  
935 940 945

ggt cag gtg gaa tcc gtg gtg att ctg gtc gat gag gtt cgt tcc tca  
2995

Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser  
950 955 960 965

caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt  
3043

Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu  
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Val Gly Trp

<210> 594

<211> 984

<212> PRT

<213> Corynebacterium glutamicum

<400> 594

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Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln 50 55 60		
Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln 65 70 75 80		
Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr 85 90 95		
Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val 100 105 110		
Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu 115 120 125		
His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu 130 135 140		
Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile 145 150 155 160		
Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile 165 170 175		
Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val 180 185 190		
Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala 195 200 205		
Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met 210 215 220		
Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala 225 230 235 240		
Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala 245 250 255		
Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu 260 265 270		
Ile Pro Ile Val Val Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn 275 280 285		
Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu 290 295 300		
Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu 305 310 315 320		
Val Leu Leu His Leu Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr 325 330 335		
Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser 340 345 350		



Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu  
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 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu  
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 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala  
 405 410 415  
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe  
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 450 455 460  
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro  
 465 470 475 480  
 Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val  
 485 490 495  
 Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser  
 500 505 510  
 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val  
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 Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe  
 530 535 540  
 Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln  
 545 550 555 560  
 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp  
 565 570 575  
 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala  
 580 585 590  
 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu  
 595 600 605  
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn  
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 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala  
 625 630 635 640  
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala  
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 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala  
 660 665 670

Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala  
 675 680 685  
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp  
 690 695 700  
 Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu  
 705 710 715 720  
 Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala  
 725 730 735  
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr  
 740 745 750  
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu  
 755 760 765  
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr  
 770 775 780  
 Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val  
 785 790 795 800  
 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser  
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 Ser Thr Asn Glu Gln Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser  
 820 825 830  
 Ala Thr Pro Glu Pro Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln  
 835 840 845  
 Ala Arg Thr Trp Asp Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr  
 850 855 860  
 Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu  
 865 870 875 880  
 Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr  
 885 890 895  
 Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr  
 900 905 910  
 Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile  
 915 920 925  
 Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp  
 930 935 940  
 Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu Val Asp  
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 <223> RXA01807

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 Met Pro Ser Ala Gly  
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 Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu Phe Asp Gln Arg Arg  
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 Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly  
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 Leu Ser Ala Ala Ile Pro Val Met His Asn Glu Gly Leu Arg Val Val  
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 Ala Val Pro Thr Val Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser  
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 His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp  
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 Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser Thr Ile Ser Thr Gly  
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 Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln  
 105 110 115  
 aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc 499  
 Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile  
 120 125 130  
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 Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr  
 135 140 145  
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 Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn  
 150 155 160 165  
 gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg 643  
 Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu  
 170 175 180

ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act 691  
 Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr Ser Ala Thr Glu Thr  
                   185                                  190                                  195

gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa 739  
 Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu  
                   200                                  205                                  210

atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc 787  
 Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val  
                   215                                  220                                  225

tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc 835  
 Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile  
                   230                                  235                                  240                                  245

gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc 883  
 Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr  
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<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 596

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                   20                                  25                                  30

Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu  
                   35                                  40                                  45

Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro  
                   50                                  55                                  60

Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala  
   65                                  70                                  75                                  80

Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser  
                                   85                                  90                                  95

Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val  
                   100                                  105                                  110

Ala Ala Trp Leu Gln Lys Ile Arg Glu Thr His Pro His Val Arg Ile  
                   115                                  120                                  125

Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala  
                   130                                  135                                  140

Asp Glu Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr  
   145                                  150                                  155                                  160

Gly Ile Ile Pro Asn Ala Phe Glu Leu Ser His Met Val Gly Ser Gly  
 165 170 175

Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr  
 180 185 190

Ser Ala Thr Glu Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg  
 195 200 205

Asp Ser Val Gln Glu Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys  
 210 215 220

Gly Ala Gly Asp Val Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys  
 225 230 235 240

Asp Phe Ser Leu Ile Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys  
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Ala Gly Leu Gln Thr Lys Ala Leu  
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<210> 597

<211> 1461

<212> DNA

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<222> (101)..(1438)

<223> RXN02754

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 Val Asn Thr Asn Pro  
 1 5

tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163  
 Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr  
 10 15 20

gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc 211  
 Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg  
 25 30 35

ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga 259  
 Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg  
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tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac 307  
 Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp  
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ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac 355  
 Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp  
 70 75 80 85

cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat 403  
 Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp

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gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu 120 125 130			499
tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met 135 140 145			547
gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg 150 155 160 165			595
acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala 170 175 180			643
gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile 185 190 195			691
cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn 200 205 210			739
gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu 215 220 225			787
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caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca gac ctt ggt ggc Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro Asp Leu Gly Gly 250 255 260			883
gta cgt atc gac tcc ggc gac cta ggt gtg ctt gcc cga aag gtc cgc Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu Ala Arg Lys Val Arg 265 270 275			931
aag cag ctc gac gat ctc aac gcc cac aac acc aag att gtg gtc tcc Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr Lys Ile Val Val Ser 280 285 290			979
tcc gac ctg gat gaa ttc gcc atc gcg ggt ctt cgc ggc gaa cca gtt 1027 Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu Arg Gly Glu Pro Val 295 300 305			
gac gtc ttt ggc gtt ggc acc tcc gtt gtc aca ggt tct ggc gca cca 1075 Asp Val Phe Gly Val Gly Thr Ser Val Val Thr Gly Ser Gly Ala Pro 310 315 320 325			

acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg  
 1123  
 Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val  
                     330                    335                    340

gcc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct  
 1171  
 Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly Gly Gly Lys Lys Ala  
                     345                    350                    355

gtg cgc acc cac cgc aag tcc ggt acc gca atc gaa gaa atc gtc tac  
 1219  
 Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr  
                     360                    365                    370

cca ttc aat gcc gaa gca cca gat act gga aag ctc gac act ttg agc  
 1267  
 Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser  
                     375                    380                    385

ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct  
 1315  
 Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile Val Pro Gly Leu Pro  
                     390                    395                    400                    405

act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta  
 1363  
 Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu  
                     410                    415                    420

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 1411  
 Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr  
                     425                    430                    435

cgt ttc gtg ggt ttc ccg ccg gcc gct tagacaattc ggtctcacca  
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                     440                    445

aac  
 1461

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<400> 598  
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                     20                    25                    30  
 Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu  
                     35                    40                    45  
 Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu  
   50                    55                    60

Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu  
 65 70 75 80  
 Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe  
 85 90 95  
 Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln  
 100 105 110  
 Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu  
 115 120 125  
 Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser  
 130 135 140  
 Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu  
 145 150 155 160  
 Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg  
 165 170 175  
 Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala  
 180 185 190  
 Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr  
 195 200 205  
 Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe  
 210 215 220  
 Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp  
 225 230 235 240  
 Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly  
 245 250 255  
 Pro Asp Leu Gly Gly Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu  
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 Ala Arg Lys Val Arg Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr  
 275 280 285  
 Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu  
 290 295 300  
 Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr Ser Val Val Thr  
 305 310 315 320  
 Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val  
 325 330 335  
 Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly  
 340 345 350  
 Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile  
 355 360 365  
 Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys  
 370 375 380



Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile  
385 390 395 400

Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys  
405 410 415

Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu  
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Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro Ala Ala  
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<211> 871

<212> DNA

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<220>

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<222> (101)..(871)

<223> FRXA02405

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Val Asn Thr Asn Pro  
1 5

tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163  
Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr  
10 15 20

gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc 211  
Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg  
25 30 35

ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga 259  
Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg  
40 45 50

tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac 307  
Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp  
55 60 65

ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac 355  
Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp  
70 75 80 85

cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat 403  
Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp  
90 95 100

ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act 451  
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr  
105 110 115

gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg 499  
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu  
120 125 130

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 135 140 145  
 gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc 595  
 Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg  
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 Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala  
 170 175 180  
 gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att 691  
 Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile  
 185 190 195  
 cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac 739  
 Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn  
 200 205 210  
 gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa 787  
 Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu  
 215 220 225  
 tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc 835  
 Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr  
 230 235 240 245  
 caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca 871  
 Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro  
 250 255

&lt;210&gt; 600

&lt;211&gt; 257

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 600

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 Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu  
 35 40 45  
 Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu  
 50 55 60  
 Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu  
 65 70 75 80  
 Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe  
 85 90 95  
 Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln  
 100 105 110

Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu  
 115 120 125

Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser  
 130 135 140

Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu  
 145 150 155 160

Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg  
 165 170 175

Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala  
 180 185 190

Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr  
 195 200 205

Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe  
 210 215 220

Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp  
 225 230 235 240

Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly  
 245 250 255

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (1)..(486)  
 <223> FRXA02754

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atc gcg ggt ctt cgc ggc gaa cca gtt gac gtc ttt ggc gtt ggc acc 96  
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 20 25 30

tcc gtt gtc aca ggt tct ggc gca cca acc gct ggc ctc gtg tac aag 144  
 Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys  
 35 40 45

atc ggg gaa gtt gcc ggt cac cct gtg gcc aag cgt tcc cga aac aag 192  
 Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys  
 50 55 60

gaa agc tac ggt ggt ggc aag aag gct gtg cgc acc cac cgc aag tcc 240  
 Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser  
 65 70 75 80

ggt acc gca atc gaa gaa atc gtc tac cca ttc aat gcc gaa gca cca 288  
 Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro  
                     85                    90                    95

gat act gga aag ctc gac act ttg agc ctg acc atc cca ttg atg cgc 336  
 Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg  
                     100                    105                    110

gac ggt gaa atc gtt cca ggt ttg cct act ttg gaa gat tcc cga gcg 384  
 Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala  
                     115                    120                    125

tat ttg gcc aag caa ttg gtc tct tta cca tgg gaa ggc ctt gca ctg 432  
 Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu  
                     130                    135                    140

tct cgc gat gag cct gtt ttg cac act cgt ttc gtg ggt ttc ccg ccg 480  
 Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro  
 145                    150                    155                    160

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 Ala Ala

<210> 602  
 <211> 162  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 602  
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                     20                    25                    30  
 Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys  
                     35                    40                    45  
 Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys  
                     50                    55                    60  
 Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser  
                     65                    70                    75                    80  
 Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro  
                     85                    90                    95  
 Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg  
                     100                    105                    110  
 Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala  
                     115                    120                    125  
 Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu  
                     130                    135                    140  
 Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro  
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Ala Ala

&lt;210&gt; 603

&lt;211&gt; 960

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(937)

&lt;223&gt; RXA02112

&lt;400&gt; 603

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                                         Met Thr Thr His Ile
                                         1                               5

gac cgc atc gtt ggc gca gcg tta tcc gag gat gcg cca tgg ggc gac 163
Asp Arg Ile Val Gly Ala Ala Leu Ser Glu Asp Ala Pro Trp Gly Asp
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att acc tcc gac act ttt atc cca gga tcg gcg cag ctg agc gcc aag 211
Ile Thr Ser Asp Thr Phe Ile Pro Gly Ser Ala Gln Leu Ser Ala Lys
                        25                        30                        35

gtt gtt gcc cgg gag cca ggt gtg ttc agc ggg cag gcg ctt tta gac 259
Val Val Ala Arg Glu Pro Gly Val Phe Ser Gly Gln Ala Leu Leu Asp
                        40                        45                        50

gcc tcc ttc cgg ctc gtc gat cct agg ata aac gca tcc ctt aag gtg 307
Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn Ala Ser Leu Lys Val
                        55                        60                        65

gct gat ggt gac agc ttt gaa acc ggg gac atc cta gga aca att acc 355
Ala Asp Gly Asp Ser Phe Glu Thr Gly Asp Ile Leu Gly Thr Ile Thr
                        70                        75                        80                        85

ggc agt gct aga agc atc ctc cgt tca gag cgc att gct ctc aac ttc 403
Gly Ser Ala Arg Ser Ile Leu Arg Ser Glu Arg Ile Ala Leu Asn Phe
                        90                        95                        100

att cag agg acg tcc ggc atc gct aca ttg aca tcg tgc tat gtt gca 451
Ile Gln Arg Thr Ser Gly Ile Ala Thr Leu Thr Ser Cys Tyr Val Ala
                        105                        110                        115

gag gtt aaa ggc acc aaa gcc cgc att gtt gat acc cgg aaa acc aca 499
Glu Val Lys Gly Thr Lys Ala Arg Ile Val Asp Thr Arg Lys Thr Thr
                        120                        125                        130

ccc ggc ctg cgc atc att gaa cgc caa gct gtc cgt gac ggt ggc gga 547
Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val Arg Asp Gly Gly Gly
                        135                        140                        145

ttt aat cac cga gcc acc ttg tcc gat gct gtc atg gtg aaa gat aac 595
Phe Asn His Arg Ala Thr Leu Ser Asp Ala Val Met Val Lys Asp Asn
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cat ctc gca gcc atc gca tcc cag ggg ctc agc atc act gaa gcg ctg 643  
 His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser Ile Thr Glu Ala Leu  
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tcg aat atg aaa gct aaa ctc ccc cac acc acc cat gtg gaa gtc gaa 691  
 Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr His Val Glu Val Glu  
                   185                                  190                                  195

gtt gat cat ata gag cag atc gaa cca gtt ctt gct gct ggt gtg gac 739  
 Val Asp His Ile Glu Gln Ile Glu Pro Val Leu Ala Ala Gly Val Asp  
                   200                                  205                                  210

acc atc atg ttg gat aat ttc acc att gat cag ctc atc gaa ggc gtt 787  
 Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln Leu Ile Glu Gly Val  
                   215                                  220                                  225

gat ctc att ggt gga cgt gca ctg gtg gaa gca tct ggc gga gtc aac 835  
 Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala Ser Gly Gly Val Asn  
                   230                                  235                                  240                                  245

ctc aac acc gcg gga aag att gca tca acc ggt gtc gac gtc att tcc 883  
 Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly Val Asp Val Ile Ser  
                   250                                  255                                  260

gtt gga gcg ctt acc cat tct gtg cat gca ctt gac cta gga ctc gat 931  
 Val Gly Ala Leu Thr His Ser Val His Ala Leu Asp Leu Gly Leu Asp  
                   265                                  270                                  275

att ttc taatgctcta ccttgataat gca 960  
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&lt;210&gt; 604

&lt;211&gt; 279

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 604

Met Thr Thr His Ile Asp Arg Ile Val Gly Ala Ala Leu Ser Glu Asp  
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Ala Pro Trp Gly Asp Ile Thr Ser Asp Thr Phe Ile Pro Gly Ser Ala  
                   20                                  25                                  30

Gln Leu Ser Ala Lys Val Val Ala Arg Glu Pro Gly Val Phe Ser Gly  
                   35                                  40                                  45

Gln Ala Leu Leu Asp Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn  
                   50                                  55                                  60

Ala Ser Leu Lys Val Ala Asp Gly Asp Ser Phe Glu Thr Gly Asp Ile  
                   65                                  70                                  75                                  80

Leu Gly Thr Ile Thr Gly Ser Ala Arg Ser Ile Leu Arg Ser Glu Arg  
                   85                                  90                                  95

Ile Ala Leu Asn Phe Ile Gln Arg Thr Ser Gly Ile Ala Thr Leu Thr  
                   100                                  105                                  110

Ser Cys Tyr Val Ala Glu Val Lys Gly Thr Lys Ala Arg Ile Val Asp  
 115 120 125  
 Thr Arg Lys Thr Thr Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val  
 130 135 140  
 Arg Asp Gly Gly Gly Phe Asn His Arg Ala Thr Leu Ser Asp Ala Val  
 145 150 155 160  
 Met Val Lys Asp Asn His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser  
 165 170 175  
 Ile Thr Glu Ala Leu Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr  
 180 185 190  
 His Val Glu Val Glu Val Asp His Ile Glu Gln Ile Glu Pro Val Leu  
 195 200 205  
 Ala Ala Gly Val Asp Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln  
 210 215 220  
 Leu Ile Glu Gly Val Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala  
 225 230 235 240  
 Ser Gly Gly Val Asn Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly  
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 Asp Leu Gly Leu Asp Ile Phe  
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 Met Thr Thr Ser Ile  
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 acc cca tct gtc aac ctt gca ttg aaa aat gcc aat agc tgc aac agt 163  
 Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala Asn Ser Cys Asn Ser  
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 gaa ctc aaa gac gga ccc tgg ttc ctc gac cag ccc gga atg ccg gat 211  
 Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln Pro Gly Met Pro Asp  
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 gtc tac ggc ccc ggc gcg tca caa aac gat ccg atc cct gcg cat gct 259  
 Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro Ile Pro Ala His Ala

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gaa ctg cat cgt agg atc cgg gaa gcg aaa gac acc ctg ggt gac aaa Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp Thr Leu Gly Asp Lys 70 75 80 85			355
gtg gtt atc cta gga cac ttc tac cag cgc gat gaa gtt atc caa cac Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp Glu Val Ile Gln His 90 95 100			403
gca gat ttt gtt ggt gac tct ttc caa ctt gcc cgc gct gcc aaa acc Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala Arg Ala Ala Lys Thr 105 110 115			451
cga ccc gag gcg gaa gcg att gtg ttc tgc ggt gtg cac ttc atg gct Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly Val His Phe Met Ala 120 125 130			499
gaa acc gct gat ctg tta tcc acg gat gaa caa tca gtg atc ctc ccc Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln Ser Val Ile Leu Pro 135 140 145			547
aac ctt gcc gca ggt tgc tcc atg gca gac atg gct gac ctt gat tcc Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met Ala Asp Leu Asp Ser 150 155 160 165			595
gtc gaa gac tgc tgg gag caa ctc acc tca att tat ggc gat gac acc Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile Tyr Gly Asp Asp Thr 170 175 180			643
ctg atc cct gtg acc tac atg aat tcc tct gca gcg ctc aaa ggt ttc Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala Ala Leu Lys Gly Phe 185 190 195			691
gtg ggt gag cac ggc gga att gta tgc acc tcc tca aat gca cgt tcc Val Gly Glu His Gly Gly Ile Val Cys Thr Ser Ser Asn Ala Arg Ser 200 205 210			739
gta ttg gag tgg gcg ttt gaa cgc ggc caa cga gtc ctg ttc ttc ccc Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg Val Leu Phe Phe Pro 215 220 225			787
gat cag cac ttg ggt cga aac acc gcg aaa gcc atg ggc att ggg atc Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala Met Gly Ile Gly Ile 230 235 240 245			835
gat caa atg ccc ctg tgg aat ccc aac aaa cca ctg ggt ggc aac acc Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro Leu Gly Gly Asn Thr 250 255 260			883
gtt tcc gag cta gaa aac gca aag gta ctg ctc tgg cat ggt ttc tgc Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu Trp His Gly Phe Cys 265 270 275			931
tct gta cac aag cgc ttt act gtc gag cag atc aac aaa gcc cgc gcc Ser Val His Lys Arg Phe Thr Val Glu Gln Ile Asn Lys Ala Arg Ala 280 285 290			979



gag tac ccc gac gtt cac gtc atc gtg cac cct gaa tcc ccc atg cca  
1027

Glu Tyr Pro Asp Val His Val Ile Val His Pro Glu Ser Pro Met Pro  
295 300 305

gtt gtt gac gcc gcc gac tca tcc gga tcc act gac ttc att gtg aaa  
1075

Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr Asp Phe Ile Val Lys  
310 315 320 325

gcc att caa gca gca ccg gca gga tct acc ttt gcg atc ggc acc gaa  
1123

Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe Ala Ile Gly Thr Glu  
330 335 340

atc aac ttg gtt cag cgc ctg gca gcc cag tac ccg cag cac acc atc  
1171

Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr Pro Gln His Thr Ile  
345 350 355

ttc tgc ctc gac cct gtc atc tgc cca tgc tcc acc atg tat cgc att  
1219

Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser Thr Met Tyr Arg Ile  
360 365 370

cac cct ggt tac ctg gcc tgg gca ctt gag gag ttg gtg gct gga aac  
1267

His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu Leu Val Ala Gly Asn  
375 380 385

gtg att aac cag att tct gtc tct gaa tcc gtg gcg gca ccg gcg cga  
1315

Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val Ala Ala Pro Ala Arg  
390 395 400 405

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1363

Val Ala Leu Glu Arg Met Leu Ser Val Val Pro Ala Ala Pro Val Thr  
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<211> 428

<212> PRT

<213> Corynebacterium glutamicum

<400> 606

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Pro Gly Met Pro Asp Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro  
35 40 45

Ile Pro Ala His Ala Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln  
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 Arg Ala Ser Asp Asp Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp  
 65 70 75 80  
 Thr Leu Gly Asp Lys Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp  
 85 90 95  
 Glu Val Ile Gln His Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala  
 100 105 110  
 Arg Ala Ala Lys Thr Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly  
 115 120 125  
 Val His Phe Met Ala Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln  
 130 135 140  
 Ser Val Ile Leu Pro Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met  
 145 150 155 160  
 Ala Asp Leu Asp Ser Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile  
 165 170 175  
 Tyr Gly Asp Asp Thr Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala  
 180 185 190  
 Ala Leu Lys Gly Phe Val Gly Glu His Gly Gly Ile Val Cys Thr Ser  
 195 200 205  
 Ser Asn Ala Arg Ser Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg  
 210 215 220  
 Val Leu Phe Phe Pro Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala  
 225 230 235 240  
 Met Gly Ile Gly Ile Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro  
 245 250 255  
 Leu Gly Gly Asn Thr Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu  
 260 265 270  
 Trp His Gly Phe Cys Ser Val His Lys Arg Phe Thr Val Glu Gln Ile  
 275 280 285  
 Asn Lys Ala Arg Ala Glu Tyr Pro Asp Val His Val Ile Val His Pro  
 290 295 300  
 Glu Ser Pro Met Pro Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr  
 305 310 315 320  
 Asp Phe Ile Val Lys Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe  
 325 330 335  
 Ala Ile Gly Thr Glu Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr  
 340 345 350  
 Pro Gln His Thr Ile Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser  
 355 360 365

Thr Met Tyr Arg Ile His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu  
 370 375 380

Leu Val Ala Gly Asn Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val  
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Ala Ala Pro Val Thr Pro Ser Ser Ser Lys Asp Ala  
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<211> 954

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(931)

<223> RXA01073

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 Met Thr Asn Thr Gln  
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acc gag atc att aat gaa cta aag gtg agc cca gca atc gac gtg gcc 163  
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aag gaa gtt gaa ttc cgt gtg cag ttc ctc gtc gat tac ctg cgg gct 211  
 Lys Glu Val Glu Phe Arg Val Gln Phe Leu Val Asp Tyr Leu Arg Ala  
 25 30 35

tcc cat aca aaa ggc ttt gtt ctt ggt att tca ggt ggc cag gat tcc 259  
 Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser Gly Gly Gln Asp Ser  
 40 45 50

act ctt gcg gga cga ctc acg cag ctg gca gta gag cgc att cgt gcg 307  
 Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val Glu Arg Ile Arg Ala  
 55 60 65

gaa gaa aac agc acg gat tat gtc ttc tac gca gtt cgc ctc ccc tac 355  
 Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala Val Arg Leu Pro Tyr  
 70 75 80 85

gcg atc cag gca gat gag gac gat gcg caa gtt gca ttg gaa ttc atc 403  
 Ala Ile Gln Ala Asp Glu Asp Asp Ala Gln Val Ala Leu Glu Phe Ile  
 90 95 100

gca cct gac aag agc gtg acc gtc aac gtt aaa gac gca acg gac gcc 451  
 Ala Pro Asp Lys Ser Val Thr Val Asn Val Lys Asp Ala Thr Asp Ala  
 105 110 115

acc gaa gca act gtt gca gct gct ttg gaa ctt cct gag ctg acc gac 499  
 Thr Glu Ala Thr Val Ala Ala Ala Leu Glu Leu Pro Glu Leu Thr Asp  
 120 125 130

ttc aat cgg ggc aat att aaa gct cgc caa cgc atg gtt gcc cag tac 547  
 Phe Asn Arg Gly Asn Ile Lys Ala Arg Gln Arg Met Val Ala Gln Tyr  
 135 140 145

gca atc gca ggc cag ttg ggc ttg ctg gtt att ggc act gat cac gcg 595  
 Ala Ile Ala Gly Gln Leu Gly Leu Leu Val Ile Gly Thr Asp His Ala  
 150 155 160 165

gct gaa aac gtc acg ggg ttc ttc acc aaa ttc ggt gat ggc gca gct 643  
 Ala Glu Asn Val Thr Gly Phe Phe Thr Lys Phe Gly Asp Gly Ala Ala  
 170 175 180

gac ctg ctt cct ttg gca ggt ttg agc aag cgt caa gga gct gcc att 691  
 Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg Gln Gly Ala Ala Ile  
 185 190 195

ctg gag cac ctg ggt gca cct tca agc acg tgg acc aag gtt cct acc 739  
 Leu Glu His Leu Gly Ala Pro Ser Ser Thr Trp Thr Lys Val Pro Thr  
 200 205 210

gct gat ttg gaa gag gat cgc cca gcg ttg cca gat gag gaa gca ctt 787  
 Ala Asp Leu Glu Glu Asp Arg Pro Ala Leu Pro Asp Glu Glu Ala Leu  
 215 220 225

ggt gtg tcg tat gcg gac atc gat aat tac ctg gaa aac aag ccc gat 835  
 Gly Val Ser Tyr Ala Asp Ile Asp Asn Tyr Leu Glu Asn Lys Pro Asp  
 230 235 240 245

gtc agt gaa aaa gcc cag cag cgc att gag cac ctg tgg aag gtg ggc 883  
 Val Ser Glu Lys Ala Gln Gln Arg Ile Glu His Leu Trp Lys Val Gly  
 250 255 260

cag cac aag cgc cac ctc cct gct acc ccg cag gaa aat tgg tgg cgt 931  
 Gln His Lys Arg His Leu Pro Ala Thr Pro Gln Glu Asn Trp Trp Arg  
 265 270 275

taatccaaca gtttgagtgt cgc 954

<210> 608  
 <211> 277  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 608  
 Met Thr Asn Thr Gln Thr Glu Ile Ile Asn Glu Leu Lys Val Ser Pro  
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 Asp Tyr Leu Arg Ala Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser  
 35 40 45  
 Gly Gly Gln Asp Ser Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val  
 50 55 60  
 Glu Arg Ile Arg Ala Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala  
 65 70 75 80

Val Arg Leu Pro Tyr Ala Ile Gln Ala Asp Glu Asp Asp Ala Gln Val  
 85 90 95  
 Ala Leu Glu Phe Ile Ala Pro Asp Lys Ser Val Thr Val Asn Val Lys  
 100 105 110  
 Asp Ala Thr Asp Ala Thr Glu Ala Thr Val Ala Ala Ala Leu Glu Leu  
 115 120 125  
 Pro Glu Leu Thr Asp Phe Asn Arg Gly Asn Ile Lys Ala Arg Gln Arg  
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 Met Val Ala Gln Tyr Ala Ile Ala Gly Gln Leu Gly Leu Leu Val Ile  
 145 150 155 160  
 Gly Thr Asp His Ala Ala Glu Asn Val Thr Gly Phe Phe Thr Lys Phe  
 165 170 175  
 Gly Asp Gly Ala Ala Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg  
 180 185 190  
 Gln Gly Ala Ala Ile Leu Glu His Leu Gly Ala Pro Ser Ser Thr Trp  
 195 200 205  
 Thr Lys Val Pro Thr Ala Asp Leu Glu Glu Asp Arg Pro Ala Leu Pro  
 210 215 220  
 Asp Glu Glu Ala Leu Gly Val Ser Tyr Ala Asp Ile Asp Asn Tyr Leu  
 225 230 235 240  
 Glu Asn Lys Pro Asp Val Ser Glu Lys Ala Gln Gln Arg Ile Glu His  
 245 250 255  
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 Glu Asn Trp Trp Arg  
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 <223> RXN02754

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 Val Asn Thr Asn Pro  
 1 5  
 tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163  
 Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr  
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Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg	
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ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga	259
Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg	
40 45 50	
tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac	307
Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp	
55 60 65	
ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac	355
Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp	
70 75 80 85	
cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat	403
Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp	
90 95 100	
ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act	451
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr	
105 110 115	
gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg	499
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu	
120 125 130	
tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg	547
Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met	
135 140 145	
gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc	595
Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg	
150 155 160 165	
acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct	643
Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala	
170 175 180	
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Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile	
185 190 195	
cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac	739
Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn	
200 205 210	
gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa	787
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu	
215 220 225	
tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc	835
Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr	
230 235 240 245	
caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca gac ctt ggt ggc	883
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro Asp Leu Gly Gly	
250 255 260	
gta cgt atc gac tcc ggc gac cta ggt gtg ctt gcc cga aag gtc cgc	931

Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu Ala Arg Lys Val Arg  
 265 270 275  
 aag cag ctc gac gat ctc aac gcc cac aac acc aag att gtg gtc tcc 979  
 Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr Lys Ile Val Val Ser  
 280 285 290  
 tcc gac ctg gat gaa ttc gcc atc gcg ggt ctt cgc ggc gaa cca gtt  
 1027  
 Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu Arg Gly Glu Pro Val  
 295 300 305  
 gac gtc ttt ggc gtt ggc acc tcc gtt gtc aca ggt tct ggc gca cca  
 1075  
 Asp Val Phe Gly Val Gly Thr Ser Val Val Thr Gly Ser Gly Ala Pro  
 310 315 320 325  
 acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg  
 1123  
 Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val  
 330 335 340  
 gcc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct  
 1171  
 Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly Gly Gly Lys Lys Ala  
 345 350 355  
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 1219  
 Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr  
 360 365 370  
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 1267  
 Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser  
 375 380 385  
 ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct  
 1315  
 Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile Val Pro Gly Leu Pro  
 390 395 400 405  
 act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta  
 1363  
 Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu  
 410 415 420  
 cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act  
 1411  
 Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr  
 425 430 435  
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 1461

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 610

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 Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu  
 35 40 45  
 Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu  
 50 55 60  
 Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu  
 65 70 75 80  
 Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe  
 85 90 95  
 Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln  
 100 105 110  
 Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu  
 115 120 125  
 Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser  
 130 135 140  
 Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu  
 145 150 155 160  
 Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg  
 165 170 175  
 Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala  
 180 185 190  
 Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr  
 195 200 205  
 Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe  
 210 215 220  
 Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp  
 225 230 235 240  
 Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly  
 245 250 255  
 Pro Asp Leu Gly Gly Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu  
 260 265 270  
 Ala Arg Lys Val Arg Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr  
 275 280 285  
 Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu



290	295	300	
Arg Gly Glu Pro Val	Asp Val Phe Gly Val	Gly Thr Ser Val Val Thr	
305	310	315	320
Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val			
	325	330	335
Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly			
	340	345	350
Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile			
	355	360	365
Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys			
	370	375	380
Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile			
	385	390	395
Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys			
	405	410	415
Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu			
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Met Leu Arg Thr Ile 1 5			
ctc gga agt aag att cac cga gcc act gtc act caa gct gat cta gat 163			
Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr Gln Ala Asp Leu Asp 10 15 20			
tat gtt ggc tct gta acc atc gac gcc gac ctg gtt cac gcc gcc gga 211			
Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu Val His Ala Ala Gly 25 30 35			
ttg atc gaa ggc gaa aaa gtt gcc atc gta gac atc acc aac ggc gct 259			
Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp Ile Thr Asn Gly Ala 40 45 50			
cgt ctg gaa act tat gtc att gtg ggc gac gcc gga acg ggc aat att 307			
Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala Gly Thr Gly Asn Ile			

55                                      60                                      65  
 tgc atc aat ggt gcc gct gca cac ctt att aat cct ggc gat ctt gtg 355  
 Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn Pro Gly Asp Leu Val  
 70                                      75                                      80                                      85  
 atc atc atg agc tac ctt cag gca act gat gcg gaa gcc aag gcg tat 403  
 Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala Glu Ala Lys Ala Tyr  
 90                                      95                                      100  
 gag cca aag att gtg cac gtg gac gcc gac aac cgc atc gtt gcg ctc 451  
 Glu Pro Lys Ile Val His Val Asp Ala Asp Asn Arg Ile Val Ala Leu  
 105                                      110                                      115  
 ggc aac gat ctt gcg gaa gca cta cct gga tcc ggg ctt ttg acg tcg 499  
 Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser Gly Leu Leu Thr Ser  
 120                                      125                                      130  
 aga agc att tagcgtttta gctcgccaat att 531  
 Arg Ser Ile  
 135  
 <210> 612  
 <211> 136  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 612  
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 1                                      5                                      10                                      15  
 Gln Ala Asp Leu Asp Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu  
 20                                      25                                      30  
 Val His Ala Ala Gly Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp  
 35                                      40                                      45  
 Ile Thr Asn Gly Ala Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala  
 50                                      55                                      60  
 Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn  
 65                                      70                                      75                                      80  
 Pro Gly Asp Leu Val Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala  
 85                                      90                                      95  
 Glu Ala Lys Ala Tyr Glu Pro Lys Ile Val His Val Asp Ala Asp Asn  
 100                                      105                                      110  
 Arg Ile Val Ala Leu Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser  
 115                                      120                                      125  
 Gly Leu Leu Thr Ser Arg Ser Ile  
 130                                      135  
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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(937)

&lt;223&gt; RXA01928

&lt;400&gt; 613

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tccacgcggg taccttccca ggcgaagcgg agtcctttta atg cag gta gca acc 115
                                     Met Gln Val Ala Thr
                                     1                               5

aca aag cag gcg ctt atc gac gcc ctc ctc cac cac aaa tcc gtc ggg 163
Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His His Lys Ser Val Gly
                10                        15                        20

ctc gtc ccc acc atg ggt gcg cta cac agc gga cac gcc tcg ttg gtt 211
Leu Val Pro Thr Met Gly Ala Leu His Ser Gly His Ala Ser Leu Val
                25                        30                        35

aaa gca gca cgc gct gaa aac gac act gtt gta gcc agt att ttt gtc 259
Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val Ala Ser Ile Phe Val
                40                        45                        50

aat ccc ctg cag ttt gaa gca ctc ggt gat tgc gat gat tac cgc aac 307
Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys Asp Asp Tyr Arg Asn
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tat ccc cgc caa ctc gac gcc gat tta gca ctg ctt gaa gag gca ggt 355
Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu Leu Glu Glu Ala Gly
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gtg gat att gtg ttc gca ccc gat gtg gag gaa atg tac ccc ggt ggc 403
Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu Met Tyr Pro Gly Gly
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ttg cca cta gtg tgg gcg cgc acc ggt tcc atc gga aca aaa ttg gag 451
Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile Gly Thr Lys Leu Glu
                105                        110                        115

ggt gcc agc agg cct ggc cat ttc gat ggt gtg gct acc gtg gtg gcg 499
Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val Ala Thr Val Val Ala
                120                        125                        130

aag ctg ttc aat ttg gtg cgc cct gat cgt gca tat ttt gga caa aaa 547
Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala Tyr Phe Gly Gln Lys
                135                        140                        145

gat gct cag cag gtt gcg gtg att cgg cga ttg gtt gcc gat cta gac 595
Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu Val Ala Asp Leu Asp
                150                        155                        160                        165

att ccc gtg gag att cgt ccc gtt ccg att att cgt ggc gcc gat ggc 643
Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile Arg Gly Ala Asp Gly
                170                        175                        180

tta gcc gaa tcc agc cgc aat caa cgt ctt tct gcg gat cag cga gcg 691
Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser Ala Asp Gln Arg Ala
                185                        190                        195

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caa gct ctg gtg ctg ccg cag gtg ttg agt ggg ttg cag cgt cga aaa 739  
 Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly Leu Gln Arg Arg Lys  
           200                                  205                                  210

gca gct ggt gaa gcg cta gat atc caa ggt gcg cgc gac acc ttg gcc 787  
 Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala Arg Asp Thr Leu Ala  
           215                                  220                                  225

agc gcc gac ggc gtg cgc ttg gat cac ctg gaa att gtc gat cca gcc 835  
 Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu Ile Val Asp Pro Ala  
           230                                  235                                  240                                  245

acc ctc gaa cca tta gaa atc gac ggc ctg ctc acc caa cca gcg ttg 883  
 Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu Thr Gln Pro Ala Leu  
                                   250                                  255                                  260

gtg gtc ggc gcg att ttc gtg ggg ccg gtg cgg ttg atc gac aat atc 931  
 Val Val Gly Ala Ile Phe Val Gly Pro Val Arg Leu Ile Asp Asn Ile  
                                   265                                  270                                  275

gag ctc tagtaccac cctgcgttgc agc 960  
 Glu Leu

<210> 614

<211> 279

<212> PRT

<213> Corynebacterium glutamicum

<400> 614

Met Gln Val Ala Thr Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His  
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His Lys Ser Val Gly Leu Val Pro Thr Met Gly Ala Leu His Ser Gly  
                                   20                                  25                                  30

His Ala Ser Leu Val Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val  
                                   35                                  40                                  45

Ala Ser Ile Phe Val Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys  
                                   50                                  55                                  60

Asp Asp Tyr Arg Asn Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu  
   65                                  70                                  75                                  80

Leu Glu Glu Ala Gly Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu  
                                   85                                  90                                  95

Met Tyr Pro Gly Gly Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile  
                                   100                                  105                                  110

Gly Thr Lys Leu Glu Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val  
                                   115                                  120                                  125

Ala Thr Val Val Ala Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala  
                                   130                                  135                                  140

Tyr Phe Gly Gln Lys Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu  
   145                                  150                                  155                                  160

Val Ala Asp Leu Asp Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile  
 165 170 175

Arg Gly Ala Asp Gly Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser  
 180 185 190

Ala Asp Gln Arg Ala Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly  
 195 200 205

Leu Gln Arg Arg Lys Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala  
 210 215 220

Arg Asp Thr Leu Ala Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu  
 225 230 235 240

Ile Val Asp Pro Ala Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu  
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Thr Gln Pro Ala Leu Val Val Gly Ala Ile Phe Val Gly Pro Val Arg  
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Leu Ile Asp Asn Ile Glu Leu  
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<210> 615  
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(913)  
 <223> RXN01929

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 Met Pro Met Ser Gly  
 1 5

att gat gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta 163  
 Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val  
 10 15 20

aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg 211  
 Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala  
 25 30 35

cgc att ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc 259  
 Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser  
 40 45 50

gct gcc aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg 307  
 Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu  
 55 60 65

gat gag atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt 355  
 Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg  
 70 75 80 85

gcg ctt gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca 403  
 Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro  
 90 95 100

aat cag gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg 451  
 Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala  
 105 110 115

gct gcg gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga 499  
 Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg  
 120 125 130

cgc att gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc 547  
 Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr  
 135 140 145

ccg cag tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc 595  
 Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly  
 150 155 160 165

gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg 643  
 Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala  
 170 175 180

ggt gcg ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc 691  
 Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg  
 185 190 195

gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc 739  
 Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly  
 200 205 210

aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc 787  
 Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu  
 215 220 225

aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc 835  
 Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly  
 230 235 240 245

gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg 883  
 Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala  
 250 255 260

ggt acc ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca 933  
 Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe  
 265 270

aag 936

<210> 616  
 <211> 271  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 616  
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 Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu  
                   35                                  40                                  45  
 Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr  
                   50                                  55                                  60  
 Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr  
                   65                                  70                                  75                                  80  
 Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr  
                                   85                                  90                                  95  
 Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met  
                                   100                                  105                                  110  
 Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile  
                   115                                  120                                  125  
 Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly  
                   130                                  135                                  140  
 His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val  
                   145                                  150                                  155                                  160  
 Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg  
                                   165                                  170                                  175  
 Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro  
                                   180                                  185                                  190  
 Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile  
                   195                                  200                                  205  
 Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln  
                   210                                  215                                  220  
 Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu  
                   225                                  230                                  235                                  240  
 Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile  
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 Ala Asp Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe  
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&lt;210&gt; 617

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(907)

&lt;223&gt; FRXA01929

&lt;400&gt; 617

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				Met	Ser	Gly	Ile	Asp		
				1				5		
gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc	163									
Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly										
	10			15				20		
cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att	211									
Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile										
	25			30				35		
ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc	259									
Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala										
	40			45				50		
aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag	307									
Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu										
	55			60				65		
atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt	355									
Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg Ala Leu										
	70			75				80	85	
gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca aat cag	403									
Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro Asn Gln										
	90					95			100	
gcg gtg gag tcc gcg atc ccg gtc atg cgt gaa acg ggt gcg gct gcg	451									
Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala Ala Ala										
	105					110			115	
gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga cgc att	499									
Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg Arg Ile										
	120					125			130	
gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc ccg cag	547									
Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr Pro Gln										
	135					140			145	
tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc gcg agt	595									
Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly Ala Ser										
	150					155			160	165
tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg ggt gcg	643									
Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala Gly Ala										
	170					175			180	
ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc gag gtt	691									
Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg Glu Val										
	185					190			195	
acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc aat ggc	739									
Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly Asn Gly										
	200					205			210	
aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc aac cgc	787									
Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu Asn Arg										
	215					220			225	



ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc gat tcc 835  
 Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly Asp Ser  
 230 235 240 245

ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg ggt acc 883  
 Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala Gly Thr  
 250 255 260

ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca aag 930  
 Phe Pro Gly Glu Ala Glu Ser Phe  
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<210> 618

<211> 269

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 618

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 20 25 30

Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val  
 35 40 45

Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser  
 50 55 60

Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala  
 65 70 75 80

Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu  
 85 90 95

Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu  
 100 105 110

Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln  
 115 120 125

Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile  
 130 135 140

Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln  
 145 150 155 160

Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu  
 165 170 175

Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu  
 180 185 190

Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile  
 195 200 205

Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala  
 210 215 220

Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala  
 225 230 235 240

Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp  
 245 250 255

Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe  
 260 265

<210> 619

<211> 921

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(898)

<223> RXA01521

<400> 619

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 Leu Ser Phe Thr His  
 1 5  
 ggt cag ggc aga gtt ttt gat acc gtc gag cag atc cgc atg ttc ggc 163  
 Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln Ile Arg Met Phe Gly  
 10 15 20  
 agc gcc ctg cgc aaa acc ggc aaa cca gtg gtg ctc gta ccc ttg gga 211  
 Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val Leu Val Pro Leu Gly  
 25 30 35  
 aat ggc ctc cac gca ggc cat att gcg ctc atc cgc gca gca aaa cgc 259  
 Asn Gly Leu His Ala Gly His Ile Ala Leu Ile Arg Ala Ala Lys Arg  
 40 45 50  
 atc ccc ggt gcg gtg gtc gtc gtc gcc tat gcc ggc ccg gaa tcg gat 307  
 Ile Pro Gly Ala Val Val Val Val Ala Tyr Ala Gly Pro Glu Ser Asp  
 55 60 65  
 cac gca cgt tta agg gaa gag ctt atc gac gcg atc ttc ccg ttc aat 355  
 His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala Ile Phe Pro Phe Asn  
 70 75 80 85  
 ccc gaa acg cta tgg cct cac ggc atc cgg gtg gaa gtt aca ggt ggc 403  
 Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val Glu Val Thr Gly Gly  
 90 95 100  
 cca aca ctt acc cca caa ggt gcg gaa gta acc aag gtg ctg ggg ctg 451  
 Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr Lys Val Leu Gly Leu  
 105 110 115  
 ttg gga atc acc gga gca act gat gtg gtg ctc ggt gaa aag gac tat 499  
 Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu Gly Glu Lys Asp Tyr  
 120 125 130  
 gag ctg gtg gtt cta gtc cag cgc gcc ctt aat gat ctg cat att cca 547  
 Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn Asp Leu His Ile Pro

135	140	145	
gta aaa ctg cat tct gtt cca acc gtg cgc atg cca gat gga cta gcc Val Lys Leu His Ser Val Pro Thr Val Arg Met Pro Asp Gly Leu Ala 150 155 160 165			595
att tcc ctg cgt aat att tca gtg ccc gaa gac tcc cgc gaa acg gca Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp Ser Arg Glu Thr Ala 170 175 180			643
ttg agc ctg gca gca gcc ctc acc gcc ggt gcg cat tcg gca gaa cac Leu Ser Leu Ala Ala Leu Thr Ala Gly Ala His Ser Ala Glu His 185 190 195			691
ggc gag gca gtg gtt aaa gaa aca gtc acg caa gtg ctc aaa gcc gca Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln Val Leu Lys Ala Ala 200 205 210			739
ggc gtg acc ccc gat tat gta gaa atc cgt ggc ctg gat ctt gga cca Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly Leu Asp Leu Gly Pro 215 220 225			787
gcc ccc gaa atc gga gac gcc cga ctc ttc gca gcc atc acg ctt ggc Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala Ala Ile Thr Leu Gly 230 235 240 245			835
gat gtc caa ctc cac gac aac gtc ggc cta ccc ctt gga atc ggc ttc Asp Val Gln Leu His Asp Asn Val Gly Leu Pro Leu Gly Ile Gly Phe 250 255 260			883
aaa aac atc gaa ggc tgatcccggt ttacccagtt cgc Lys Asn Ile Glu Gly 265			921
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Ile Arg Met Phe Gly Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val 20 25 30			
Leu Val Pro Leu Gly Asn Gly Leu His Ala Gly His Ile Ala Leu Ile 35 40 45			
Arg Ala Ala Lys Arg Ile Pro Gly Ala Val Val Val Val Ala Tyr Ala 50 55 60			
Gly Pro Glu Ser Asp His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala 65 70 75 80			
Ile Phe Pro Phe Asn Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val 85 90 95			
Glu Val Thr Gly Gly Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr 100 105 110			

Lys Val Leu Gly Leu Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu  
 115 120 125  
 Gly Glu Lys Asp Tyr Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn  
 130 135 140  
 Asp Leu His Ile Pro Val Lys Leu His Ser Val Pro Thr Val Arg Met  
 145 150 155 160  
 Pro Asp Gly Leu Ala Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp  
 165 170 175  
 Ser Arg Glu Thr Ala Leu Ser Leu Ala Ala Ala Leu Thr Ala Gly Ala  
 180 185 190  
 His Ser Ala Glu His Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln  
 195 200 205  
 Val Leu Lys Ala Ala Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly  
 210 215 220  
 Leu Asp Leu Gly Pro Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala  
 225 230 235 240  
 Ala Ile Thr Leu Gly Asp Val Gln Leu His Asp Asn Val Gly Leu Pro  
 245 250 255  
 Leu Gly Ile Gly Phe Lys Asn Ile Glu Gly  
 260 265

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 <213> Corynebacterium glutamicum

<220>  
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 <223> RXS01145

<400> 621  
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 Met Ala Ile Glu Leu  
 1 5  
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163  
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val  
 10 15 20  
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211  
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu  
 25 30 35  
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259  
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys  
 40 45 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307  
 Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala  
 55 60 65

gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355  
 Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr  
 70 75 80 85

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403  
 Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala  
 90 95 100

ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451  
 Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu  
 105 110 115

atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499  
 Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly  
 120 125 130

cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547  
 Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro  
 135 140 145

tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg 595  
 Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu  
 150 155 160 165

acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc 643  
 Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile  
 170 175 180

cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag 691  
 Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln  
 185 190 195

gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag 739  
 Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu  
 200 205 210

gtt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt 787  
 Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val  
 215 220 225

ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc 835  
 Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile  
 230 235 240 245

agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac 883  
 Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr  
 250 255 260

ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag 931  
 Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys  
 265 270 275

gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc 979  
 Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile  
 280 285 290

gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc  
1027

Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser  
295 300 305

tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc  
1075

Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu  
310 315 320 325

atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtttcac  
1124

Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala  
330 335

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1137

<210> 622

<211> 338

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 622

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20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu  
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu  
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu  
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp  
130 135 140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly  
145 150 155 160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala  
165 170 175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp  
180 185 190

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val  
 195 200 205  
 Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met  
 210 215 220  
 Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met  
 225 230 235 240  
 Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala  
 245 250 255  
 Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr  
 260 265 270  
 Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe  
 275 280 285  
 Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu  
 290 295 300  
 Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala  
 305 310 315 320  
 Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu  
 325 330 335  
 Thr Ala

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> FRXA01145

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 Met Ala Ile Glu Leu  
 1 5  
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163  
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val  
 10 15 20  
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211  
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu  
 25 30 35  
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259  
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys  
 40 45 50  
 tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala  
 55 60 65  
 gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355  
 Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr  
 70 75 80 85  
 tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403  
 Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala  
 90 95 100  
 ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451  
 Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu  
 105 110 115  
 atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499  
 Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly  
 120 125 130  
 cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547  
 Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro  
 135 140 145  
 tgc ctc atc 556  
 Cys Leu Ile  
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 <210> 624  
 <211> 152  
 <212> PRT  
 <213> Corynebacterium glutamicum  
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 20 25 30  
 His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu  
 35 40 45  
 Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
 50 55 60  
 Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu  
 65 70 75 80  
 Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu  
 85 90 95  
 Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
 100 105 110  
 Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
 115 120 125  
 Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp  
 130 135 140



Gly Lys Gly Val Pro Cys Leu Ile  
145 150

<210> 625  
<211> 1389  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
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<222> (101)..(1366)  
<223> RXA02239

<400> 625  
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gtgtgggaac ccagccagcc tcttactttg aaggattgtt gtg ccc atg act cat 115  
Val Pro Met Thr His  
1 5  
gtt tca agc ccc tcc gca ccc cgc aac gtg gtt gtt ggt gtt gcc ggc 163  
Val Ser Ser Pro Ser Ala Pro Arg Asn Val Val Val Gly Val Ala Gly  
10 15 20  
gga atc gca gcg tac aag gcg tgt cac atc gtg cgc gcg ttt aaa gaa 211  
Gly Ile Ala Ala Tyr Lys Ala Cys His Ile Val Arg Ala Phe Lys Glu  
25 30 35  
gcg ggc gat aat gtg cgg gtg gtt cct acg gaa tcc gcg ttg aag ttt 259  
Ala Gly Asp Asn Val Arg Val Val Pro Thr Glu Ser Ala Leu Lys Phe  
40 45 50  
gtg ggg aag gcg acg ttt gaa gcg ttg tct ggc aat ccg gtg tct aca 307  
Val Gly Lys Ala Thr Phe Glu Ala Leu Ser Gly Asn Pro Val Ser Thr  
55 60 65  
acg gtg ttt gat gcg gtg gat tcg gtg cag cat gtg aaa gtt ggc cag 355  
Thr Val Phe Asp Ala Val Asp Ser Val Gln His Val Lys Val Gly Gln  
70 75 80 85  
gaa gct gat ttg atc gtg att gcg ccg gcg aca gcc gat ttg atg gcg 403  
Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr Ala Asp Leu Met Ala  
90 95 100  
cgt gtg gtg gca ggt ctc ggt gac gat ctg ttg gcg gcg acg ctg ctg 451  
Arg Val Val Ala Gly Leu Gly Asp Asp Leu Leu Ala Ala Thr Leu Leu  
105 110 115  
gtg gca acg tgc ccc gtg gtt att gcg ccg gcc atg cat acg gag atg 499  
Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala Met His Thr Glu Met  
120 125 130  
tgg ttt aat ccg gct acc gta gcc aat gtg gca acg ctg agg cag cgg 547  
Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala Thr Leu Arg Gln Arg  
135 140 145  
ggg att acc gtg att gag cct gcg cat ggt cga ctc acc ggt aaa gat 595  
Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg Leu Thr Gly Lys Asp  
150 155 160 165

aca ggc cct ggc cgg ctg ccg gat cca gag cag att gtt gat tta gcc 643  
 Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln Ile Val Asp Leu Ala  
 170 175 180

aat gcg gtg cac gcc ggg gcg agg ttg cct cag gat ttg gcg ggc aag 691  
 Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln Asp Leu Ala Gly Lys  
 185 190 195

aaa gtg ctg atc act gct ggt ggc acg cat gag cat att gat cct gtg 739  
 Lys Val Leu Ile Thr Ala Gly Gly Thr His Glu His Ile Asp Pro Val  
 200 205 210

cgc ttt att ggc aat agt tcc tcg ggc cgt caa ggt ttt gcg ttg ggt 787  
 Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln Gly Phe Ala Leu Gly  
 215 220 225

gaa atc gca gca cag cga ggt gct cat gtc agc atc gtg gcg gga aat 835  
 Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser Ile Val Ala Gly Asn  
 230 235 240 245

gct gcg gag ctg ccc act ccg gca ggc gca gag atc gtg ccg gtg gtg 883  
 Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu Ile Val Pro Val Val  
 250 255 260

tcc aca caa gac atg ttt gat gca gtc cag gaa cga gct ggc caa tct 931  
 Ser Thr Gln Asp Met Phe Asp Ala Val Gln Glu Arg Ala Gly Gln Ser  
 265 270 275

gat ttc atc gtc atg gcg gca gcg gta gct gat ttc acg ccc gca tcg 979  
 Asp Phe Ile Val Met Ala Ala Ala Val Ala Asp Phe Thr Pro Ala Ser  
 280 285 290

cag gcg aca tcg aag ttg aag aag ggc tca gat tct gat gaa gac gca  
 1027  
 Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp Ser Asp Glu Asp Ala  
 295 300 305

ttg agc acc atc tcg ttg gtg gaa aac ccg gat att ttg gct acc acg  
 1075  
 Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp Ile Leu Ala Thr Thr  
 310 315 320 325

gtg aag cgt cgt gaa gca gga gag ctg gac agt aat cct gtc atc gtg  
 1123  
 Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser Asn Pro Val Ile Val  
 330 335 340

ggt ttt gct gcg gaa act gga gac gag cac acc acc gcc ttg gag tat  
 1171  
 Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr Thr Ala Leu Glu Tyr  
 345 350 355

gcg cgc aag aaa ctg cag aag aag ggc tgc gac ctc ctc atg tgt aat  
 1219  
 Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp Leu Leu Met Cys Asn  
 360 365 370

gag gtg ggc atg ggc aaa gtg ttt ggg caa aag cac aat gag ggc tgg  
 1267  
 Glu Val Gly M t Gly Lys Val Phe Gly Gln Lys His Asn Glu Gly Trp  
 375 380 385

att ttg gat gct cac ggt ggg gta gtc gat gtg gag cac ggc agc aaa  
1315

Ile Leu Asp Ala His Gly Gly Val Val Asp Val Glu His Gly Ser Lys  
390 395 400 405

atc gag gtt gct gcg caa att tgg gac gcg gca ctg gcg tat cgc gaa  
1363

Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala Leu Ala Tyr Arg Glu  
410 415 420

gtc tagaaaaatc cagctagacc act

1389

Val

<210> 626

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 626

Val Pro Met Thr His Val Ser Ser Pro Ser Ala Pro Arg Asn Val Val  
1 5 10 15

Val Gly Val Ala Gly Gly Ile Ala Ala Tyr Lys Ala Cys His Ile Val  
20 25 30

Arg Ala Phe Lys Glu Ala Gly Asp Asn Val Arg Val Val Pro Thr Glu  
35 40 45

Ser Ala Leu Lys Phe Val Gly Lys Ala Thr Phe Glu Ala Leu Ser Gly  
50 55 60

Asn Pro Val Ser Thr Thr Val Phe Asp Ala Val Asp Ser Val Gln His  
65 70 75 80

Val Lys Val Gly Gln Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr  
85 90 95

Ala Asp Leu Met Ala Arg Val Val Ala Gly Leu Gly Asp Asp Leu Leu  
100 105 110

Ala Ala Thr Leu Leu Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala  
115 120 125

Met His Thr Glu Met Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala  
130 135 140

Thr Leu Arg Gln Arg Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg  
145 150 155 160

Leu Thr Gly Lys Asp Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln  
165 170 175

Ile Val Asp Leu Ala Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln  
180 185 190

Asp Leu Ala Gly Lys Lys Val Leu Ile Thr Ala Gly Gly Thr His Glu  
195 200 205

His Ile Asp Pro Val Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln  
 210 215 220  
 Gly Phe Ala Leu Gly Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser  
 225 230 235 240  
 Ile Val Ala Gly Asn Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu  
 245 250 255  
 Ile Val Pro Val Val Ser Thr Gln Asp Met Phe Asp Ala Val Gln Glu  
 260 265 270  
 Arg Ala Gly Gln Ser Asp Phe Ile Val Met Ala Ala Ala Val Ala Asp  
 275 280 285  
 Phe Thr Pro Ala Ser Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp  
 290 295 300  
 Ser Asp Glu Asp Ala Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp  
 305 310 315 320  
 Ile Leu Ala Thr Thr Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser  
 325 330 335  
 Asn Pro Val Ile Val Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr  
 340 345 350  
 Thr Ala Leu Glu Tyr Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp  
 355 360 365  
 Leu Leu Met Cys Asn Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys  
 370 375 380  
 His Asn Glu Gly Trp Ile Leu Asp Ala His Gly Gly Val Val Asp Val  
 385 390 395 400  
 Glu His Gly Ser Lys Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala  
 405 410 415  
 Leu Ala Tyr Arg Glu Val  
 420

<210> 627  
 <211> 1092  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1069)  
 <223> RXA00581

<400> 627  
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 Met Ala Glu Gln Asn  
 1 5

gct gca agc aca act ggt gtg aaa cct tcc cca cgc aca cca gat ttc 163  
 Ala Ala Ser Thr Thr Gly Val Lys Pro Ser Pro Arg Thr Pro Asp Phe  
 10 15 20

agc ccc tac ctt gat ttc gac cgc gca caa tgg cgc gag ctg aga aac 211  
 Ser Pro Tyr Leu Asp Phe Asp Arg Ala Gln Trp Arg Glu Leu Arg Asn  
 25 30 35

tca atg cct cag gtg ctg acc caa aaa gaa gtc att gaa ctt cga ggc 259  
 Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val Ile Glu Leu Arg Gly  
 40 45 50

atc gga gaa aac att gac ctc gct gaa gtg gca gaa gtc tac ctt ccg 307  
 Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala Glu Val Tyr Leu Pro  
 55 60 65

ctg tcc cgt ctg att cac ctc cag gta gcg gcc cga cag caa ctt act 355  
 Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala Arg Gln Gln Leu Thr  
 70 75 80 85

gca gcc acc gaa acc ttc ctc gga act tcc ccc tct atc tct gtg ccg 403  
 Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro Ser Ile Ser Val Pro  
 90 95 100

ttt gtc att ggt gtc gcg gga tcc gtc gcc gtc ggt aaa tca acc acc 451  
 Phe Val Ile Gly Val Ala Gly Ser Val Ala Val Gly Lys Ser Thr Thr  
 105 110 115

gcc cga ctc ctc caa gtt ctg ctt cag cgc tgg aat tcc cac ccc cgc 499  
 Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp Asn Ser His Pro Arg  
 120 125 130

gtg gac ctc gtc acc acc gac gga ttc ctc tat ccc ggc gcg gaa cta 547  
 Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr Pro Gly Ala Glu Leu  
 135 140 145

atc cgc cgc gga tta atg tcc cga aaa gga ttc ccc gaa agc tac gac 595  
 Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe Pro Glu Ser Tyr Asp  
 150 155 160 165

caa cgt gca ctc ctc cgc ttt gtc acc gac gta aaa tcc gga aaa ctc 643  
 Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val Lys Ser Gly Lys Leu  
 170 175 180

gaa gtc aac gca cct gtc tac tcc cac acc gcg tac gac cga gtt cca 691  
 Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala Tyr Asp Arg Val Pro  
 185 190 195

ggc gaa ttc acc aca gtc cgc caa ccc gac att ttg atc gtc gaa ggc 739  
 Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile Leu Ile Val Glu Gly  
 200 205 210

tta aac gtc ctc caa act ggc cca aca ttg atg gtc agt gac ctt ttc 787  
 Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met Val Ser Asp Leu Phe  
 215 220 225

gac ttc agc gtc tac gta gat gcc cgc acc gaa gat atc gaa aaa tgg 835  
 Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu Asp Ile Glu Lys Trp  
 230 235 240 245

tac atc gac cgc ttc ctc aaa ctc cgc gac act gca ttc cgt cgc ccc 883

Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr Ala Phe Arg Arg Pro  
 250 255 260

ggt gcc cac ttc tcc cat tac gcc gac atg gct gat cca gag tcc atc 931  
 Gly Ala His Phe Ser His Tyr Ala Asp Met Ala Asp Pro Glu Ser Ile  
 265 270 275

gcc gtc gct cga gaa ctg tgg caa tcg atc aac ctg ccc aac ttg gtg 979  
 Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn Leu Pro Asn Leu Val  
 280 285 290

gag aat att ctt ccc acc cga gtt cgc gcg tcg ttg gta ctg aaa aaa  
 1027  
 Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser Leu Val Leu Lys Lys  
 295 300 305

ggt agc gat cac ttg gtg gaa cgg gtg agg atg cgc aag atc  
 1069  
 Gly Ser Asp His Leu Val Glu Arg Val Arg Met Arg Lys Ile  
 310 315 320

taggggttct tgctggtttt gag  
 1092

<210> 628

<211> 323

<212> PRT

<213> Corynebacterium glutamicum

<400> 628

Met Ala Glu Gln Asn Ala Ala Ser Thr Thr Gly Val Lys Pro Ser Pro  
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Arg Thr Pro Asp Phe Ser Pro Tyr Leu Asp Phe Asp Arg Ala Gln Trp  
 20 25 30

Arg Glu Leu Arg Asn Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val  
 35 40 45

Ile Glu Leu Arg Gly Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala  
 50 55 60

Glu Val Tyr Leu Pro Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala  
 65 70 75 80

Arg Gln Gln Leu Thr Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro  
 85 90 95

Ser Ile Ser Val Pro Phe Val Ile Gly Val Ala Gly Ser Val Ala Val  
 100 105 110

Gly Lys Ser Thr Thr Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp  
 115 120 125

Asn Ser His Pro Arg Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr  
 130 135 140

Pro Gly Ala Glu Leu Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe  
 145 150 155 160

Pro Glu Ser Tyr Asp Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val  
 165 170 175  
 Lys Ser Gly Lys Leu Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala  
 180 185 190  
 Tyr Asp Arg Val Pro Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile  
 195 200 205  
 Leu Ile Val Glu Gly Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met  
 210 215 220  
 Val Ser Asp Leu Phe Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu  
 225 230 235 240  
 Asp Ile Glu Lys Trp Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr  
 245 250 255  
 Ala Phe Arg Arg Pro Gly Ala His Phe Ser His Tyr Ala Asp Met Ala  
 260 265 270  
 Asp Pro Glu Ser Ile Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn  
 275 280 285  
 Leu Pro Asn Leu Val Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser  
 290 295 300  
 Leu Val Leu Lys Lys Gly Ser Asp His Leu Val Glu Arg Val Arg Met  
 305 310 315 320  
 Arg Lys Ile

<210> 629  
 <211> 1023  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1000)  
 <223> RXS00838

<400> 629  
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 Met Lys Ile Ala Ile  
 1 5  
 gtt ggc gct ggt gca gtt ggt gga tat ttc gga gcg ttg tta caa gaa 163  
 Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly Ala Leu Leu Gln Glu  
 10 15 20  
 tct ggt gca gat atc acg atg gtt gca cgt gga cga aca tta gaa gcc 211  
 Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala  
 25 30 35  
 ttg aag tct aaa gga ctc cac atc aac gat gca aga ggc gaa cgc tac 259  
 Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala Arg Gly Glu Arg Tyr

40	45	50	
gta cca att cct gca gtt gcg agc gtg caa gaa cta aaa gat gca gat Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu Leu Lys Asp Ala Asp 55 60 65			307
gta gtg atg att gct act aaa gca tta tcg cgg tct tta gat ctc gct Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg Ser Leu Asp Leu Ala 70 75 80 85			355
gaa ctt ttg ggt ggg ata cct gcg aat tcg gtg gtc gcg att act cag Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val Val Ala Ile Thr Gln 90 95 100			403
aat tcg att gaa tct gct gat cta gca gcg aag agt atc ggt gct gat Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys Ser Ile Gly Ala Asp 105 110 115			451
cgt gtg tgg cct ggt gtg gtt cgt ggg ttc ttt gtt cat gag ggg cca Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe Val His Glu Gly Pro 120 125 130			499
gcc tca gtg tca tac aag gga ggc cca ctg tcc tac acg ttt ggt gat Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser Tyr Thr Phe Gly Asp 135 140 145			547
tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly 150 155 160 165			595
att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys 170 175 180			643
gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys 185 190 195			691
caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu 200 205 210			739
atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro 215 220 225			787
agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu 230 235 240 245			835
aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser 250 255 260			883
gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val 265 270 275			931
ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu 280 285 290			979



aaa gaa gag gaa aat tca ctt tagggataga atcaagatcc atg  
1023

Lys Glu Glu Glu Asn Ser Leu  
295 300

<210> 630

<211> 300

<212> PRT

<213> Corynebacterium glutamicum

<400> 630

Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly  
1 5 10 15

Ala Leu Leu Gln Glu Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly  
20 25 30

Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala  
35 40 45

Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu  
50 55 60

Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg  
65 70 75 80

Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val  
85 90 95

Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys  
100 105 110

Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe  
115 120 125

Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser  
130 135 140

Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr  
145 150 155 160

Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val  
165 170 175

Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly  
180 185 190

Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala  
195 200 205

Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala  
210 215 220

Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala  
225 230 235 240

Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala  
245 250 255

Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg  
 260 265 270

Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr  
 275 280 285

Ala Gly Leu Lys Leu Lys Glu Glu Asn Ser Leu  
 290 295 300

<210> 631

<211> 408

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(385)

<223> RXC02238

<400> 631

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 ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115  
 Val Thr Asn Val Ser  
 1 5  
 aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163  
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile  
 10 15 20  
 acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211  
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr  
 25 30 35  
 gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259  
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe  
 40 45 50  
 tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307  
 Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val  
 55 60 65  
 act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355  
 Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile  
 70 75 80 85  
 aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405  
 Asn Ala Gly Leu Leu Asp His Glu Glu Gly  
 90 95  
 cac 408

<210> 632

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 632

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp

897

105 110 115  
 atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata 499  
 Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile  
 120 125 130  
 cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga 547  
 Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly  
 135 140 145  
 atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc 593  
 Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro  
 150 155 160  
 tataaaccacaaa 606  
  
 <210> 634  
 <211> 161  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 634  
 Val Ser Lys Leu Lys Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly  
 1 5 10 15  
 Asp His Ser Phe Ala Asp Leu Ala Gly Arg Gln Val Ala His Val Asp  
 20 25 30  
 Val Val Asp Pro Leu Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr  
 35 40 45  
 Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn  
 50 55 60  
 Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly  
 65 70 75 80  
 Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp  
 85 90 95  
 Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile  
 100 105 110  
 Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu  
 115 120 125  
 Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg  
 130 135 140  
 Arg Ile Arg Arg Gly Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys  
 145 150 155 160  
 Pro

<210> 635  
 <211> 606  
 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(583)

&lt;223&gt; FRXA02903

&lt;400&gt; 635

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gcccatttgg aatcacaaca ccgcatatcg gccatggctg gtg tca aag ctc aaa 115  
 Val Ser Lys Leu Lys  
 1 5

ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc 163  
 Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala  
 10 15 20

gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt 211  
 Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu  
 25 30 35

att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc 259  
 Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala  
 40 45 50

atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307  
 Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu  
 55 60 65

aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta 355  
 Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val  
 70 75 80 85

ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta 403  
 Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu  
 90 95 100

caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa 451  
 Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln  
 105 110 115

atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata 499  
 Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile  
 120 125 130

cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga 547  
 Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly  
 135 140 145

atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc 593  
 Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro  
 150 155 160

tataaaccaa aaa 606

&lt;210&gt; 636

&lt;211&gt; 161

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 636

Val Ser Lys Leu Lys Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly  
 1 5 10 15

Asp His Ser Phe Ala Asp Leu Ala Gly Arg Gln Val Ala His Val Asp  
 20 25 30

Val Val Asp Pro Leu Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr  
 35 40 45

Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn  
 50 55 60

Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly  
 65 70 75 80

Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp  
 85 90 95

Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile  
 100 105 110

Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu  
 115 120 125

Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg  
 130 135 140

Arg Ile Arg Arg Gly Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys  
 145 150 155 160

Pro

&lt;210&gt; 637

&lt;211&gt; 783

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(760)

&lt;223&gt; RXA00166

&lt;400&gt; 637

ggcgttttagc gatcttcaac atcgagcaac cagcgccagc gctttttaccc aaggcagcac 60

gacttatcac gatgtccgac ctggatatcc ggctgaggcc gtg gag tta gcc cgt 115  
 Val Glu Leu Ala Arg  
 1 5

ggg ttt ggc cga gtc ctg gat gtc ggt gca ggt acc gga aaa cta acc 163  
 Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly Thr Gly Lys Leu Thr  
 10 15 20

agt gag cta aca gct gat cag gtc cta gcc ctt gat cca agc atg gac 211  
 Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu Asp Pro Ser Met Asp  
 25 30 35

atg ttg cgg gtg ttt cgc tcc gcg ctt ccg gcg gtt ccc tgc tgg caa 259

Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala Val Pro Cys Trp Gln  
 40 45 50  
 gcg aca gca gaa cac aca gga ata cgt gac aac gcg gtt gat ctg att 307  
 Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn Ala Val Asp Leu Ile  
 55 60 65  
 acg tgc gca caa acg tgg cat tgg gtt gac gtg acg gct gcc tca gcg 355  
 Thr Cys Ala Gln Thr Trp His Trp Val Asp Val Thr Ala Ala Ser Ala  
 70 75 80 85  
 gaa ttt gat cgg gtg att gca cct gag ggt gca gtc ctg ctc gtg tgg 403  
 Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala Val Leu Leu Val Trp  
 90 95 100  
 aat aac ctg gac acc tcc atc gcg tgg gta cac cga ctc agt cgc att 451  
 Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His Arg Leu Ser Arg Ile  
 105 110 115  
 atg cat gcc ggc gat gta ctc aag ccg gga ttc acc cca gaa acc gca 499  
 Met His Ala Gly Asp Val Leu Lys Pro Gly Phe Thr Pro Glu Thr Ala  
 120 125 130  
 gct ccc tgg ata att gat cga gaa att cgc acc acg tgg aat cag cac 547  
 Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr Thr Trp Asn Gln His  
 135 140 145  
 ctc acc cct gaa gaa atc atc cag ctc gct cac acg agg tcc tac tgg 595  
 Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His Thr Arg Ser Tyr Trp  
 150 155 160 165  
 tta aac gcg tca gag aaa atc aaa gag cgt gtt gat cag aac ctt cag 643  
 Leu Asn Ala Ser Glu Lys Ile Lys Glu Arg Val Asp Gln Asn Leu Gln  
 170 175 180  
 tgg tat ctc tac gag cat ttg ggt ttc agt ccc gac aat cca gtg gaa 691  
 Trp Tyr Leu Tyr Glu His Leu Gly Phe Ser Pro Asp Asn Pro Val Glu  
 185 190 195  
 ctt ccc tat cgc tgt gat gca ttt tta ctt tca cgt tcc ggt acc ctg 739  
 Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser Arg Ser Gly Thr Leu  
 200 205 210  
 gca ggc aga tct tcc aat ctt taggagccct cgccatgtac ctg 783  
 Ala Gly Arg Ser Ser Asn Leu  
 215 220

&lt;210&gt; 638

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 638

Val Glu Leu Ala Arg Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly  
 1 5 10 15

Thr Gly Lys Leu Thr Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu  
 20 25 30

Asp Pro Ser Met Asp Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala

35 40 45  
 Val Pro Cys Trp Gln Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn  
 50 55 60  
 Ala Val Asp Leu Ile Thr Cys Ala Gln Thr Trp His Trp Val Asp Val  
 65 70 75 80  
 Thr Ala Ala Ser Ala Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala  
 85 90 95  
 Val Leu Leu Val Trp Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His  
 100 105 110  
 Arg Leu Ser Arg Ile Met His Ala Gly Asp Val Leu Lys Pro Gly Phe  
 115 120 125  
 Thr Pro Glu Thr Ala Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr  
 130 135 140  
 Thr Trp Asn Gln His Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His  
 145 150 155 160  
 Thr Arg Ser Tyr Trp Leu Asn Ala Ser Glu Lys Ile Lys Glu Arg Val  
 165 170 175  
 Asp Gln Asn Leu Gln Trp Tyr Leu Tyr Glu His Leu Gly Phe Ser Pro  
 180 185 190  
 Asp Asn Pro Val Glu Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser  
 195 200 205  
 Arg Ser Gly Thr Leu Ala Gly Arg Ser Ser Asn Leu  
 210 215 220  
  
 <210> 639  
 <211> 1392  
 <212> DNA  
 <213> Corynebacterium glutamicum  
  
 <220>  
 <221> CDS  
 <222> (101)..(1369)  
 <223> RXA00633  
  
 <400> 639  
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 tacactgcag atatacatcc aaaccaagtg acggaggaaa atg gaa aac ccc agc 115  
 Met Glu Asn Pro Ser  
 1 5  
 ttg cgc gag ctt gat cac cga aac atc tgg cac ccg tat gcc gcg ccg 163  
 Leu Arg Glu Leu Asp His Arg Asn Ile Trp His Pro Tyr Ala Ala Pro  
 10 15 20  
 ggc gtg cgc aat aga ctc gtc acc aaa acc gat gga gtg ttt ttg acg 211  
 Gly Val Arg Asn Arg Leu Val Thr Lys Thr Asp Gly Val Phe Leu Thr  
 25 30 35



ctg gaa gat ggc agc acc gtg att gac gcg atg agc tcc tgg tgg tcg 259  
 Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met Ser Ser Trp Trp Ser  
           40                          45                          50

gca att cat gga cac gga cac ccc cga ctg aaa gct gcc gcc caa aaa 307  
 Ala Ile His Gly His Gly His Pro Arg Leu Lys Ala Ala Ala Gln Lys  
           55                          60                          65

caa atc gac acc atg agt cac gtc atg ttt ggc gga cta acc cac gag 355  
 Gln Ile Asp Thr Met Ser His Val Met Phe Gly Gly Leu Thr His Glu  
           70                          75                          80                          85

ccc gcc att aag ctc acc cac aaa ctc ctc aat ctc act gga aat tcc 403  
 Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn Leu Thr Gly Asn Ser  
                           90                          95                          100

ttt gac cac gtc ttt tat tcc gat tcg ggc tcg gtc tca gtg gag gtc 451  
 Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser Val Ser Val Glu Val  
                           105                          110                          115

gcc atc aaa atg gca ctg cag gcc tcc aaa gga caa ggc cac ccg gaa 499  
 Ala Ile Lys Met Ala Leu Gln Ala Ser Lys Gly Gln Gly His Pro Glu  
                           120                          125                          130

cgg aca aaa ctc ctc acc tgg cgg tcc ggc tac cac gga gac aca ttc 547  
 Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr His Gly Asp Thr Phe  
           135                          140                          145

acc gcg atg agc gtg tgc gac cca gaa aat ggc atg cat agc ctc tgg 595  
 Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly Met His Ser Leu Trp  
           150                          155                          160                          165

aaa ggc aca ctc ccc gag cag att ttc gcc ccc gcc cca cca gtt cgg 643  
 Lys Gly Thr Leu Pro Glu Gln Ile Phe Ala Pro Ala Pro Pro Val Arg  
                           170                          175                          180

ggg tca tcg ccg cag gcg att tcc gag tac ctg cgc agc atg gaa ttg 691  
 Gly Ser Ser Pro Gln Ala Ile Ser Glu Tyr Leu Arg Ser Met Glu Leu  
                           185                          190                          195

ctt atc gac gag gcg gtc tcc gca atc atc atc gaa ccg atc gtc caa 739  
 Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile Glu Pro Ile Val Gln  
           200                          205                          210

ggc gct gga ggc atg cgc ttt cac gat gtc gca ctc att gaa gga gtc 787  
 Gly Ala Gly Gly Met Arg Phe His Asp Val Ala Leu Ile Glu Gly Val  
           215                          220                          225

gcc aca ctg tgc aag aag cac gat cgt ttc ttg atc gtc gat gaa att 835  
 Ala Thr Leu Cys Lys Lys His Asp Arg Phe Leu Ile Val Asp Glu Ile  
           230                          235                          240                          245

gcc act ggt ttc ggc cgc acc ggt gaa cta ttt gcc acg tta agc aat 883  
 Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe Ala Thr Leu Ser Asn  
                           250                          255                          260

ggc cta caa cca gac atc atg tgt gtg ggc aag gcc ctc acc ggt gga 931  
 Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys Ala Leu Thr Gly Gly  
                           265                          270                          275

ttc atg tcc ttc gcc gct act tta tgc acg gac aag gtg gct caa tta 979

Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp Lys Val Ala Gln Leu  
 280 285 290  
 atc agc acc cca aat ggc gga ggt gcg ctg atg cac ggc ccc act ttt  
 1027  
 Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met His Gly Pro Thr Phe  
 295 300 305  
 atg gct aat cct ctg gcc tgt gcg gtt tcg cat gct tca tta gaa atc  
 1075  
 Met Ala Asn Pro Leu Ala Cys Ala Val Ser His Ala Ser Leu Glu Ile  
 310 315 320 325  
 att gag acc ggc atg tgg cag aaa cag gta aaa aga atc gaa gcc gaa  
 1123  
 Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys Arg Ile Glu Ala Glu  
 330 335 340  
 ctt atc gca ggc ctt tcc cca ctt caa cac ctt cca ggg gtt gcc gat  
 1171  
 Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu Pro Gly Val Ala Asp  
 345 350 355  
 gtc cgg gtt ctc ggc gcg att ggt gtc atc gaa atg gaa caa aat gtc  
 1219  
 Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu Met Glu Gln Asn Val  
 360 365 370  
 aat gtc gaa gaa gct act cag gct gca tta gat cac ggt gtg tgg atc  
 1267  
 Asn Val Glu Glu Ala Thr Gln Ala Ala Leu Asp His Gly Val Trp Ile  
 375 380 385  
 cgc ccc ttt gga cgc ttg ctc tat gtc atg cct cca tat atc acc acg  
 1315  
 Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro Pro Tyr Ile Thr Thr  
 390 395 400 405  
 tca gag cag tgc gca cag atc tgc act gcg ctt cat gct gca gtt aaa  
 1363  
 Ser Glu Gln Cys Ala Gln Ile Cys Thr Ala Leu His Ala Ala Val Lys  
 410 415 420  
 ggg aaa taaaccatgc cattttttatt tgt  
 1392  
 Gly Lys

&lt;210&gt; 640

&lt;211&gt; 423

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 640

Met Glu Asn Pro Ser Leu Arg Glu Leu Asp His Arg Asn Ile Trp His  
 1 5 10 15

Pro Tyr Ala Ala Pro Gly Val Arg Asn Arg Leu Val Thr Lys Thr Asp  
 20 25 30

Gly Val Phe Leu Thr Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met  
 35 40 45  
 Ser Ser Trp Trp Ser Ala Ile His Gly His Gly His Pro Arg Leu Lys  
 50 55 60  
 Ala Ala Ala Gln Lys Gln Ile Asp Thr Met Ser His Val Met Phe Gly  
 65 70 75 80  
 Gly Leu Thr His Glu Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn  
 85 90 95  
 Leu Thr Gly Asn Ser Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser  
 100 105 110  
 Val Ser Val Glu Val Ala Ile Lys Met Ala Leu Gln Ala Ser Lys Gly  
 115 120 125  
 Gln Gly His Pro Glu Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr  
 130 135 140  
 His Gly Asp Thr Phe Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly  
 145 150 155 160  
 Met His Ser Leu Trp Lys Gly Thr Leu Pro Glu Gln Ile Phe Ala Pro  
 165 170 175  
 Ala Pro Pro Val Arg Gly Ser Ser Pro Gln Ala Ile Ser Glu Tyr Leu  
 180 185 190  
 Arg Ser Met Glu Leu Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile  
 195 200 205  
 Glu Pro Ile Val Gln Gly Ala Gly Gly Met Arg Phe His Asp Val Ala  
 210 215 220  
 Leu Ile Glu Gly Val Ala Thr Leu Cys Lys Lys His Asp Arg Phe Leu  
 225 230 235 240  
 Ile Val Asp Glu Ile Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe  
 245 250 255  
 Ala Thr Leu Ser Asn Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys  
 260 265 270  
 Ala Leu Thr Gly Gly Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp  
 275 280 285  
 Lys Val Ala Gln Leu Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met  
 290 295 300  
 His Gly Pro Thr Phe Met Ala Asn Pro Leu Ala Cys Ala Val Ser His  
 305 310 315 320  
 Ala Ser Leu Glu Ile Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys  
 325 330 335  
 Arg Ile Glu Ala Glu Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu  
 340 345 350  
 Pro Gly Val Ala Asp Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu

906

Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala Leu Asn Ala Pro Leu  
 120 125 130  
 gtg att gtg aca agc acc gga ttg gga agc ctc aac gct gct gaa tta 547  
 Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu Asn Ala Ala Glu Leu  
 135 140 145  
 agc gtt gag gca gca aac cgc cga gga ctc aca gtg ttg gga gtc ctc 595  
 Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr Val Leu Gly Val Leu  
 150 155 160 165  
 ggc ggt tcg atc cct caa aat cct gat cta gct acg atg ctt aat ctc 643  
 Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala Thr Met Leu Asn Leu  
 170 175 180  
 gaa gaa ttt gag aga gtc acc ggc gtg ccc ttt tgg gga gct ttg ccg 691  
 Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe Trp Gly Ala Leu Pro  
 185 190 195  
 gaa ggg ttg tca cgg gtg gag ggg ttc gtc gaa aag caa tct ttt ccg 739  
 Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu Lys Gln Ser Phe Pro  
 200 205 210  
 gcc ctt gat gcc ttt aag aaa ccg ccg gca agg tgatcgtgaa caccgtgcct 792  
 Ala Leu Asp Ala Phe Lys Lys Pro Pro Ala Arg  
 215 220  
 tcg 795  
 <210> 642  
 <211> 224  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 642  
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 Phe Ser Thr Ala Val Leu Val Arg Tyr Leu Ala Asp Gln Gly His Asp  
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 Val Leu Pro Val Lys Leu Val Gln Thr Gly Glu Leu Pro Gly Glu Gly  
 35 40 45  
 Asp Ile Phe Asn Ile Glu Arg Leu Thr Gly Ile Ala Gly Glu Glu Phe  
 50 55 60  
 Ala Arg Phe Lys Asp Pro Leu Ala Pro Asn Leu Ala Ala Arg Arg Glu  
 65 70 75 80  
 Gly Val Glu Pro Ile Gln Phe Asp Gln Ile Ile Ser Trp Leu Arg Gly  
 85 90 95  
 Phe Asp Asp Pro Asp Arg Ile Ile Val Val Glu Gly Ala Gly Gly Leu  
 100 105 110  
 Leu Val Arg Leu Gly Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala  
 115 120 125  
 Leu Asn Ala Pro Leu Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu



aaa cag acc gca aaa act ggc gct acc gaa ttc tgt atc gtc gcc gca 451  
 Lys Gln Thr Ala Lys Thr Gly Ala Thr Glu Phe Cys Ile Val Ala Ala  
 105 110 115

gtc aag ggg cct gat gag agg ctc atg acc cag ctg gag gaa gca gtc 499  
 Val Lys Gly Pro Asp Glu Arg Leu Met Thr Gln Leu Glu Glu Ala Val  
 120 125 130

ctc gcg att cac tct gaa gtt gaa att gaa gtc gca gca tcg atc gga 547  
 Leu Ala Ile His Ser Glu Val Glu Ile Glu Val Ala Ala Ser Ile Gly  
 135 140 145

acg tta aat aag gaa cag gtg gat cgc ctc gct gct gcc ggc gtg cac 595  
 Thr Leu Asn Lys Glu Gln Val Asp Arg Leu Ala Ala Ala Gly Val His  
 150 155 160 165

cgc tac aac cat aat ttg gaa act gcg cgt tcc tat ttc cct gaa gtt 643  
 Arg Tyr Asn His Asn Leu Glu Thr Ala Arg Ser Tyr Phe Pro Glu Val  
 170 175 180

gtc acc act cat aca tgg gaa gag cgc cgc gaa act ttg cgc ctg gtg 691  
 Val Thr Thr His Thr Trp Glu Glu Arg Arg Glu Thr Leu Arg Leu Val  
 185 190 195

gca gaa gct gga atg gaa gtc tgt tcc ggc gga atc tta gga atg ggc 739  
 Ala Glu Ala Gly Met Glu Val Cys Ser Gly Gly Ile Leu Gly Met Gly  
 200 205 210

gaa act tta gag cag cgc gcc gag ttt gcc gtg cag ctg gcg gag ctt 787  
 Glu Thr Leu Glu Gln Arg Ala Glu Phe Ala Val Gln Leu Ala Glu Leu  
 215 220 225

gat ccg cac gaa gtc ccc atg aac ttc ctt gat cct cgc ccg ggc acc 835  
 Asp Pro His Glu Val Pro Met Asn Phe Leu Asp Pro Arg Pro Gly Thr  
 230 235 240 245

cca ttt gcc gat agg gaa ttg atg gac agc cgt gac gct ctg cgc tct 883  
 Pro Phe Ala Asp Arg Glu Leu Met Asp Ser Arg Asp Ala Leu Arg Ser  
 250 255 260

att ggt gcg ttc cgc ctt gcg atg cct cac acc atg ctt cgt ttt gct 931  
 Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr Met Leu Arg Phe Ala  
 265 270 275

ggc ggt cgc gag ctg act ttg ggc gac aag ggt tcc gag caa gcc ctc 979  
 Gly Gly Arg Glu Leu Thr Leu Gly Asp Lys Gly Ser Glu Gln Ala Leu  
 280 285 290

ctg gga ggc atc aat gcg atg atc gtc gga aac tac ctg act acg ctc  
 1027  
 Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn Tyr Leu Thr Thr Leu  
 295 300 305

ggc cgc cca atg gaa gat gac ctc gac atg atg gat cgt ctc cag ctg  
 1075  
 Gly Arg Pro Met Glu Asp Asp Leu Asp Met Met Asp Arg Leu Gln Leu  
 310 315 320 325

ccc atc aaa gtc ctt aat aag gtc atc taagaagcac gcgcatgaac  
 1122

Pro Ile Lys Val Leu Asn Lys Val Ile  
330

gac  
1125

<210> 644  
<211> 334  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 644  
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Glu Gln Gly Ile Gly Leu Asn Gln Gln Gln Leu Met Glu Val Leu Thr  
20 25 30  
Leu Pro Glu Glu Gln Ile Pro Asp Leu Met Glu Leu Ala His Gln Val  
35 40 45  
Arg Leu Lys Trp Cys Gly Glu Glu Ile Glu Val Glu Gly Ile Ile Ser  
50 55 60  
Leu Lys Thr Gly Gly Cys Pro Glu Asp Cys His Phe Cys Ser Gln Ser  
65 70 75 80  
Gly Leu Phe Glu Ser Pro Val Arg Ser Val Trp Leu Asp Ile Pro Asn  
85 90 95  
Leu Val Glu Ala Ala Lys Gln Thr Ala Lys Thr Gly Ala Thr Glu Phe  
100 105 110  
Cys Ile Val Ala Ala Val Lys Gly Pro Asp Glu Arg Leu Met Thr Gln  
115 120 125  
Leu Glu Glu Ala Val Leu Ala Ile His Ser Glu Val Glu Ile Glu Val  
130 135 140  
Ala Ala Ser Ile Gly Thr Leu Asn Lys Glu Gln Val Asp Arg Leu Ala  
145 150 155 160  
Ala Ala Gly Val His Arg Tyr Asn His Asn Leu Glu Thr Ala Arg Ser  
165 170 175  
Tyr Phe Pro Glu Val Val Thr Thr His Thr Trp Glu Glu Arg Arg Glu  
180 185 190  
Thr Leu Arg Leu Val Ala Glu Ala Gly Met Glu Val Cys Ser Gly Gly  
195 200 205  
Ile Leu Gly Met Gly Glu Thr Leu Glu Gln Arg Ala Glu Phe Ala Val  
210 215 220  
Gln Leu Ala Glu Leu Asp Pro His Glu Val Pro Met Asn Phe Leu Asp  
225 230 235 240  
Pro Arg Pro Gly Thr Pro Phe Ala Asp Arg Glu Leu Met Asp Ser Arg  
245 250 255



Asp Ala Leu Arg Ser Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr  
 260 265 270

Met Leu Arg Phe Ala Gly Gly Arg Glu Leu Thr Leu Gly Asp Lys Gly  
 275 280 285

Ser Glu Gln Ala Leu Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn  
 290 295 300

Tyr Leu Thr Thr Leu Gly Arg Pro Met Glu Asp Asp Leu Asp Met Met  
 305 310 315 320

Asp Arg Leu Gln Leu Pro Ile Lys Val Leu Asn Lys Val Ile  
 325 330

<210> 645

<211> 1212

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1189)

<223> RXA00223

<400> 645

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tttgaacact ttttatctgg accatgcagc caccacacca atg cgt gag gtg gcc 115  
 Met Arg Glu Val Ala  
 1 5

gca gct gcg tgg atg gaa aac gcg cag gca ttg aat ccc gcg agt cag 163  
 Ala Ala Ala Trp Met Glu Asn Ala Gln Ala Leu Asn Pro Ala Ser Gln  
 10 15 20

tac ggt tcg ggg cgt aag gcg cgc agc gtt gcg gat tcg gct cgt gaa 211  
 Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala Asp Ser Ala Arg Glu  
 25 30 35

gaa att gct tct ttg ctg ggc tgt gaa cct atc gag gtt gtg ttt acc 259  
 Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile Glu Val Val Phe Thr  
 40 45 50

gcg tcc ggc acg gag gca gat aac ctc gct gtg cag ggg tta ttc cac 307  
 Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val Gln Gly Leu Phe His  
 55 60 65

gca tcg cct ctc aat cgg att att tct acg ccg atc gag cac ccc ggg 355  
 Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro Ile Glu His Pro Gly  
 70 75 80 85

att ctg gaa acc gtc aag gct cta gaa ctt ggc ggg gca gag gcg gag 403  
 Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly Gly Ala Glu Ala Glu  
 90 95 100

ctc atg ccg atc ggt cca gat gga cga gtg tct tcc ttc gaa gcg ctg 451  
 Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser Ser Phe Glu Ala Leu  
 105 110 115

gac aag cct gcc gcg gtt gcc act atg atg tgg gcg aac aat gag acc 499  
 Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp Ala Asn Asn Glu Thr  
 120 125 130

ggc gcg att cag ccg gtt tct gag ttc atc gcc gcc gcg cag gcg tcc 547  
 Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala Ala Ala Gln Ala Ser  
 135 140 145

ggc acg cca aca cac atc gat gcg gtt cag gtc gtt ggc cat ctg ccg 595  
 Gly Thr Pro Thr His Ile Asp Ala Val Gln Val Val Gly His Leu Pro  
 150 155 160 165

gtc aat ttt gat gag ctc ggc gcc acc act ttg gct gcc tcc gcg cac 643  
 Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu Ala Ala Ser Ala His  
 170 175 180

aaa ttc ggt gga cca cgt ggc gtc ggc ctg ctg ttg gtg agg cgc tca 691  
 Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu Leu Val Arg Arg Ser  
 185 190 195

cca gca cct tca gcc gta ttg cac gga ggt ggt cag gag cgc ggc atc 739  
 Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly Gln Glu Arg Gly Ile  
 200 205 210

cgt cca ggc acc ctt gat gtc gcc ggc gca gct gcc acc gca gcc gca 787  
 Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala Ala Thr Ala Ala Ala  
 215 220 225

tta cgc gaa gca gtg gcc gag ctt gac ggc gaa gcc acc cgc ctg cgc 835  
 Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu Ala Thr Arg Leu Arg  
 230 235 240 245

gga ctt aaa aag atg ctt ctc gac gcc atc ctc cac acc atc ccc aac 883  
 Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu His Thr Ile Pro Asn  
 250 255 260

gta ctg gtc cac acc acc gaa cca tcc ctg cca gga cac ctg cat ctc 931  
 Val Leu Val His Thr Thr Glu Pro Ser Leu Pro Gly His Leu His Leu  
 265 270 275

tcc ttc cca gga gca gaa ggc gat agt ttg atc atg ctg ctc gac tcc 979  
 Ser Phe Pro Gly Ala Glu Gly Asp Ser Leu Ile Met Leu Leu Asp Ser  
 280 285 290

ttg cgg atc gaa gcc tcc aca ggt tcg gcc tgc tcc aac ggt gta aac  
 1027  
 Leu Arg Ile Glu Ala Ser Thr Gly Ser Ala Cys Ser Asn Gly Val Asn  
 295 300 305

cgt gcc agc cac gtc ctt ttg gcc atg gga att tcc gaa acc gac gcc  
 1075  
 Arg Ala Ser His Val Leu Leu Ala Met Gly Ile Ser Glu Thr Asp Ala  
 310 315 320 325

cgt ggt gcc atc cga ttc acc ctc gga aga acc acc act gaa gaa tcc  
 1123  
 Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr Thr Thr Glu Glu Ser  
 330 335 340

atc aag gca gtg atc gcc gtg atc gaa gac gta gtg acc agg gct cgt  
 1171

Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val Val Thr Arg Ala Arg  
 345 350 355

act gcg gga atg gct ttt tagcgaccgt aaatcgcata gtg  
 1212

Thr Ala Gly Met Ala Phe  
 360

<210> 646

<211> 363

<212> PRT

<213> Corynebacterium glutamicum

<400> 646

Met Arg Glu Val Ala Ala Ala Ala Trp Met Glu Asn Ala Gln Ala Leu  
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Asn Pro Ala Ser Gln Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala  
 20 25 30

Asp Ser Ala Arg Glu Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile  
 35 40 45

Glu Val Val Phe Thr Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val  
 50 55 60

Gln Gly Leu Phe His Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro  
 65 70 75 80

Ile Glu His Pro Gly Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly  
 85 90 95

Gly Ala Glu Ala Glu Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser  
 100 105 110

Ser Phe Glu Ala Leu Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp  
 115 120 125

Ala Asn Asn Glu Thr Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala  
 130 135 140

Ala Ala Gln Ala Ser Gly Thr Pro Thr His Ile Asp Ala Val Gln Val  
 145 150 155 160

Val Gly His Leu Pro Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu  
 165 170 175

Ala Ala Ser Ala His Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu  
 180 185 190

Leu Val Arg Arg Ser Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly  
 195 200 205

Gln Glu Arg Gly Ile Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala  
 210 215 220

Ala Thr Ala Ala Ala Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu  
 225 230 235 240

Ala Thr Arg Leu Arg Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu



cgt ggc cgg cac ctc atc acc acc ccg atc gag cat gac agt gtc cta 403  
 Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu His Asp Ser Val Leu  
 90 95 100

gaa act gct gct tat ctt gaa agg ttt cat gat ttc gag atc acc tac 451  
 Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr  
 105 110 115

cta tcc ccc gat cac act ggg ctg atc tcc ccg gag ggt ctc cgc aaa 499  
 Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys  
 120 125 130

gca gtc agg ccg gac acc aca ttg atc agc att ggt tat gcc aac aat 547  
 Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn  
 135 140 145

gag gtg gga acc att cag ccg ata gct gag ttg gcg gcg gta agc agt 595  
 Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser  
 150 155 160 165

acg cct ttt cac acc gat gca gtg caa gct gca cat tta acc ttt gac 643  
 Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp  
 170 175 180

ttg gga gtt gac gcg tta agt ttg tcg ggt cat aaa ttc ggt gcg cct 691  
 Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro  
 185 190 195

aaa ggg att gga gtg tta tgg tca aag ctt ccc ctg gag ccg gta atc 739  
 Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile  
 200 205 210

cat ggc ggc ggc cag gaa aaa ggg ccg cgt agt ggc acg gaa aac gtt 787  
 His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val  
 215 220 225

gcg ggg gct atc gcc ttt gcc act gcc ttg gaa ttg gcc agg gcg gaa 835  
 Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu  
 230 235 240 245

tcc tat cca gat ctt ggc gaa ttc atc gag gaa gtt ctc act atc ccg 883  
 Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro  
 250 255 260

gga gca cac ctg act gga cat cct agg atg cgc att gat gga cac gca 931  
 Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala  
 265 270 275

tct ttt ctc ttc gac agc ata gga tct gaa act gtt ctt ctg gaa ttg 979  
 Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu  
 280 285 290

gaa cgc caa ggc att gtg tgc tcc cct ggt tct gcc tgt ggt tcc gga 1027  
 Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly  
 295 300 305

gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt gag gag gat caa gca 1075  
 Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala  
 310 315 320 325

cga acg gct gtg cgc tgt act ttt agt aca aca cac agc cgt gaa gat  
1123

Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp  
330 335 340

gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg gtc gcc tta atc aga  
1171

Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg  
345 350 355

ggg tgacgctagt cagaggttta cgg

1197

Gly

<210> 648

<211> 358

<212> PRT

<213> Corynebacterium glutamicum

<400> 648

Met Leu Tyr Leu Asp Asn Ala Ala Thr Thr Ser Val Arg Asn Glu Ala  
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Leu Glu Ala Met Trp Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser  
20 25 30

Ser Pro His Glu Val Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala  
35 40 45

Arg Thr Arg Val Ala Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr  
50 55 60

Phe Thr Ser Gly Gly Ser Glu Ala Asn Asn Leu Ala Ile Lys Gly Ala  
65 70 75 80

Cys Leu Ala Asn Pro Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu  
85 90 95

His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp  
100 105 110

Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro  
115 120 125

Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile  
130 135 140

Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu  
145 150 155 160

Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala  
165 170 175

His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His  
180 185 190

Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro  
195 200 205

Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser  
 210 215 220  
 Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu  
 225 230 235 240  
 Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu  
 245 250 255  
 Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg  
 260 265 270  
 Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr  
 275 280 285  
 Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser  
 290 295 300  
 Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu  
 305 310 315 320  
 Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr  
 325 330 335  
 His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala  
 340 345 350  
 Val Ala Leu Ile Arg Gly  
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<210> 649  
 <211> 920  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (79) .. (897)  
 <223> FRXA00262

<400> 649  
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 Val Ala Gly His Leu Ile Thr Thr Pro Ile Glu  
 1 5 10  
 cat gac agt gtc cta gaa act gct gct tat ctt gaa agg ttt cat gat 159  
 His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp  
 15 20 25  
 ttc gag atc acc tac cta tcc ccc gat cac act ggg ctg atc tcc ccg 207  
 Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro  
 30 35 40  
 gag ggt ctc cgc aaa gca gtc agg ccg gac acc aca ttg atc agc att 255  
 Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile  
 45 50 55

ggt tat gcc aac aat gag gtg gga acc att cag ccg ata gct gag ttg 303  
 Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu  
 60 65 70 75

gcg gcg gta agc agt acg cct ttt cac acc gat gca gtg caa gct gca 351  
 Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala  
 80 85 90

cat tta acc ttt gac ttg gga gtt gac gcg tta agt ttg tcg ggt cat 399  
 His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His  
 95 100 105

aaa ttc ggt gcg cct aaa ggg att gga gtg tta tgg tca aag ctt ccc 447  
 Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro  
 110 115 120

ctg gag ccg gta atc cat ggc ggc ggc cag gaa aaa ggg cgg cgt agt 495  
 Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser  
 125 130 135

ggc acg gaa aac gtt gcg ggg gct atc gcc ttt gcc act gcc ttg gaa 543  
 Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu  
 140 145 150 155

ttg gcc agg gcg gaa tcc tat cca gat ctt ggc gaa ttc atc gag gaa 591  
 Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu  
 160 165 170

gtt ctc act atc ccg gga gca cac ctg act gga cat cct agg atg cgc 639  
 Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg  
 175 180 185

att gat gga cac gca tct ttt ctc ttc gac agc ata gga tct gaa act 687  
 Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr  
 190 195 200

gtt ctt ctg gaa ttg gaa cgc caa ggc att gtg tgc tcc cct ggt tct 735  
 Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser  
 205 210 215

gcc tgt ggt tcc gga gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt 783  
 Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu  
 220 225 230 235

gag gag gat caa gca cga acg gct gtg cgc tgt act ttt agt aca aca 831  
 Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr  
 240 245 250

cac agc cgt gaa gat gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg 879  
 His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala  
 255 260 265

gtc gcc tta atc aga ggg tgacgctagt cagaggttta cgg 920  
 Val Ala Leu Ile Arg Gly  
 270

&lt;210&gt; 650

&lt;211&gt; 273

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



<400> 650  
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 Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr  
 20 25 30  
 Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys  
 35 40 45  
 Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn  
 50 55 60  
 Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser  
 65 70 75 80  
 Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp  
 85 90 95  
 Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro  
 100 105 110  
 Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile  
 115 120 125  
 His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val  
 130 135 140  
 Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu  
 145 150 155 160  
 Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro  
 165 170 175  
 Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala  
 180 185 190  
 Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu  
 195 200 205  
 Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly  
 210 215 220  
 Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala  
 225 230 235 240  
 Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp  
 245 250 255  
 Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg  
 260 265 270

Gly

<210> 651  
 <211> 1296  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1273)

&lt;223&gt; RXN00435

&lt;400&gt; 651

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gtggaaggaa atgctgtggc ggttgaaagg agtgcctttc gtg ggt ttt gat gtg 115  
Val Gly Phe Asp Val  
1 5

gcc agg gtt cgg ggg ctt tat acc tct ttg ggc gat ggc tgg acg tac 163  
Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr  
10 15 20

ctt aat tca cat caa att ccg cag gtt ccg gag cgg gtg gcg tcg gga 211  
Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu Arg Val Ala Ser Gly  
25 30 35

gtt gcg gcg gct ttc cgc acg cat gcg cag att tct gag gtg acg tcg 259  
Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile Ser Glu Val Thr Ser  
40 45 50

cag ccg att gcg gtg gat cag ttg gag gct gct cgc gag gca gtt gcg 307  
Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala Arg Glu Ala Val Ala  
55 60 65

tcg ttg gcg ggt gtg gat ccg gac tgt gtt gtg ctg ggt ccc acg agg 355  
Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val Leu Gly Pro Thr Arg  
70 75 80 85

cag ttt ttg gct cat aca ttg gcg cgc ggt ttg ggt ggg ttt gta cgt 403  
Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu Gly Gly Phe Val Arg  
90 95 100

cga aaa gcg ggc gtg gtg ttg tcg cgc gcg gac gcg gac tgg ctg acc 451  
Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Ala Asp Trp Leu Thr  
105 110 115

gcg ccg ttc cgc tcc ctc gac ggc gtt ttt agc tgg gcc gag ccc gat 499  
Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Glu Pro Asp  
120 125 130

ttg ggc acc ggc atg ctg ccg gat tgg cag tac gag aag ctt gtt gac 547  
Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Glu Lys Leu Val Asp  
135 140 145

ggc tcg acg cgc ctt gtc gtg ctc agc gcc gcg cac ccg ctg ctc ggc 595  
Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala His Pro Leu Leu Gly  
150 155 160 165

acg gtc gcc cca gtg ggc aag att gtg gat aaa gtg cgg gcg cgt tcg 643  
Thr Val Ala Pro Val Gly Lys Ile Val Asp Lys Val Arg Ala Arg Ser  
170 175 180

cgt gcc tgg gtg ctt gtc gac gcc acc acc tac gca gcc tac cgc ccc 691  
Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro  
185 190 195

ctg cgc cta gac gag tgg gaa gcc gat atc gtc atg ctt gat ctc ggc 739  
 Leu Arg Leu Asp Glu Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly  
 200 205 210

gag ttg ggc ggc ccg cag att tcg gcg ttg att ttc cgt gat acc tcg 787  
 Glu Leu Gly Gly Pro Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser  
 215 220 225

atg ttc ccg cgc ctg gat cgc acc gtt cca ctc gaa ctg ccc gca agc 835  
 Met Phe Pro Arg Leu Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser  
 230 235 240 245

tcc ctg ccg cat ggg ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac 883  
 Ser Leu Pro His Gly Leu Leu Gly Gly Val Pro Asn Leu Val Arg His  
 250 255 260

ctg gga aac ctg gat gaa aac gcc ccg tcc gtc gtt gag gcg atg ggc 931  
 Leu Gly Asn Leu Asp Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly  
 265 270 275

gag atg gcg aaa ttc cac aag gga ctt ttt gag cat ctt gtg gaa tcg 979  
 Glu Met Ala Lys Phe His Lys Gly Leu Phe Glu His Leu Val Glu Ser  
 280 285 290

ctc gaa gga ctt cac gcg gtg cat atc gtg gga att tcc ggc gat gcc  
 1027  
 Leu Glu Gly Leu His Ala Val His Ile Val Gly Ile Ser Gly Asp Ala  
 295 300 305

gca ggt caa gac gcc ccg ttc ctg gat cga gtg ccc cgc ttg acc ttc  
 1075  
 Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe  
 310 315 320 325

acc atg gaa ggc gtg ccc gca gat atg gtg tac cgc cga ttg gtg gac  
 1123  
 Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp  
 330 335 340

aat cgt ttg atc act acc gtc agc cct gct gac ccg ctg ctc gaa gca  
 1171  
 Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala  
 345 350 355

atg ggt gtg act gaa gct ggc gga tcg atc act atc gga cta agc ccg  
 1219  
 Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro  
 360 365 370

ttt agc acc tac tat gaa gtg gat cag ctg acc agg gtg ctg gca tcg  
 1267  
 Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser  
 375 380 385

ctt gcc taaaccgcaa gcacgagctt gcc  
 1296  
 Leu Ala  
 390

&lt;210&gt; 652

&lt;211&gt; 391

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 652

Val Gly Phe Asp Val Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly  
 1 5 10 15  
 Asp Gly Trp Thr Tyr Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu  
 20 25 30  
 Arg Val Ala Ser Gly Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile  
 35 40 45  
 Ser Glu Val Thr Ser Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala  
 50 55 60  
 Arg Glu Ala Val Ala Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val  
 65 70 75 80  
 Leu Gly Pro Thr Arg Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu  
 85 90 95  
 Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp  
 100 105 110  
 Ala Asp Trp Leu Thr Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser  
 115 120 125  
 Trp Ala Glu Pro Asp Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr  
 130 135 140  
 Glu Lys Leu Val Asp Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala  
 145 150 155 160  
 His Pro Leu Leu Gly Thr Val Ala Pro Val Gly Lys Ile Val Asp Lys  
 165 170 175  
 Val Arg Ala Arg Ser Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr  
 180 185 190  
 Ala Ala Tyr Arg Pro Leu Arg Leu Asp Glu Trp Glu Ala Asp Ile Val  
 195 200 205  
 Met Leu Asp Leu Gly Glu Leu Gly Gly Pro Gln Ile Ser Ala Leu Ile  
 210 215 220  
 Phe Arg Asp Thr Ser Met Phe Pro Arg Leu Asp Arg Thr Val Pro Leu  
 225 230 235 240  
 Glu Leu Pro Ala Ser Ser Leu Pro His Gly Leu Leu Gly Gly Val Pro  
 245 250 255  
 Asn Leu Val Arg His Leu Gly Asn Leu Asp Glu Asn Ala Pro Ser Val  
 260 265 270  
 Val Glu Ala Met Gly Glu Met Ala Lys Phe His Lys Gly Leu Phe Glu  
 275 280 285  
 His Leu Val Glu Ser Leu Glu Gly Leu His Ala Val His Ile Val Gly  
 290 295 300

Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val  
305 310 315 320

Pro Arg Leu Thr Phe Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr  
325 330 335

Arg Arg Leu Val Asp Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp  
340 345 350

Pro Leu Leu Glu Ala Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr  
355 360 365

Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr  
370 375 380

Arg Val Leu Ala Ser Leu Ala  
385 390

<210> 653

<211> 638

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(615)

<223> FRXA00435

<400> 653

gtc gac gcc acc acc tac gca gcc tac cgc ccc ctg cgc cta gac gag 48  
Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro Leu Arg Leu Asp Glu  
1 5 10 15

tgg gaa gcc gat atc gtc atg ctt gat ctc ggc gag ttg ggc ggc ccg 96  
Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly Glu Leu Gly Gly Pro  
20 25 30

cag att tcg gcg ttg att ttc cgt gat acc tcg atg ttc ccg cgc ctg 144  
Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser Met Phe Pro Arg Leu  
35 40 45

gat cgc acc gtt cca ctc gaa ctg ccc gca agc tcc ctg ccg cat ggg 192  
Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser Ser Leu Pro His Gly  
50 55 60

ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac ctg gga aac ctg gat 240  
Leu Leu Gly Gly Val Pro Asn Leu Val Arg His Leu Gly Asn Leu Asp  
65 70 75 80

gaa aac gcc ccg tcc gtc gtt gag gcg atg ggg gag atg gcg aaa ttc 288  
Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly Glu Met Ala Lys Phe  
85 90 95

cac aag gga ctt ttt gag cat ctt gtg gaa tcg ctc gaa gga ctt cac 336  
His Lys Gly Leu Phe Glu His Leu Val Glu Ser Leu Glu Gly Leu His  
100 105 110

gcg gtg cat atc gtg gga att tcc ggc gat gcc gca ggt caa gac gcc 384  
Ala Val His Ile Val Gly Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala

115	120	125	
ccg ttc ctg gat cga gtg ccc cgc ttg acc ttc acc atg gaa ggc gtg			432
Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe Thr Met Glu Gly Val			
130	135	140	
ccc gca gat atg gtg tac cgc cga ttg gtg gac aat cgt ttg atc act			480
Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp Asn Arg Leu Ile Thr			
145	150	155	160
acc gtc agc cct gct gac ccg ctg ctc gaa gca atg ggt gtg act gaa			528
Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala Met Gly Val Thr Glu			
	165	170	175
gct ggc gga tcg atc act atc gga cta agc ccg ttt agc acc tac tat			576
Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr			
	180	185	190
gaa gtg gat cag ctg acc agg gtg ctg gca tcg ctt gcc taaaccgcaa			625
Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser Leu Ala			
	195	200	205
gcacgagctt gcc			638
<210> 654			
<211> 205			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 654			
Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro Leu Arg Leu Asp Glu			
1	5	10	15
Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly Glu Leu Gly Gly Pro			
	20	25	30
Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser Met Phe Pro Arg Leu			
	35	40	45
Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser Ser Leu Pro His Gly			
	50	55	60
Leu Leu Gly Gly Val Pro Asn Leu Val Arg His Leu Gly Asn Leu Asp			
	65	70	75
Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly Glu Met Ala Lys Phe			
	85	90	95
His Lys Gly Leu Phe Glu His Leu Val Glu Ser Leu Glu Gly Leu His			
	100	105	110
Ala Val His Ile Val Gly Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala			
	115	120	125
Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe Thr Met Glu Gly Val			
	130	135	140
Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp Asn Arg Leu Ile Thr			
	145	150	155
			160

Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala Met Gly Val Thr Glu  
 165 170 175

Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr  
 180 185 190

Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser Leu Ala  
 195 200 205

<210> 655

<211> 535

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA02801

<400> 655

cgacaggtga attcatgcac gtttgagtgt cccgtgtgtg gggtaatgtt gtccaagaga 60  
 gtggaaggaa atgctgtggc ggttgaaagg agtgcctttc gtg ggt ttt gat gtg 115  
 Val Gly Phe Asp Val  
 1 5

gcc agg gtt cgg ggg ctt tat acc tct ttg ggc gat ggc tgg acg tac 163  
 Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr  
 10 15 20

ctt aat tca cat caa att ccg cag gtt ccg gag cgg gtg gcg tcg gga 211  
 Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu Arg Val Ala Ser Gly  
 25 30 35

gtt gcg gcg gct ttc cgc acg cat gcg cag att tct gag gtg acg tcg 259  
 Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile Ser Glu Val Thr Ser  
 40 45 50

cag ccg att gcg gtg gat cag ttg gag gct gct cgc gag gca gtt gcg 307  
 Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala Arg Glu Ala Val Ala  
 55 60 65

tcg ttg gcg ggt gtg gat ccg gac tgt gtt gtg ctg ggt ccc acg agg 355  
 Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val Leu Gly Pro Thr Arg  
 70 75 80 85

cag ttt ttg gct cat aca ttg gcg cgc ggt ttg ggt ggg ttt gta cgt 403  
 Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu Gly Gly Phe Val Arg  
 90 95 100

cga aaa gcg ggc gtg gtg ttg tcg cgc gcg gac gcg gac tgg ctg acc 451  
 Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Ala Asp Trp Leu Thr  
 105 110 115

gcg ccg ttc cgc tcc ctc gac ggc gtt ttt agc tgg gcc gag ccc gat 499  
 Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Glu Pro Asp  
 120 125 130

ttg ggc acc ggc atg ctg ccg gat tgg cag tac cag 535  
 Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Gln

135

140

145

&lt;210&gt; 656

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 656

Val Gly Phe Asp Val Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly  
 1 5 10 15

Asp Gly Trp Thr Tyr Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu  
 20 25 30

Arg Val Ala Ser Gly Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile  
 35 40 45

Ser Glu Val Thr Ser Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala  
 50 55 60

Arg Glu Ala Val Ala Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val  
 65 70 75 80

Leu Gly Pro Thr Arg Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu  
 85 90 95

Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp  
 100 105 110

Ala Asp Trp Leu Thr Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser  
 115 120 125

Trp Ala Glu Pro Asp Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr  
 130 135 140

Gln  
 145

&lt;210&gt; 657

&lt;211&gt; 1386

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1363)

&lt;223&gt; RXA02516

&lt;400&gt; 657

ttcattcacg ttttcgcgaa tggccagatt gtgaccaccg gtggcgctga gcttgctgac 60

aagctcgagg ctgacggcta cgaccagttc atcaagtaac atg tcc gat ttc ctc 115  
 Met Ser Asp Phe Leu  
 1 5

aat gca gat gga tcc ctc aat gtg gat aag gtg cgg gaa gaa ttc cca 163  
 Asn Ala Asp Gly Ser Leu Asn Val Asp Lys Val Arg Glu Glu Phe Pro  
 10 15 20



atc ctg aag cgc act gtt agg gat ggg aaa ccg ctt gct tac ctg gac 211  
 Ile Leu Lys Arg Thr Val Arg Asp Gly Lys Pro Leu Ala Tyr Leu Asp  
                   25                                  30                                  35

tca ggt gcg aca tcg cag cga ccc gag cgg gtg tgg cgt gca gag gag 259  
 Ser Gly Ala Thr Ser Gln Arg Pro Glu Arg Val Trp Arg Ala Glu Glu  
                   40                                  45                                  50

cac ttt gtg ctg cac acc aac gcc ccc gtg cac cgc ggt gcc tac caa 307  
 His Phe Val Leu His Thr Asn Ala Pro Val His Arg Gly Ala Tyr Gln  
                   55                                  60                                  65

ctg gct gag gaa gca acg gat gct tat gaa ggt gcc cgc gag aag atc 355  
 Leu Ala Glu Glu Ala Thr Asp Ala Tyr Glu Gly Ala Arg Glu Lys Ile  
                   70                                  75                                  80                                  85

gct gcc ttt gtt ggt gcc gag cag cat gaa att gcg ttc act aag aat 403  
 Ala Ala Phe Val Gly Ala Glu Gln His Glu Ile Ala Phe Thr Lys Asn  
                                   90                                  95                                  100

gca act gaa gca ctc aat ctt gtt gcg tac acc ttg ggt gat gac cgt 451  
 Ala Thr Glu Ala Leu Asn Leu Val Ala Tyr Thr Leu Gly Asp Asp Arg  
                                   105                                  110                                  115

tcc ggt aag tat cgt gtc cag gcc ggg gat acc gtg gtc atc acg gag 499  
 Ser Gly Lys Tyr Arg Val Gln Ala Gly Asp Thr Val Val Ile Thr Glu  
                   120                                  125                                  130

cta gag cac cac gca aac ttg gtg cca tgg cag gag ctg tgc cgt cga 547  
 Leu Glu His His Ala Asn Leu Val Pro Trp Gln Glu Leu Cys Arg Arg  
                   135                                  140                                  145

acc ggt gcg aca ttg aag tgg tac aag gtg act gaa gat ggt cgc att 595  
 Thr Gly Ala Thr Leu Lys Trp Tyr Lys Val Thr Glu Asp Gly Arg Ile  
                   150                                  155                                  160                                  165

gat ctc gat tca ctc gag ctt gat gaa act gtc aag gtc gtt gcc ttc 643  
 Asp Leu Asp Ser Leu Glu Leu Asp Glu Thr Val Lys Val Val Ala Phe  
                                   170                                  175                                  180

act cac cag tcc aat gtg acc ggt gct gtg gct gat gtt cca gag ttg 691  
 Thr His Gln Ser Asn Val Thr Gly Ala Val Ala Asp Val Pro Glu Leu  
                                   185                                  190                                  195

gtt cgt cgt gcc aag gct gtc ggc gct ctc acg gtg ctt gat gcg tgc 739  
 Val Arg Arg Ala Lys Ala Val Gly Ala Leu Thr Val Leu Asp Ala Cys  
                   200                                  205                                  210

cag tct gtt cct cat atg cca gtg aat ttc cac gag ctg gat gta gat 787  
 Gln Ser Val Pro His Met Pro Val Asn Phe His Glu Leu Asp Val Asp  
                   215                                  220                                  225

ttc tct gca ttc tct ggc cat aag atg ctg gga cct gca ggc gtg ggc 835  
 Phe Ser Ala Phe Ser Gly His Lys Met Leu Gly Pro Ala Gly Val Gly  
                   230                                  235                                  240                                  245

gtt gtg tat gca aag tcc cca atc ttg gat gaa ctg cca cca ttt ttg 883  
 Val Val Tyr Ala Lys Ser Pro Ile Leu Asp Glu Leu Pro Pro Phe Leu  
                                   250                                  255                                  260

act ggt ggt tcc atg att gaa gtt gtc acc atg gag ggt tcc acc tac 931

Thr Gly Gly Ser Met Ile Glu Val Val Thr Met Glu Gly Ser Thr Tyr  
 265 270 275  
 gct gcc gca cct caa cgt ttt gag gcc ggc acg cag atg acc agc cag 979  
 Ala Ala Ala Pro Gln Arg Phe Glu Ala Gly Thr Gln Met Thr Ser Gln  
 280 285 290  
 gtt gtg ggc ttg ggt gct gcc gtg gac atg ctg aat gaa atc ggt atg  
 1027  
 Val Val Gly Leu Gly Ala Ala Val Asp Met Leu Asn Glu Ile Gly Met  
 295 300 305  
 gaa gca atc gca gcg cat gag cac gca ttg act gct tac gcg ttg gaa  
 1075  
 Glu Ala Ile Ala Ala His Glu His Ala Leu Thr Ala Tyr Ala Leu Glu  
 310 315 320 325  
 aag ctc acg gca att aag gga cta acc att gct ggt cct ttg act gca  
 1123  
 Lys Leu Thr Ala Ile Lys Gly Leu Thr Ile Ala Gly Pro Leu Thr Ala  
 330 335 340  
 gag cag cgc ggc ggt gca atc agc ttc ggt gtc gag ggc att cac cca  
 1171  
 Glu Gln Arg Gly Gly Ala Ile Ser Phe Gly Val Glu Gly Ile His Pro  
 345 350 355  
 cac gat cta ggc caa gtg ctt gac gat cag ggc gtg aat atc cgc gtc  
 1219  
 His Asp Leu Gly Gln Val Leu Asp Asp Gln Gly Val Asn Ile Arg Val  
 360 365 370  
 ggc cac cac tgc gcg tgg ccc gtg cac cgc agc atg aac gta caa tcg  
 1267  
 Gly His His Cys Ala Trp Pro Val His Arg Ser Met Asn Val Gln Ser  
 375 380 385  
 aca gca aga gca tct ttc tat ctc tat aac acc ttc gaa gaa atc gac  
 1315  
 Thr Ala Arg Ala Ser Phe Tyr Leu Tyr Asn Thr Phe Glu Glu Ile Asp  
 390 395 400 405  
 cgc ctc gcg gca gcg atc gag aag gcc aag caa ttc ttt gga gtt gag  
 1363  
 Arg Leu Ala Ala Ala Ile Glu Lys Ala Lys Gln Phe Phe Gly Val Glu  
 410 415 420  
 taatgaacct tgagcagatg tac  
 1386  
 <210> 658  
 <211> 421  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 658  
 Met Ser Asp Phe Leu Asn Ala Asp Gly Ser Leu Asn Val Asp Lys Val  
 1 5 10 15  
 Arg Glu Glu Phe Pro Ile Leu Lys Arg Thr Val Arg Asp Gly Lys Pro

20	25	30
Leu Ala Tyr Leu Asp Ser Gly Ala Thr Ser Gln Arg Pro Glu Arg Val 35 40 45		
Trp Arg Ala Glu Glu His Phe Val Leu His Thr Asn Ala Pro Val His 50 55 60		
Arg Gly Ala Tyr Gln Leu Ala Glu Glu Ala Thr Asp Ala Tyr Glu Gly 65 70 75 80		
Ala Arg Glu Lys Ile Ala Ala Phe Val Gly Ala Glu Gln His Glu Ile 85 90 95		
Ala Phe Thr Lys Asn Ala Thr Glu Ala Leu Asn Leu Val Ala Tyr Thr 100 105 110		
Leu Gly Asp Asp Arg Ser Gly Lys Tyr Arg Val Gln Ala Gly Asp Thr 115 120 125		
Val Val Ile Thr Glu Leu Glu His His Ala Asn Leu Val Pro Trp Gln 130 135 140		
Glu Leu Cys Arg Arg Thr Gly Ala Thr Leu Lys Trp Tyr Lys Val Thr 145 150 155 160		
Glu Asp Gly Arg Ile Asp Leu Asp Ser Leu Glu Leu Asp Glu Thr Val 165 170 175		
Lys Val Val Ala Phe Thr His Gln Ser Asn Val Thr Gly Ala Val Ala 180 185 190		
Asp Val Pro Glu Leu Val Arg Arg Ala Lys Ala Val Gly Ala Leu Thr 195 200 205		
Val Leu Asp Ala Cys Gln Ser Val Pro His Met Pro Val Asn Phe His 210 215 220		
Glu Leu Asp Val Asp Phe Ser Ala Phe Ser Gly His Lys Met Leu Gly 225 230 235 240		
Pro Ala Gly Val Gly Val Val Tyr Ala Lys Ser Pro Ile Leu Asp Glu 245 250 255		
Leu Pro Pro Phe Leu Thr Gly Gly Ser Met Ile Glu Val Val Thr Met 260 265 270		
Glu Gly Ser Thr Tyr Ala Ala Ala Pro Gln Arg Phe Glu Ala Gly Thr 275 280 285		
Gln Met Thr Ser Gln Val Val Gly Leu Gly Ala Ala Val Asp Met Leu 290 295 300		
Asn Glu Ile Gly Met Glu Ala Ile Ala Ala His Glu His Ala Leu Thr 305 310 315 320		
Ala Tyr Ala Leu Glu Lys Leu Thr Ala Ile Lys Gly Leu Thr Ile Ala 325 330 335		
Gly Pro Leu Thr Ala Glu Gln Arg Gly Gly Ala Ile Ser Phe Gly Val 340 345 350		

Glu Gly Ile His Pro His Asp Leu Gly Gln Val Leu Asp Asp Gln Gly  
 355 360 365

Val Asn Ile Arg Val Gly His His Cys Ala Trp Pro Val His Arg Ser  
 370 375 380

Met Asn Val Gln Ser Thr Ala Arg Ala Ser Phe Tyr Leu Tyr Asn Thr  
 385 390 395 400

Phe Glu Glu Ile Asp Arg Leu Ala Ala Ala Ile Glu Lys Ala Lys Gln  
 405 410 415

Phe Phe Gly Val Glu  
 420

<210> 659

<211> 570

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(547)

<223> RXA02517

<400> 659

cgacagcaag agcatctttc tatctctata acaccttcga agaaatcgac cgcctcgcgg 60

cagcgatcga gaaggccaag caattctttg gagttgagta atg aac ctt gag cag 115  
 Met Asn Leu Glu Gln  
 1 5

atg tac cag gag gtg atc ctg gac cac tac aaa aac cca cag cac aag 163  
 Met Tyr Gln Glu Val Ile Leu Asp His Tyr Lys Asn Pro Gln His Lys  
 10 15 20

ggc ctt cgg gat cct ttc gat gct gag gtt cac cac gtc aac cct tct 211  
 Gly Leu Arg Asp Pro Phe Asp Ala Glu Val His His Val Asn Pro Ser  
 25 30 35

tgt ggc gac gaa ttg act ctg cgc gtg aag ctg tct gag gac ggc tcc 259  
 Cys Gly Asp Glu Leu Thr Leu Arg Val Lys Leu Ser Glu Asp Gly Ser  
 40 45 50

acc gtg gag gac gtc tcc tac gaa gca gtt ggt tgc tca atc agc cag 307  
 Thr Val Glu Asp Val Ser Tyr Glu Ala Val Gly Cys Ser Ile Ser Gln  
 55 60 65

gcc tcc acg tcc gtt atg gcc gag gag atc gtg ggc caa ccc gtc gac 355  
 Ala Ser Thr Ser Val Met Ala Glu Glu Ile Val Gly Gln Pro Val Asp  
 70 75 80 85

aag gcg ctg gaa aag ctc aca gaa ttt gag aag atg atc gtt tcc cgc 403  
 Lys Ala Leu Glu Lys Leu Thr Glu Phe Glu Lys Met Ile Val Ser Arg  
 90 95 100

ggt cag ttt gtt ggc gat gaa gat ctc atc gga gat ggc gtt gct ttc 451  
 Gly Gln Phe Val Gly Asp Glu Asp Leu Ile Gly Asp Gly Val Ala Phe  
 105 110 115

tcc gga gtc gcc aag tac ccg gca cgc gtg aag tgc gcg ctg ctt ggg 499  
 Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys Cys Ala Leu Leu Gly  
           120                          125                          130

tgg aag gct ttc cag gcg gca acc gct gac gct gtt gcg cac gca cat 547  
 Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala Val Ala His Ala His  
           135                          140                          145

tagcccgctg tattaattgg agg 570

<210> 660

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 660

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Asn Pro Gln His Lys Gly Leu Arg Asp Pro Phe Asp Ala Glu Val His  
           20                          25                          30

His Val Asn Pro Ser Cys Gly Asp Glu Leu Thr Leu Arg Val Lys Leu  
           35                          40                          45

Ser Glu Asp Gly Ser Thr Val Glu Asp Val Ser Tyr Glu Ala Val Gly  
           50                          55                          60

Cys Ser Ile Ser Gln Ala Ser Thr Ser Val Met Ala Glu Glu Ile Val  
       65                          70                          75                          80

Gly Gln Pro Val Asp Lys Ala Leu Glu Lys Leu Thr Glu Phe Glu Lys  
           85                          90                          95

Met Ile Val Ser Arg Gly Gln Phe Val Gly Asp Glu Asp Leu Ile Gly  
           100                          105                          110

Asp Gly Val Ala Phe Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys  
           115                          120                          125

Cys Ala Leu Leu Gly Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala  
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Val Ala His Ala His  
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<210> 661

<211> 1167

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1144)

<223> RXA01747

<400> 661

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	Val Thr Ile Ala Pro	
	1 5	
gaa gga cga cga ctg cta cgc gtc gaa gct cga aac tca gaa acc ccg	163	
Glu Gly Arg Arg Leu Leu Arg Val Glu Ala Arg Asn Ser Glu Thr Pro		
	10 15 20	
att gag acg aag cct cga tgg att aga aac cag gtc aaa aac gga cct	211	
Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Gln Val Lys Asn Gly Pro		
	25 30 35	
gag tat cag gat atg aag gaa cgt gtc gct ggc gca tca cta cac act	259	
Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly Ala Ser Leu His Thr		
	40 45 50	
gtg tgt cag gag gct ggc tgt cct aat atc cat gag tgt tgg gaa tcc	307	
Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His Glu Cys Trp Glu Ser		
	55 60 65	
cgt gag gca acc ttc ctc att ggt ggc gcc aac tgc tct cgc cgc tgt	355	
Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn Cys Ser Arg Arg Cys		
	70 75 80 85	
gat ttc tgc atg atc aac tcg gct cgc cct gag cca ctc gac cgc ggt	403	
Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu Pro Leu Asp Arg Gly		
	90 95 100	
gag cca ctg cgt gtc gct gag tct gtt cgt gag atg cag ctg aat tac	451	
Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu Met Gln Leu Asn Tyr		
	105 110 115	
tcc acc atc acc ggt gtt acc cgt gat gat ctg gat gat gaa ggc gca	499	
Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu Asp Asp Glu Gly Ala		
	120 125 130	
tgg ctg tac tca gaa gtg gtt cgt aag atc cac gag ctg aac cca cac	547	
Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His Glu Leu Asn Pro His		
	135 140 145	
acc ggt gtg gaa aac ctg gtg cct gat ttc tcc ggc aag aag gat ctg	595	
Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser Gly Lys Lys Asp Leu		
	150 155 160 165	
ctg cag gaa gtt ttt gaa tcc cgc cca gag gtt ttc gct cac aac gtg	643	
Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val Phe Ala His Asn Val		
	170 175 180	
gaa act gtg cca cgt att ttc aag cgc att cgc cca gca ttc cgc tac	691	
Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg Pro Ala Phe Arg Tyr		
	185 190 195	
gag cgt tca ctt gat gtg atc cgt cag gct cgc gat ttc ggt ctg gtg	739	
Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg Asp Phe Gly Leu Val		
	200 205 210	
acc aag tcc aac ctg att ttg ggc atg ggt gaa acc aag gaa gaa atc	787	
Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu Thr Lys Glu Glu Ile		
	215 220 225	

acc gag gcg ctg cag gat ctg cac gac gct ggc tgt gac atc atc acc 835  
 Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly Cys Asp Ile Ile Thr  
 230 235 240 245

atc acc cag tac ctg cgt cct ggt cct ttg ttc cac ccc atc gag cgt 883  
 Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe His Pro Ile Glu Arg  
 250 255 260

tgg gtg aag cct gag gag ttc ctc gag cac gct gat gct gca aag gaa 931  
 Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala Asp Ala Ala Lys Glu  
 265 270 275

atg ggc ttc gct gct gtt atg tcc ggc cca ttg gtt cgt tcc tct tac 979  
 Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu Val Arg Ser Ser Tyr  
 280 285 290

cgt gca ggc cgt ctg tac gcg cag gcc atg gag ttc cgt ggc gag gaa  
 1027  
 Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu Phe Arg Gly Glu Glu  
 295 300 305

atc cca gca cac ctc gcg cac ctg aag gat act tcc gga gga tcc acc  
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 Ile Pro Ala His Leu Ala His Leu Lys Asp Thr Ser Gly Gly Ser Thr  
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gcc cag gaa gca tct aca ctt ctg gag cgt tac ggt gct tcc gaa gac  
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 Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr Gly Ala Ser Glu Asp  
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 Thr Pro Val Val Ser Phe Asn  
 345

<210> 662  
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 <212> PRT  
 <213> *Corynebacterium glutamicum*

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 Val Lys Asn Gly Pro Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly  
 35 40 45  
 Ala Ser Leu His Thr Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His  
 50 55 60  
 Glu Cys Trp Glu Ser Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn  
 65 70 75 80  
 Cys Ser Arg Arg Cys Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu  
 85 90 95

Pro Leu Asp Arg Gly Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu  
 100 105 110  
 Met Gln Leu Asn Tyr Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu  
 115 120 125  
 Asp Asp Glu Gly Ala Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His  
 130 135 140  
 Glu Leu Asn Pro His Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser  
 145 150 155 160  
 Gly Lys Lys Asp Leu Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val  
 165 170 175  
 Phe Ala His Asn Val Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg  
 180 185 190  
 Pro Ala Phe Arg Tyr Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg  
 195 200 205  
 Asp Phe Gly Leu Val Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu  
 210 215 220  
 Thr Lys Glu Glu Ile Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly  
 225 230 235 240  
 Cys Asp Ile Ile Thr Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe  
 245 250 255  
 His Pro Ile Glu Arg Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala  
 260 265 270  
 Asp Ala Ala Lys Glu Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu  
 275 280 285  
 Val Arg Ser Ser Tyr Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu  
 290 295 300  
 Phe Arg Gly Glu Glu Ile Pro Ala His Leu Ala His Leu Lys Asp Thr  
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 Ser Gly Gly Ser Thr Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr  
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 Gly Ala Ser Glu Asp Thr Pro Val Val Ser Phe Asn  
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&lt;210&gt; 663

&lt;211&gt; 876

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(853)

&lt;223&gt; RXA01746

&lt;400&gt; 663

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Met Thr Ala Pro Arg	
1 5	
gat cct ttt ttc ccc gca gat ctt tct atc cgc gcg tct gca gag ccc	163
Asp Pro Phe Phe Pro Ala Asp Leu Ser Ile Arg Ala Ser Ala Glu Pro	
10 15 20	
att gaa att cag cgg ttg ggt ttg atc gat tat caa gag gcc tgg gat	211
Ile Glu Ile Gln Arg Leu Gly Leu Ile Asp Tyr Gln Glu Ala Trp Asp	
25 30 35	
tat caa gca gag ctt gct acc cgt agg gct aat gat gaa atc cct gat	259
Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn Asp Glu Ile Pro Asp	
40 45 50	
cag ctg ctt att ttg gag cac ccg tcg gtg tat acc gca ggt aag cgc	307
Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr Thr Ala Gly Lys Arg	
55 60 65	
acc cag ccg gaa gat ctt ccc acc aac gga ctg ccg gtg atc aat gct	355
Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu Pro Val Ile Asn Ala	
70 75 80 85	
gat cgt ggt ggt cgc atc acg tgg cat ggt cct ggc caa ttg gtg atc	403
Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro Gly Gln Leu Val Ile	
90 95 100	
tat ccg atc atc aaa tta gcc gat ccg atc gat gtg gtt gat tac gta	451
Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp Val Val Asp Tyr Val	
105 110 115	
aga cgc ctc gag gaa gcg ctc atc caa gtt gtc ggc gat atg ggt gtt	499
Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val Gly Asp Met Gly Val	
120 125 130	
gcc ggc gct ggg cgc att gat ggg cgt tcg ggt gtg tgg gtg cca gct	547
Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly Val Trp Val Pro Ala	
135 140 145	
cat gat ggt tgg gtg gac agc aag gtt gcg gcc atc ggc att cga ata	595
His Asp Gly Trp Val Asp Ser Lys Val Ala Ala Ile Gly Ile Arg Ile	
150 155 160 165	
act cgt ggt gtt gca atg cac ggt gtg gcc atc aac tgc aac aac acg	643
Thr Arg Gly Val Ala Met His Gly Val Ala Ile Asn Cys Asn Asn Thr	
170 175 180	
ttg gat ttc tat gag cac atc att ccg tgt ggc att gct gat gca ggc	691
Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly Ile Ala Asp Ala Gly	
185 190 195	
ttg agc aca ctc tcg agg gaa ctg aaa agg gac gtt tca gtt gag gaa	739
Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp Val Ser Val Glu Glu	
200 205 210	
tta gtc gag cca tcg atc cgc gca ttg gat gat gct ttg gct ggt cgg	787
Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp Ala Leu Ala Gly Arg	
215 220 225	

ctg gtt gtt tct gat cat tct ttc ggc agc gcg ccc gac cca act aag 835  
 Leu Val Val Ser Asp His Ser Phe Gly Ser Ala Pro Asp Pro Thr Lys  
 230 235 240 245

aat ctc cct aaa cgg ggg tagtacgagg aattttgtcg gtg 876  
 Asn Leu Pro Lys Arg Gly  
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<210> 664

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 664

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Gln Glu Ala Trp Asp Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn  
 35 40 45

Asp Glu Ile Pro Asp Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr  
 50 55 60

Thr Ala Gly Lys Arg Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu  
 65 70 75 80

Pro Val Ile Asn Ala Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro  
 85 90 95

Gly Gln Leu Val Ile Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp  
 100 105 110

Val Val Asp Tyr Val Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val  
 115 120 125

Gly Asp Met Gly Val Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly  
 130 135 140

Val Trp Val Pro Ala His Asp Gly Trp Val Asp Ser Lys Val Ala Ala  
 145 150 155 160

Ile Gly Ile Arg Ile Thr Arg Gly Val Ala Met His Gly Val Ala Ile  
 165 170 175

Asn Cys Asn Asn Thr Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly  
 180 185 190

Ile Ala Asp Ala Gly Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp  
 195 200 205

Val Ser Val Glu Glu Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp  
 210 215 220

Ala Leu Ala Gly Arg Leu Val Val Ser Asp His Ser Phe Gly Ser Ala  
 225 230 235 240

Pro Asp Pro Thr Lys Asn Leu Pro Lys Arg Gly

245

250

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<211> 1179
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1156)  
<223> RXA02106
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				Met	Asn	Asn	His	Phe									
				1								5					
gag	ctc	aaa	gta	cct	ggt	gga	aag	ctt	gtc	gtc	ggt	gat	gtg	acc	acc	163	
Glu	Leu	Lys	Val	Pro	Gly	Gly	Lys	Leu	Val	Val	Val	Asp	Val	Thr	Thr		
				10								15				20	
gat	ctg	gat	tcc	att	gct	gac	gtg	aag	att	tcc	ggc	gat	ttc	ttc	ctc	211	
Asp	Leu	Asp	Ser	Ile	Ala	Asp	Val	Lys	Ile	Ser	Gly	Asp	Phe	Phe	Leu		
				25								30				35	
gaa	ccc	gat	gag	gca	ttc	ttc	gcc	ctt	ggc	cgg	gcg	ctg	cag	ggg	gcg	259	
Glu	Pro	Asp	Glu	Ala	Phe	Phe	Ala	Leu	Gly	Arg	Ala	Leu	Gln	Gly	Ala		
				40								45				50	
tcg	gtg	ggt	gat	aac	act	gat	cgt	ttg	cag	gca	aag	ttg	gat	gga	gcg	307	
Ser	Val	Gly	Asp	Asn	Thr	Asp	Arg	Leu	Gln	Ala	Lys	Leu	Asp	Ala	Ala		
				55								60				65	
ttg	gcg	gaa	tat	gat	gac	gtt	gag	cta	cac	ggc	ttt	agc	act	gcg	gat	355	
Leu	Ala	Glu	Tyr	Asp	Asp	Val	Glu	Leu	His	Gly	Phe	Ser	Thr	Ala	Asp		
				70								75				80	85
att	gct	tta	gct	gtg	cgt	cgg	gca	gtc	acc	ggc	gcg	caa	gat	ttc	acc	403	
Ile	Ala	Leu	Ala	Val	Arg	Arg	Ala	Val	Thr	Gly	Ala	Gln	Asp	Phe	Thr		
				90								95				100	
gat	tat	gaa	tgg	gaa	atc	ctg	cac	cca	ggg	gtg	ctt	cct	acc	cca	ctt	451	
Asp	Tyr	Glu	Trp	Glu	Ile	Leu	His	Pro	Gly	Val	Leu	Pro	Thr	Pro	Leu		
				105								110				115	
aac	gtt	gcg	ttg	gat	gag	ctc	ctt	ttg	gac	caa	gtt	gcc	agt	ggg	cag	499	
Asn	Val	Ala	Leu	Asp	Glu	Leu	Leu	Leu	Asp	Gln	Val	Ala	Ser	Gly	Gln		
				120								125				130	
cgt	ggc	ccg	acg	atg	cgc	att	tgg	gat	tgg	gat	gat	cgc	gcc	aca	gtg	547	
Arg	Gly	Pro	Thr	Met	Arg	Ile	Trp	Asp	Trp	Asp	Asp	Arg	Ala	Thr	Val		
				135								140				145	
atc	ggg	agt	ttc	cag	tca	tat	gtc	aat	gaa	atc	aac	caa	gaa	ggc	gtt	595	
Ile	Gly	Ser	Phe	Gln	Ser	Tyr	Val	Asn	Glu	Ile	Asn	Gln	Glu	Gly	Val		
				150								155				160	165
at	gaa	cat	ggg	gtg	acc	gtg	gta	cga	cgc	atg	tct	ggg	ggc	ggg	gca	643	

Asn Glu His Gly Val Thr Val Val Arg Arg Met Ser Gly Gly Gly Ala  
 170 175 180  
 atg ttt atg gag ggc ggc aac tgc atc acc tat tcc ctg tat gca ccg 691  
 Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr Ser Leu Tyr Ala Pro  
 185 190 195  
 gaa tct ctc gtt gct ggt ttg agc tat gag cag tcc tat gaa tat ttg 739  
 Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln Ser Tyr Glu Tyr Leu  
 200 205 210  
 gat cgt tgg gtg att gct gcg ctg aag aca cac gat gtt gac gct tgg 787  
 Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His Asp Val Asp Ala Trp  
 215 220 225  
 tac gtg cct atc aat gac atc acc tcc acc ggc gga aaa atc ggt ggc 835  
 Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly Gly Lys Ile Gly Gly  
 230 235 240 245  
 gct gca cag aaa cgt cgc agt ggc gca gtc ctc cac cac gtg acc atg 883  
 Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu His His Val Thr Met  
 250 255 260  
 tcc tat gac atc gat gcg gac atg atg acc cag gtg ttg cgc att gga 931  
 Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln Val Leu Arg Ile Gly  
 265 270 275  
 aag gtg aag att tcc gac aag ggt ctt cgc agc gca aag aag cgc gtt 979  
 Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser Ala Lys Lys Arg Val  
 280 285 290  
 gat cct ctg cgc cgc caa aca ggt gca tca cgt gag caa atc atc gac  
 1027  
 Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg Glu Gln Ile Ile Asp  
 295 300 305  
 acc cta aag tcc aca ttc agt gct agg tac ggc gcg caa gaa gta gag  
 1075  
 Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly Ala Gln Glu Val Glu  
 310 315 320 325  
 ctc agc gat gaa gat ttc gcg gca ggc cac gac cta gta aaa acc aaa  
 1123  
 Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp Leu Val Lys Thr Lys  
 330 335 340  
 tac gcc acc gag gag tgg act aag cga gtt caa tagtttctat ggatctgcac  
 1176  
 Tyr Ala Thr Glu Glu Trp Thr Lys Arg Val Gln  
 345 350  
 aag  
 1179

&lt;210&gt; 666

&lt;211&gt; 352

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 666

Met Asn Asn His Phe Glu Leu Lys Val Pro Gly Gly Lys Leu Val Val  
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 Val Asp Val Thr Thr Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser  
 20 25 30  
 Gly Asp Phe Phe Leu Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg  
 35 40 45  
 Ala Leu Gln Gly Ala Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala  
 50 55 60  
 Lys Leu Asp Ala Ala Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly  
 65 70 75 80  
 Phe Ser Thr Ala Asp Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly  
 85 90 95  
 Ala Gln Asp Phe Thr Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val  
 100 105 110  
 Leu Pro Thr Pro Leu Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln  
 115 120 125  
 Val Ala Ser Gly Gln Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp  
 130 135 140  
 Asp Arg Ala Thr Val Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile  
 145 150 155 160  
 Asn Gln Glu Gly Val Asn Glu His Gly Val Thr Val Val Arg Arg Met  
 165 170 175  
 Ser Gly Gly Gly Ala Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr  
 180 185 190  
 Ser Leu Tyr Ala Pro Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln  
 195 200 205  
 Ser Tyr Glu Tyr Leu Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His  
 210 215 220  
 Asp Val Asp Ala Trp Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly  
 225 230 235 240  
 Gly Lys Ile Gly Gly Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu  
 245 250 255  
 His His Val Thr Met Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln  
 260 265 270  
 Val Leu Arg Ile Gly Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser  
 275 280 285  
 Ala Lys Lys Arg Val Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg  
 290 295 300  
 Glu Gln Ile Ile Asp Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly  
 305 310 315 320  
 Ala Gln Glu Val Glu Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp

325

330

335

Leu Val Lys Thr Lys Tyr Ala Thr Glu Glu Trp Thr Lys Arg Val Gln  
 340 345 350

&lt;210&gt; 667

&lt;211&gt; 403

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(403)

&lt;223&gt; RXS01183

&lt;400&gt; 667

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ttccgttttta acgacacgac ttgcgaggag tcttaaaata atg gcg ttc tcc gta 115  
 Met Ala Phe Ser Val  
 1 5

gag atg ccc gag ctg ggc gaa tca gta acc gaa ggc acg atc acc cag 163  
 Glu Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln  
 10 15 20

tgg ttg aag tct gtt ggt gac act gtt gag gta gat gag ccg ttg ctc 211  
 Trp Leu Lys Ser Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu  
 25 30 35

gag gtc tca act gac aag gtc gac acc gag att ccc tct cct gtc gcc 259  
 Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala  
 40 45 50

ggt gtc atc cta gag att aag gct gaa gag gat gac acc gtc gac gtc 307  
 Gly Val Ile Leu Glu Ile Lys Ala Glu Glu Asp Asp Thr Val Asp Val  
 55 60 65

ggc ggt gtc att gca ata atc ggc gat gct gat gag act cct gcc aac 355  
 Gly Gly Val Ile Ala Ile Ile Gly Asp Ala Asp Glu Thr Pro Ala Asn  
 70 75 80 85

gaa gct cct gcc gac gag gca cca gct cct gcc gaa gag gaa gaa cca 403  
 Glu Ala Pro Ala Asp Glu Ala Pro Ala Pro Ala Glu Glu Glu Glu Pro  
 90 95 100

&lt;210&gt; 668

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 668

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Gly Thr Ile Thr Gln Trp Leu Lys Ser Val Gly Asp Thr Val Glu Val

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 35 40 45  
 Pro Ser Pro Val Ala Gly Val Ile Leu Glu Ile Lys Ala Glu Glu Asp  
 50 55 60  
 Asp Thr Val Asp Val Gly Gly Val Ile Ala Ile Ile Gly Asp Ala Asp  
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 Glu Thr Pro Ala Asn Glu Ala Pro Ala Asp Glu Ala Pro Ala Pro Ala  
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<210> 669  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1282)  
 <223> RXS01260

<400> 669  
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 Val Thr Phe Asn Tyr  
 1 5  
 gag gat gct cac aag cgt tcc cgt ggc gtt tcc gac aag atc gtt gga 163  
 Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly  
 10 15 20  
 ggc gtt cat tac ttg atg aag aag aac aag atc atc gaa att cat ggt 211  
 Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Ile Glu Ile His Gly  
 25 30 35  
 ctt gga aac ttc aag gat gct aag act ctt gag gtc acc gac ggt aag 259  
 Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu Val Thr Asp Gly Lys  
 40 45 50  
 gat gct ggc aag acc atc acc ttt gat gac tgc atc atc gca acc ggt 307  
 Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly  
 55 60 65  
 tcg gta gtc aac acc ctc cgt ggc gtt gac ttc tca gag aac gtt gtg 355  
 Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe Ser Glu Asn Val Val  
 70 75 80 85  
 tct ttt gaa gag cag att ctt aac cct gtt gcg cca aag aag atg gtc 403  
 Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val  
 90 95 100  
 att gtt ggt gca ggc gca att gga atg gaa ttc gcc tac gtt ctt ggt 451  
 Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly

105	110	115	
aac tac ggt gta gat gta acc gtc atc gag ttc atg gat cgt gtg ctt Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu 120 125 130			499
cca aat gaa gat gct gaa gtc tcc aag gtt att gca aag gcc tac aag Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys 135 140 145			547
aag atg ggc gtt aag ctt ctt cct ggc cat gca acc act gct gtt cgg Lys Met Gly Val Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg 150 155 160 165			595
gac aac ggt gac ttt gtc gag gtt gat tac cag aag aag ggc tct gac Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp 170 175 180			643
aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe 185 190 195			691
cgt cca cgc gtt gag gga ttt ggt ctt gaa aac act ggc gtt aag ctc Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu 200 205 210			739
acc gag cgt ggc gca atc gag atc gat gat tac atg cgt acc aac gtc Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr Met Arg Thr Asn Val 215 220 225			787
gat ggc att tac gcc atc ggt gac gtg acc gcc aag ctt cag ctt gct Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala 230 235 240 245			835
cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly 250 255 260			883
gca gaa act cag act ctt ggt gat tac atg atg atg cca cgt gca acc Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr 265 270 275			931
ttc tgc aac cca cag gtt tct tcc ttt ggt tac acc gaa gag cag gcc Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr Thr Glu Glu Gln Ala 280 285 290			979
aag gag aag tgg cca gat cgt gag atc aag gtt gct tcc ttc cca ttc 1027 Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe 295 300 305			
tct gca aac ggt aaa gca gtt ggc ctg gca gaa act gat ggt ttc gca 1075 Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala 310 315 320 325			
aag atc gtt gct gat gca gaa ttc ggt gag ctg ctc ggt gca cac ctg 1123 Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Ala His Leu 330 335 340			



gtt gga gca aat gca tca gag ctc atc aat gaa ttg gtg ctt gct cag  
1171

Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln  
345 350 355

aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac  
1219

Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His  
360 365 370

cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga  
1267

Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly  
375 380 385

cac atg atc aac ttc tagaatccac ctcgttggcc ctg  
1305

His Met Ile Asn Phe  
390

<210> 670

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 670

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Asp Lys Ile Val Gly Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile  
20 25 30

Ile Glu Ile His Gly Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu  
35 40 45

Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys  
50 55 60

Ile Ile Ala Thr Gly Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe  
65 70 75 80

Ser Glu Asn Val Val Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala  
85 90 95

Pro Lys Lys Met Val Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe  
100 105 110

Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe  
115 120 125

Met Asp Arg Val Leu Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile  
130 135 140

Ala Lys Ala Tyr Lys Lys Met Gly Val Lys Leu Leu Pro Gly His Ala  
145 150 155 160

Thr Thr Ala Val Arg Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln  
165 170 175

Lys Lys Gly Ser Asp Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met

180					185					190					
Val	Ser	Val	Gly	Phe	Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	Glu	Asn
		195					200					205			
Thr	Gly	Val	Lys	Leu	Thr	Glu	Arg	Gly	Ala	Ile	Glu	Ile	Asp	Asp	Tyr
	210					215					220				
Met	Arg	Thr	Asn	Val	Asp	Gly	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Thr	Ala
225					230					235					240
Lys	Leu	Gln	Leu	Ala	His	Val	Ala	Glu	Ala	Gln	Gly	Ile	Val	Ala	Ala
				245					250					255	
Glu	Thr	Ile	Ala	Gly	Ala	Glu	Thr	Gln	Thr	Leu	Gly	Asp	Tyr	Met	Met
			260					265					270		
Met	Pro	Arg	Ala	Thr	Phe	Cys	Asn	Pro	Gln	Val	Ser	Ser	Phe	Gly	Tyr
		275					280					285			
Thr	Glu	Glu	Gln	Ala	Lys	Glu	Lys	Trp	Pro	Asp	Arg	Glu	Ile	Lys	Val
	290					295					300				
Ala	Ser	Phe	Pro	Phe	Ser	Ala	Asn	Gly	Lys	Ala	Val	Gly	Leu	Ala	Glu
305					310					315					320
Thr	Asp	Gly	Phe	Ala	Lys	Ile	Val	Ala	Asp	Ala	Glu	Phe	Gly	Glu	Leu
				325					330					335	
Leu	Gly	Ala	His	Leu	Val	Gly	Ala	Asn	Ala	Ser	Glu	Leu	Ile	Asn	Glu
			340					345					350		
Leu	Val	Leu	Ala	Gln	Asn	Trp	Asp	Leu	Thr	Thr	Glu	Glu	Ile	Ser	Arg
		355					360					365			
Ser	Val	His	Ile	His	Pro	Thr	Leu	Ser	Glu	Ala	Val	Lys	Glu	Ala	Ala
	370					375					380				
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385					390										

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(271)  
 <223> RXS01261

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 Val Thr Glu His Tyr  
 1 5  
 gac gta gta gta ctc gga gcc ggc ccc ggt ggc tat gtc tcc gcc atc 163  
 Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly Tyr Val Ser Ala Ile

	10	15	20	
cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac				211
Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr				
	25	30	35	
tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct				259
Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser				
	40	45	50	
gat caa aaa cgc tgaagttgcc cataccttta ccc				294
Asp Gln Lys Arg				
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<210> 672  
 <211> 57  
 <212> PRT  
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 Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val  
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 Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile  
 35 40 45  
 Pro Ser Lys Val Ser Asp Gln Lys Arg  
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 <212> DNA  
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<220>  
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 <223> RXA02717

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 Met Pro Pro Arg Asp  
 1 5  
 gat gca gct gaa gag cgt ctt tac cgc gca gca gag gtc ttc cat gac 163  
 Asp Ala Ala Glu Glu Arg Leu Tyr Arg Ala Ala Glu Val Phe His Asp  
 10 15 20  
 ctc ggt gca tcg ttt gtc tcc gtg act tat ggt gct ggc gga tca acc 211  
 Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Ser Thr  
 25 30 35  
 cgt gag aga acc tca cgt att gct cga cga tta gcg aaa caa ccg ttg 259  
 Arg Glu Arg Thr Ser Arg Ile Ala Arg Arg Leu Ala Lys Gln Pro L u

40	45	50	
acc act ctg gtg cac ctg acc ctg gtt aac cac act cgc gaa gag atg Thr Thr Leu Val His Leu Thr Leu Val Asn His Thr Arg Glu Glu Met 55 60 65			307
aag gca att ctt cgg gaa tac cta gag ctg gga tta aca aac ctg ttg Lys Ala Ile Leu Arg Glu Tyr Leu Glu Leu Gly Leu Thr Asn Leu Leu 70 75 80 85			355
gcg ctt cga gga gat ccg cct gga gac cca tta ggc gat tgg gtg agc Ala Leu Arg Gly Asp Pro Pro Gly Asp Pro Leu Gly Asp Trp Val Ser 90 95 100			403
acc gat gga gga ctg aac tat gcc tct gag ctc atc gat ctt att aag Thr Asp Gly Gly Leu Asn Tyr Ala Ser Glu Leu Ile Asp Leu Ile Lys 105 110 115			451
tcc act cct gag ttc cgg gaa ttc gac ctc ggt atc gcc tcc ttc ccc Ser Thr Pro Glu Phe Arg Glu Phe Asp Leu Gly Ile Ala Ser Phe Pro 120 125 130			499
gaa ggg cat ttc cgg gcg aaa act cta gaa gaa gac acc aaa tac act Glu Gly His Phe Arg Ala Lys Thr Leu Glu Glu Asp Thr Lys Tyr Thr 135 140 145			547
ctg gcg aag ctg cgt gga ggg gca gag tac tcc atc acg cag atg ttc Leu Ala Lys Leu Arg Gly Gly Ala Glu Tyr Ser Ile Thr Gln Met Phe 150 155 160 165			595
ttt gat gtg gaa gac tac ctg cga ctt cgt gat cgc ctt gtc gct gca Phe Asp Val Glu Asp Tyr Leu Arg Leu Arg Asp Arg Leu Val Ala Ala 170 175 180			643
gac ccc att cat ggt gcg aag cca atc att cct ggc atc atg ccc att Asp Pro Ile His Gly Ala Lys Pro Ile Ile Pro Gly Ile Met Pro Ile 185 190 195			691
acg agc ctg cgg tct gtg cgt cga cag gtc gaa ctc tct ggt gct caa Thr Ser Leu Arg Ser Val Arg Arg Gln Val Glu Leu Ser Gly Ala Gln 200 205 210			739
ttg ccg agc caa cta gaa gaa tca ctt gtt cga gct gca aac ggc aat Leu Pro Ser Gln Leu Glu Glu Ser Leu Val Arg Ala Ala Asn Gly Asn 215 220 225			787
gaa gaa gcg aac aaa gac gag atc cgc aag gtg ggc att gaa tat tcc Glu Glu Ala Asn Lys Asp Glu Ile Arg Lys Val Gly Ile Glu Tyr Ser 230 235 240 245			835
acc aat atg gca gag cga ctc att gcc gaa ggt gcg gaa gat ctg cac Thr Asn Met Ala Glu Arg Leu Ile Ala Glu Gly Ala Glu Asp Leu His 250 255 260			883
ttc atg acg ctt aac ttc acc cgt gca acc caa gaa gtg ttg tac aac Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln Glu Val Leu Tyr Asn 265 270 275			931
ctt ggc atg gcg cct gct tgg gga gca gag cac ggc caa gac gcg gtg Leu Gly Met Ala Pro Ala Trp Gly Ala Glu His Gly Gln Asp Ala Val 280 285 290			979

cgt taagccctct taggaatcat gaa  
1005  
Arg

<210> 674  
<211> 294  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 674

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Glu	Val	Phe	His	Asp	Leu	Gly	Ala	Ser	Phe	Val	Ser	Val	Thr	Tyr	Gly	20	25	30	
Ala	Gly	Gly	Ser	Thr	Arg	Glu	Arg	Thr	Ser	Arg	Ile	Ala	Arg	Arg	Leu	35	40	45	
Ala	Lys	Gln	Pro	Leu	Thr	Thr	Leu	Val	His	Leu	Thr	Leu	Val	Asn	His	50	55	60	
Thr	Arg	Glu	Glu	Met	Lys	Ala	Ile	Leu	Arg	Glu	Tyr	Leu	Glu	Leu	Gly	65	70	75	80
Leu	Thr	Asn	Leu	Leu	Ala	Leu	Arg	Gly	Asp	Pro	Pro	Gly	Asp	Pro	Leu	85	90	95	
Gly	Asp	Trp	Val	Ser	Thr	Asp	Gly	Gly	Leu	Asn	Tyr	Ala	Ser	Glu	Leu	100	105	110	
Ile	Asp	Leu	Ile	Lys	Ser	Thr	Pro	Glu	Phe	Arg	Glu	Phe	Asp	Leu	Gly	115	120	125	
Ile	Ala	Ser	Phe	Pro	Glu	Gly	His	Phe	Arg	Ala	Lys	Thr	Leu	Glu	Glu	130	135	140	
Asp	Thr	Lys	Tyr	Thr	Leu	Ala	Lys	Leu	Arg	Gly	Gly	Ala	Glu	Tyr	Ser	145	150	155	160
Ile	Thr	Gln	Met	Phe	Phe	Asp	Val	Glu	Asp	Tyr	Leu	Arg	Leu	Arg	Asp	165	170	175	
Arg	Leu	Val	Ala	Ala	Asp	Pro	Ile	His	Gly	Ala	Lys	Pro	Ile	Ile	Pro	180	185	190	
Gly	Ile	Met	Pro	Ile	Thr	Ser	Leu	Arg	Ser	Val	Arg	Arg	Gln	Val	Glu	195	200	205	
Leu	Ser	Gly	Ala	Gln	Leu	Pro	Ser	Gln	Leu	Glu	Glu	Ser	Leu	Val	Arg	210	215	220	
Ala	Ala	Asn	Gly	Asn	Glu	Glu	Ala	Asn	Lys	Asp	Glu	Ile	Arg	Lys	Val	225	230	235	240
Gly	Ile	Glu	Tyr	Ser	Thr	Asn	Met	Ala	Glu	Arg	Leu	Ile	Ala	Glu	Gly	245	250	255	

Ala Glu Asp Leu His Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln  
 260 265 270

Glu Val Leu Tyr Asn Leu Gly Met Ala Pro Ala Trp Gly Ala Glu His  
 275 280 285

Gly Gln Asp Ala Val Arg  
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<210> 675

<211> 601

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> RXN02027

<400> 675

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tcgtcgtacc cctccgaaaa taacggttat ccttagattt atg agc caa act aag 115  
 Met Ser Gln Thr Lys  
 1 5

cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163  
 Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu  
 10 15 20

gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211  
 Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr  
 25 30 35

tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg 259  
 Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val  
 40 45 50

cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa 307  
 Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu  
 55 60 65

act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355  
 Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp  
 70 75 80 85

tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403  
 Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly  
 90 95 100

atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451  
 Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe  
 105 110 115

tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499  
 Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile  
 120 125 130

agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547  
 Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly

135                                      140                                      145  
 gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac 595  
 Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp  
 150                                      155                                      160                                      165  
  
 gat atc  
 Asp Ile 601  
  
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 <212> PRT  
 <213> Corynebacterium glutamicum  
  
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 Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile  
                                     20                                      25                                      30  
 Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala  
                                     35                                      40                                      45  
 Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp  
                                     50                                      55                                      60  
 Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu  
                                     65                                      70                                      75                                      80  
 Asp Arg Arg Leu Asp Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val  
                                     85                                      90                                      95  
 Pro Gly Ala Phe Gly Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro  
                                     100                                      105                                      110  
 Glu Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys  
                                     115                                      120                                      125  
 Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg  
                                     130                                      135                                      140  
 Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn  
 145                                      150                                      155                                      160  
 Gly Glu Ile Arg Asp Asp Ile  
                                     165

<210> 677  
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 <212> DNA  
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 Met Ser Gln Thr Lys  
 1 5

cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163  
 Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu  
 10 15 20

gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211  
 Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr  
 25 30 35

tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg 259  
 Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val  
 40 45 50

cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa 307  
 Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu  
 55 60 65

act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355  
 Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp  
 70 75 80 85

tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403  
 Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly  
 90 95 100

atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451  
 Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe  
 105 110 115

tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499  
 Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile  
 120 125 130

agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547  
 Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly  
 135 140 145

gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac 595  
 Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp  
 150 155 160 165

&lt;210&gt; 678

&lt;211&gt; 165

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 678

Met Ser Gln Thr Lys Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg  
 1 5 10 15

Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile  
 20 25 30

Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala



35 40 45  
 Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp  
 50 55 60  
 Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu  
 65 70 75 80  
 Asp Arg Arg Leu Asp Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val  
 85 90 95  
 Pro Gly Ala Phe Gly Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro  
 100 105 110  
 Glu Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys  
 115 120 125  
 Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg  
 130 135 140  
 Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn  
 145 150 155 160  
 Gly Glu Ile Arg Asp  
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 <222> (101)..(556)  
 <223> RXA00106  
  
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 Met Ile Gly Ala Ile  
 1 5  
 tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163  
 Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro  
 10 15 20  
 tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211  
 Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly  
 25 30 35  
 cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259  
 Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys  
 40 45 50  
 ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307  
 Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly  
 55 60 65  
 gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355

Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly  
 70 75 80 85  
 tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403  
 Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala  
 90 95 100  
 gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451  
 Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr  
 105 110 115  
 ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499  
 Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu  
 120 125 130  
 tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547  
 Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr  
 135 140 145  
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 Ile Lys Val  
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 Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys  
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 Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu  
 35 40 45  
 Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser  
 50 55 60  
 Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu  
 65 70 75 80  
 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala  
 85 90 95  
 Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr  
 100 105 110  
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe  
 115 120 125  
 Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr  
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 Lys Phe Gln Arg Tyr Ile Lys Val  
 145 150

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 <222> (101)..(1021)  
 <223> RXN01321

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acttagacct gacttagtgt gggaaaattt ccagggtaga atg caa cga atg acc 115
                                         Met Gln Arg Met Thr
                                         1                               5

ccg agt tct cct gaa gtt cgt aat cgt ccg agc gct gcg cct gaa gag 163
Pro Ser Ser Pro Glu Val Arg Asn Arg Pro Ser Ala Ala Pro Glu Glu
                        10                               15                               20

cgt cag ttt gtg ctc act ttt ggc tgc cct gac tcc act gga att gtg 211
Arg Gln Phe Val Leu Thr Phe Gly Cys Pro Asp Ser Thr Gly Ile Val
                        25                               30                               35

gcg aag ttg tcg tcg ttc cta gct gag cgt ggg ggt tgg att act gag 259
Ala Lys Leu Ser Ser Phe Leu Ala Glu Arg Gly Gly Trp Ile Thr Glu
                        40                               45                               50

gct gga tat ttc acg gat cct gat tcg aat tgg ttc ttt act cgt cag 307
Ala Gly Tyr Phe Thr Asp Pro Asp Ser Asn Trp Phe Phe Thr Arg Gln
                        55                               60                               65

gcg att cgc gct gag tcg att gat acc acg att gag cag ttg cgg gag 355
Ala Ile Arg Ala Glu Ser Ile Asp Thr Thr Ile Glu Gln Leu Arg Glu
                        70                               75                               80                               85

gag ttc gct ccg ctt gcg gag gag ttc ggc ccg agg gct aag tgg agt 403
Glu Phe Ala Pro Leu Ala Glu Glu Phe Gly Pro Arg Ala Lys Trp Ser
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ttc act gac act gcg cag gtg aag aag gct gtg ttg ttg gtg tct aag 451
Phe Thr Asp Thr Ala Gln Val Lys Lys Ala Val Leu Leu Val Ser Lys
                        105                               110                               115

gag ggc cac tgc ttg cac gat ttg tta ggt cgt gtg gct gag aat gat 499
Glu Gly His Cys Leu His Asp Leu Leu Gly Arg Val Ala Glu Asn Asp
                        120                               125                               130

tat ccg atg gaa gtt gtt gcg gtt gtg ggt aac cat gag aac ttg cgt 547
Tyr Pro Met Glu Val Val Ala Val Val Gly Asn His Glu Asn Leu Arg
                        135                               140                               145

tat att gcg gag aac cat aat gtt ccg ttt ttc cat gtg ccg ttt cct 595
Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe His Val Pro Phe Pro
                        150                               155                               160                               165

aag gat gcg gtt ggt aag cgg aag gcg ttt gac cag gtc gct gag att 643
Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp Gln Val Ala Glu Ile
                        170                               175                               180

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gtg aat ggt tat gat ccg gat gcg att gtt ttg gct cgt ttt atg cag 691  
 Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu Ala Arg Phe M t Gln  
                   185                                  190                                  195

att ttg ccg ccg gat ttg tgt gag atg tgg gct ggt cgt gtg ttg aat 739  
 Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn  
                   200                                  205                                  210

att cat cac agt ttc ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat 787  
 Ile His His Ser Phe Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His  
                   215                                  220                                  225

cag gcg tat agc cgt ggt gtg aag ttg att ggt gcg acc tgc cat tat 835  
 Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr  
                   230                                  235                                  240                                  245

gcg act ggg gat ctg gat gat ggt ccg atc att gag cag gat gtt att 883  
 Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile  
                                   250                                  255                                  260

cgt gtg acg cat aag gat acg ccg act gag atg cag cgt ttg ggc cgc 931  
 Arg Val Thr His Lys Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg  
                                   265                                  270                                  275

gat gcg gag aag cag gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag 979  
 Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu  
                   280                                  285                                  290

gac cgg gtg ctg gtt tac ggt aac cgc acg gtt gtc ttt gat  
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 Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val Val Phe Asp  
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<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 682

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Ala Ala Pro Glu Glu Arg Gln Phe Val Leu Thr Phe Gly Cys Pro Asp  
                   20                                  25                                  30

Ser Thr Gly Ile Val Ala Lys Leu Ser Ser Phe Leu Ala Glu Arg Gly  
                   35                                  40                                  45

Gly Trp Ile Thr Glu Ala Gly Tyr Phe Thr Asp Pro Asp Ser Asn Trp  
                   50                                  55                                  60

Phe Phe Thr Arg Gln Ala Ile Arg Ala Glu Ser Ile Asp Thr Thr Ile  
                   65                                  70                                  75                                  80

Glu Gln Leu Arg Glu Glu Phe Ala Pro Leu Ala Glu Glu Phe Gly Pro  
                   85                                  90                                  95

Arg Ala Lys Trp Ser Phe Thr Asp Thr Ala Gln Val Lys Lys Ala Val  
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 Leu Leu Val Ser Lys Glu Gly His Cys Leu His Asp Leu Leu Gly Arg  
 115 120 125  
 Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn  
 130 135 140  
 His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe  
 145 150 155 160  
 His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp  
 165 170 175  
 Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu  
 180 185 190  
 Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala  
 195 200 205  
 Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly  
 210 215 220  
 Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly  
 225 230 235 240  
 Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile  
 245 250 255  
 Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met  
 260 265 270  
 Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu  
 275 280 285  
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 Val Phe Asp  
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 Val Ala Glu Asn Asp Tyr Pro Met Glu Val  
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 gtt gcg gtt gtg ggt aac cat gag aac ttg cgt tat att gcg gag aac 100  
 Val Ala Val Val Gly Asn His Glu Asn Leu Arg Tyr Ile Ala Glu Asn  
 15 20 25

cat aat gtt ccg ttt ttc cat gtg ccg ttt cct aag gat gcg gtt ggt 148  
 His Asn Val Pro Phe Phe His Val Pro Phe Pro Lys Asp Ala Val Gly  
                   30                                  35                                  40

aag cgg aag gcg ttt gac cag gtc gct gag att gtg aat ggt tat gat 196  
 Lys Arg Lys Ala Phe Asp Gln Val Ala Glu Ile Val Asn Gly Tyr Asp  
                   45                                  50                                  55

ccg gat gcg att gtt ttg gct cgt ttt atg cag att ttg ccg ccg gat 244  
 Pro Asp Ala Ile Val Leu Ala Arg Phe Met Gln Ile Leu Pro Pro Asp  
                   60                                  65                                  70

ttg tgt gag atg tgg gct ggt cgt gtg ttg aat att cat cac agt ttc 292  
 Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn Ile His His Ser Phe  
                   75                                  80                                  85                                  90

ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat cag gcg tat agc cgt 340  
 Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg  
                                   95                                  100                                  105

ggt gtg aag ttg att ggt gcg acc tgc cat tat gcg act ggg gat ctg 388  
 Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr Ala Thr Gly Asp Leu  
                                   110                                  115                                  120

gat gat ggt ccg atc att gag cag gat gtt att cgt gtg acg cat aag 436  
 Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile Arg Val Thr His Lys  
                   125                                  130                                  135

gat acg ccg act gag atg cag cgt ttg ggc cgc gat gcg gag aag cag 484  
 Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln  
                   140                                  145                                  150

gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag gac cgg gtg ctg gtt 532  
 Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu Asp Arg Val Leu Val  
                   155                                  160                                  165                                  170

tac ggt aac cgc acg gtt gtc ttt gat taaggctttt tgcttttcga 579  
 Tyr Gly Asn Arg Thr Val Val Phe Asp  
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cgc 582

<210> 684  
 <211> 179  
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 <213> Corynebacterium glutamicum

<400> 684  
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His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe  
                   20                                  25                                  30

His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp  
                   35                                  40                                  45

Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu  
                   50                                  55                                  60

Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala  
65 70 75 80

Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly  
85 90 95

Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly  
100 105 110

Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile  
115 120 125

Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met  
130 135 140

Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu  
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Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val  
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Val Phe Asp

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<211> 975

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(952)

<223> RXA00461

<400> 685

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Val Thr Ala Ile Lys  
1 5

ctt gat gga aac tta tac cgc ggg gaa att ttc gcc gac ttg gaa cag 163  
Leu Asp Gly Asn Leu Tyr Arg Gly Glu Ile Phe Ala Asp Leu Glu Gln  
10 15 20

cgc gtt gct gcg ttg aag gag aaa ggg att gtg ccg ggg ctt gcc acc 211  
Arg Val Ala Ala Leu Lys Glu Lys Gly Ile Val Pro Gly Leu Ala Thr  
25 30 35

gtg ctg gtg ggt gat gac cca gcg agc cac tct tac gtg aag atg aag 259  
Val Leu Val Gly Asp Asp Pro Ala Ser His Ser Tyr Val Lys Met Lys  
40 45 50

cat cgt gac tgt gag cag att ggt gtg aac tcg atc cgt aag gat ctg 307  
His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser Ile Arg Lys Asp Leu  
55 60 65

cct gct gat gtc acg cag gaa gag ctt ttc gct gtc atc gat gaa ctg 355  
Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala Val Ile Asp Glu Leu

70	75	80	85	
aac aac gat gat tct tgc act ggt tac att gtg cag ctt cct ttg cct	Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val Gln Leu Pro Leu Pro	403		
	90	95	100	
aag cac ttg gac gaa aac gct gtg ctg gag cgc att gat cca gct aag	Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg Ile Asp Pro Ala Lys	451		
	105	110	115	
gat gct gat ggc ctg cac cct gta aac ctg ggc aag ctt gtg ctc aac	Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly Lys Leu Val Leu Asn	499		
	120	125	130	
gag cca gct cca ctg cca tgc acc ccg aat ggt tcc atc agc ttg ttg	Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly Ser Ile Ser Leu Leu	547		
	135	140	145	
cgt cgt ttc ggc gtt gag ctt gat ggc gcg aag gtt gtt gtc att ggc	Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys Val Val Val Ile Gly	595		
	150	155	160	165
cgt ggc gtc acc gtt ggt cgc cca att ggc ctg atg ctg acc cgc cgt	Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu Met Leu Thr Arg Arg	643		
	170	175	180	
tcc gag aac tcc acg gtt act ttg tgc cac act ggc acg aag gat ctg	Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr Gly Thr Lys Asp Leu	691		
	185	190	195	
gct gcg gag acc cgt gcg gct gac gtc atc att gct gca gct ggt cag	Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile Ala Ala Ala Gly Gln	739		
	200	205	210	
ccg cac atg ctg acc gca gac atg gtc aag cca ggc gca gcg gtg ctc	Pro His Met Leu Thr Ala Asp Met Val Lys Pro Gly Ala Ala Val Leu	787		
	215	220	225	
gat gtc ggc gtc tcc cgc aag gac ggc aag ttg ctt ggc gac gtc cac	Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu Leu Gly Asp Val His	835		
	230	235	240	245
ccc gac gtg tgg gaa gtc gcc ggc gcg gtc tca cca aac cca ggc ggc	Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser Pro Asn Pro Gly Gly	883		
	250	255	260	
gtt ggc cct ctg acc cgt gca ttc ttg gtg cac aat gtt gtc gag cgc	Val Gly Pro Leu Thr Arg Ala Phe Leu Val His Asn Val Val Glu Arg	931		
	265	270	275	
gct gaa aag ctg gct gga ctc taaaaacaca tgactaatcc cgg	Ala Glu Lys Leu Ala Gly Leu	975		
	280			

&lt;210&gt; 686

&lt;211&gt; 284

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 686



Val Thr Ala Ile Lys Leu Asp Gly Asn Leu Tyr Arg Gly Glu Ile Phe  
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 Ala Asp Leu Glu Gln Arg Val Ala Ala Leu Lys Glu Lys Gly Ile Val  
 20 25 30  
 Pro Gly Leu Ala Thr Val Leu Val Gly Asp Asp Pro Ala Ser His Ser  
 35 40 45  
 Tyr Val Lys Met Lys His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser  
 50 55 60  
 Ile Arg Lys Asp Leu Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala  
 65 70 75 80  
 Val Ile Asp Glu Leu Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val  
 85 90 95  
 Gln Leu Pro Leu Pro Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg  
 100 105 110  
 Ile Asp Pro Ala Lys Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly  
 115 120 125  
 Lys Leu Val Leu Asn Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly  
 130 135 140  
 Ser Ile Ser Leu Leu Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys  
 145 150 155 160  
 Val Val Val Ile Gly Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu  
 165 170 175  
 Met Leu Thr Arg Arg Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr  
 180 185 190  
 Gly Thr Lys Asp Leu Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile  
 195 200 205  
 Ala Ala Ala Gly Gln Pro His Met Leu Thr Ala Asp Met Val Lys Pro  
 210 215 220  
 Gly Ala Ala Val Leu Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu  
 225 230 235 240  
 Leu Gly Asp Val His Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser  
 245 250 255  
 Pro Asn Pro Gly Gly Val Gly Pro Leu Thr Arg Ala Phe Leu Val His  
 260 265 270  
 Asn Val Val Glu Arg Ala Glu Lys Leu Ala Gly Leu  
 275 280

&lt;210&gt; 687

&lt;211&gt; 711

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

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 <223> RXA01514

<400> 687

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gagggcacac aggagaatcc ggaaaatgaa ggagacaacc gtg gat aac cac gct 115
                                   Val Asp Asn His Ala
                                   1 5

gca gtt cgc gag ttc gat gag gag cgc gca aca gct gcg att cgt gag 163
Ala Val Arg Glu Phe Asp Glu Glu Arg Ala Thr Ala Ala Ile Arg Glu
                                   10 15 20

ttg ctc atc gct gtg ggt gag gat cca gat cgc gaa ggc ctg ttg gaa 211
Leu Leu Ile Ala Val Gly Glu Asp Pro Asp Arg Glu Gly Leu Leu Glu
                                   25 30 35

acc cca gct cga gtg gct agg gcg tac aag gaa act ttc gcg ggt ctg 259
Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu Thr Phe Ala Gly Leu
                                   40 45 50

cat gag gat ccc acc act gtg ctg gag aag acg ttc tct gag ggc cat 307
His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr Phe Ser Glu Gly His
                                   55 60 65

gaa gag ttg gtt ctg gtt cgt gag atc ccg att tac tcc atg tgt gag 355
Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile Tyr Ser Met Cys Glu
                                   70 75 80 85

cac cac ttg gtg ccg ttc ttt ggc gtg gcg cac att ggt tac att ccg 403
His His Leu Val Pro Phe Phe Gly Val Ala His Ile Gly Tyr Ile Pro
                                   90 95 100

ggt aag tcc ggc aag gtg act ggc ctg tcc aag ctg gcg cgt tta gcg 451
Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys Leu Ala Arg Leu Ala
                                   105 110 115

gat atg ttt gct aag cga cct cag gtt cag gag cgc ttg acc tcc caa 499
Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu Arg Leu Thr Ser Gln
                                   120 125 130

att gcg gat gct ctc gtc gaa aag ctt gat gcc cag gcc gtg gcc gtg 547
Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala Gln Ala Val Ala Val
                                   135 140 145

gtg att gaa gct gag cac ctg tgc atg gcc atg cgc gga atc cgt aag 595
Val Ile Glu Ala Glu His Leu Cys Met Ala Met Arg Gly Ile Arg Lys
                                   150 155 160 165

cct ggt gct gtg acc acg acg tct gcg gtg cgc ggc ggt ttt aag aac 643
Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg Gly Gly Phe Lys Asn
                                   170 175 180

aac gct gcc tcc cgc gct gag gtg ttc tcc ctg att cgg ggg cac 688
Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu Ile Arg Gly His
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 <213> Corynebacterium glutamicum

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 Ala Ala Ile Arg Glu Leu Leu Ile Ala Val Gly Glu Asp Pro Asp Arg  
                   20                  25                  30  
 Glu Gly Leu Leu Glu Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu  
           35                  40                  45  
 Thr Phe Ala Gly Leu His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr  
       50                  55                  60  
 Phe Ser Glu Gly His Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile  
   65                  70                  75                  80  
 Tyr Ser Met Cys Glu His His Leu Val Pro Phe Phe Gly Val Ala His  
                   85                  90                  95  
 Ile Gly Tyr Ile Pro Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys  
           100                  105                  110  
 Leu Ala Arg Leu Ala Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu  
       115                  120                  125  
 Arg Leu Thr Ser Gln Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala  
       130                  135                  140  
 Gln Ala Val Ala Val Val Ile Glu Ala Glu His Leu Cys Met Ala Met  
   145                  150                  155                  160  
 Arg Gly Ile Arg Lys Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg  
                   165                  170                  175  
 Gly Gly Phe Lys Asn Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu  
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 Ile Arg Gly His  
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 <223> RXA01516

<400> 689  
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	Met	Ala	Asp	Arg	Ile	
	1				5	
gaa ctt aaa ggc ctt gaa tgc ttc gga cac cac ggt gtg ttc gac ttt						163
Glu Leu Lys Gly Leu Glu Cys Phe Gly His His Gly Val Phe Asp Phe						
		10		15	20	
gaa aaa gag caa ggc cag ccc ttc att gtg gat gtc acc tgc tgg atg						211
Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp Val Thr Cys Trp Met						
		25		30	35	
gat ttc gat gcc gca ggt gcc agc gat gac ctt tcc gac acc gta gat						259
Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu Ser Asp Thr Val Asp						
		40		45	50	
tac ggc gcg ttg gca ttg ttg gtt gct gaa atc gtg gaa ggc cca tcc						307
Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile Val Glu Gly Pro Ser						
		55		60	65	
agg gat ttg atc gag acg gtg gcc acg gaa tct gcg gat gct gtg atg						355
Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser Ala Asp Ala Val Met						
		70		75	80	85
gct aaa ttt gat gcg ctt cat gcg gtg gaa gta acc atc cat aag ccc						403
Ala Lys Phe Asp Ala Leu His Ala Val Glu Val Thr Ile His Lys Pro						
		90		95	100	
aaa gca ccg atc cca cgt act ttt gct gac gtc gcg gtg gtt gcc cga						451
Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val Ala Val Val Ala Arg						
		105		110	115	
cgt tcc agg aaa tcc atg gct gct gga agg agc aac gcc taatgcatgc						500
Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser Asn Ala						
		120		125	130	
agttttgtcc atc						513
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<212> PRT						
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<400> 690						
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1				5		
						10
						15
Gly	Val	Phe	Asp	Phe	Glu	Lys
						20
						25
						30
Val	Thr	Cys	Trp	Met	Asp	Phe
						35
						40
						45
Ser	Asp	Thr	Val	Asp	Tyr	Gly
						50
						55
						60
Val	Glu	Gly	Pro	Ser	Arg	Asp
						65
						70
						75
						80
Ala	Asp	Ala	Val	Met	Ala	Lys
						85
						90
						95

Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val  
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Ala Val Val Ala Arg Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser  
 115 120 125

Asn Ala  
 130

<210> 691

<211> 975

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(952)

<223> RXA01515

<400> 691

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 Met Asn Val Ser Ser  
 1 5  
 ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163  
 Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr  
 10 15 20  
 gag gat tcc ttt tcg gac ggt ggc aag tac att gac gtt gat cag gcg 211  
 Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala  
 25 30 35  
 atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat 259  
 Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp  
 40 45 50  
 gtc ggc ggc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc 307  
 Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser  
 55 60 65  
 gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355  
 Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala  
 70 75 80 85  
 ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct 403  
 Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala  
 90 95 100  
 gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg 451  
 Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp Val Ser Gly Gly Leu  
 105 110 115  
 gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg 499  
 Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val  
 120 125 130  
 tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag 547

Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln  
 135 140 145  
 gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat 595  
 Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp  
 150 155 160 165  
 gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc 643  
 Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile  
 170 175 180  
 gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg 691  
 Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp  
 185 190 195  
 cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc 739  
 Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile  
 200 205 210  
 ctg gtg gga gca tcc cgg aag cga ttc ctg gct ggc gtg cgc aaa gac 787  
 Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp  
 215 220 225  
 cgt ggc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835  
 Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala  
 230 235 240 245  
 gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883  
 Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His  
 250 255 260  
 gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931  
 Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg  
 265 270 275  
 agt gga gga act cac cat ggc tgatcgtatt gaacttaaag gcc 975  
 Ser Gly Gly Thr His His Gly  
 280

&lt;210&gt; 692

&lt;211&gt; 284

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 692

Met Asn Val Ser Ser Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly  
 1 5 10 15

Ile Val Asn Val Thr Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile  
 20 25 30

Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly  
 35 40 45

Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val  
 50 55 60

Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys  
 65 70 75 80

Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala  
85 90 95

Ser Val Ala Gln Ala Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp  
100 105 110

Val Ser Gly Gly Leu Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu  
115 120 125

Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly  
130 135 140

Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val  
145 150 155 160

His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val  
165 170 175

Ala Glu Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser  
180 185 190

Arg Glu Asp Asn Trp Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser  
195 200 205

Gly Pro Phe Pro Ile Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala  
210 215 220

Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp  
225 230 235 240

Pro Ala Thr Ala Ala Val Thr Ala Val Ser Ala His Met Gly Ala Trp  
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Gly Val Arg Val His Asp Val Pro Val Ser Arg Asp Ala Val Asp Val  
260 265 270

Ala Ala Leu Trp Arg Ser Gly Gly Thr His His Gly  
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<212> DNA  
<213> Corynebacterium glutamicum

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<223> RXA02024

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Met Ser Ser Leu Pro  
1 5

gtc atc atg gcc atc gtc aat cgc acc ccg gat tct ttc tat gac aag 163  
Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys  
10 15 20

ggt gcg aca ttt gag gac acc gct gcg cta aac agg gca gcg gag gtc	211
Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn Arg Ala Ala Glu Val	
25 30 35	
att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc	259
Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly	
40 45 50	
ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac cgc gtg gtg cca	307
Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile Asp Arg Val Val Pro	
55 60 65	
atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat att tct gtt	355
Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val	
70 75 80 85	
gat acc tgg cgg gcg tcg gtg gct gat gtc gca gtg gcg cat gga gca	403
Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala	
90 95 100	
acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag	451
Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Leu Val Gln	
105 110 115	
gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggg	499
Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly	
120 125 130	
gtg att cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtg	547
Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Asp Ile Val	
135 140 145	
gcc gat gta att acg gag acc acc aaa ttg gca gag caa gct gtt cgt	595
Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala Glu Gln Ala Val Arg	
150 155 160 165	
gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc	643
Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp Pro Thr His Asp Phe	
170 175 180	
ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag	691
Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu Arg Arg Ile Asp Glu	
185 190 195	
gtg gtt gcc acg ggc tgg ccg gtg ctg atg gcc ttg agt aat aag gat	739
Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp	
200 205 210	
ttc att ggg gaa act ttg gaa agg ggc gtc gat aag cgt gtt gct ggc	787
Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp Lys Arg Val Ala Gly	
215 220 225	
acg ctt gct gcc act gcc tgg gcg gcg gcg cgc ggc gtt gcg gct ttt	835
Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg Gly Val Ala Ala Phe	
230 235 240 245	
cgc gtg cat gaa gtt gcg gaa acc	859
Arg Val His Glu Val Ala Glu Thr	
250	



<210> 694  
 <211> 253  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 694  
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 Ser Phe Tyr Asp Lys Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn  
                     20                    25                    30  
 Arg Ala Ala Glu Val Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly  
                     35                    40                    45  
 Gly Val Lys Ala Gly Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile  
                     50                    55                    60  
 Asp Arg Val Val Pro Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp  
     65                    70                    75                    80  
 Ile Asp Ile Ser Val Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala  
                     85                    90                    95  
 Val Ala His Gly Ala Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp  
                     100                    105                    110  
 His Glu Leu Val Gln Val Ala Gly Gln His Lys Val Gly Tyr Val Cys  
                     115                    120                    125  
 Ser His Thr Gly Gly Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His  
     130                    135                    140  
 Phe Asp Asp Ile Val Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala  
     145                    150                    155                    160  
 Glu Gln Ala Val Arg Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp  
                     165                    170                    175  
 Pro Thr His Asp Phe Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu  
                     180                    185                    190  
 Arg Arg Ile Asp Glu Val Val Ala Thr Gly Trp Pro Val Leu Met Ala  
     195                    200                    205  
 Leu Ser Asn Lys Asp Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp  
     210                    215                    220  
 Lys Arg Val Ala Gly Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg  
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 Gly Val Ala Ala Phe Arg Val His Glu Val Ala Glu Thr  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>

<221> CDS  
 <222> (101)..(556)  
 <223> RXA00106

<400> 695

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gctacgatcc acacccattg atccgcggca aggtcgccgt atg atc ggt gcg att 115
                                         Met Ile Gly Ala Ile
                                         1                               5

tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163
Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro
                        10                               15                               20

tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211
Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly
                        25                               30                               35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259
Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys
                        40                               45                               50

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307
Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly
                        55                               60                               65

gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355
Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
                        70                               75                               80                               85

tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
                        90                               95                               100

gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
                        105                               110                               115

ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
                        120                               125                               130

tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
                        135                               140                               145

atc aag gtt taaggagcaa acaacatgag caa 579
Ile Lys Val
150
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<210> 696  
 <211> 152  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 696

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  1                               5                               10                               15
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                   20                                  25                                  30  
 Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu  
                   35                                  40                                  45  
 Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser  
                   50                                  55                                  60  
 Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu  
                   65                                  70                                  75                                  80  
 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala  
                                   85                                  90                                  95  
 Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr  
                                   100                                  105                                  110  
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe  
                   115                                  120                                  125  
 Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr  
                   130                                  135                                  140  
 Lys Phe Gln Arg Tyr Ile Lys Val  
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<210> 697  
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 <212> DNA  
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<220>  
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 <222> (1)..(1533)  
 <223> RXA00989

<400> 697  
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 Gly Ile Gly Leu Val Ala Asn Asn Asp Gly Ile Phe Asp Ser Glu Asn  
   1                                  5                                  10                                  15  
 gat gac atc acc gta ggc gat gtc acg ttg ggc gag act gga ctg tct 96  
 Asp Asp Ile Thr Val Gly Asp Val Thr Leu Gly Glu Thr Gly Leu Ser  
                   20                                  25                                  30  
 ttg ccc atc gat ctc gcc ggt gag gta gaa gca cct gcc tcc gag gag 144  
 Leu Pro Ile Asp Leu Ala Gly Glu Val Glu Ala Pro Ala Ser Glu Glu  
                   35                                  40                                  45  
 atc acc caa gaa gat ttg ctg cgc ctt gcc cag gtg gaa gca gag ttg 192  
 Ile Thr Gln Glu Asp Leu Leu Arg Leu Ala Gln Val Glu Ala Glu Leu  
                   50                                  55                                  60  
 gat caa cgt tgg ttg gaa acc aaa att gat ccc act ttc cga cgc atg 240  
 Asp Gln Arg Trp Leu Glu Thr Lys Ile Asp Pro Thr Phe Arg Arg Met  
                   65                                  70                                  75                                  80  
 agc tac atg atg gat ctc atg ggc caa cca cag aat tcc ttc cca gca 288  
 Ser Tyr Met Met Asp Leu Met Gly Gln Pro Gln Asn Ser Phe Pro Ala

85	90	95	
att cac gtg gct ggc acc aac ggt aag acc tcc acc acc cgc atg atc Ile His Val Ala Gly Thr Asn Gly Lys Thr Ser Thr Thr Arg Met Ile 100 105 110			336
gag tcg ttg ctg cgc gca ttc cac cgc cgc acc ggc cgg acc acc agc Glu Ser Leu Leu Arg Ala Phe His Arg Arg Thr Gly Arg Thr Thr Ser 115 120 125			384
ccg cac ctg cag ctg gta acc gaa cgc atc gcg att gat ggc aag ccc Pro His Leu Gln Leu Val Thr Glu Arg Ile Ala Ile Asp Gly Lys Pro 130 135 140			432
atc cac ccg cgt gat ttc gtg cgg atc tac gaa gag att aag ccc tac Ile His Pro Arg Asp Phe Val Arg Ile Tyr Glu Glu Ile Lys Pro Tyr 145 150 155 160			480
atg gag atg acc gac gcc tgg tca gag gcc gag ggc gga ccg aag atg Met Glu Met Thr Asp Ala Trp Ser Glu Ala Glu Gly Gly Pro Lys Met 165 170 175			528
agc aag ttt gag gca ctc gtg gcc ctc gct tac gca ggt ttt gcc gac Ser Lys Phe Glu Ala Leu Val Ala Leu Ala Tyr Ala Gly Phe Ala Asp 180 185 190			576
gct cct gtt gac gtc gcc gtc gtt gag gtt ggt ctt ggc gga cgc tgg Ala Pro Val Asp Val Ala Val Val Glu Val Gly Leu Gly Gly Arg Trp 195 200 205			624
gat gcc act aac gtg atc aac gca gct gtt tcc gtg atc acc ccg gtg Asp Ala Thr Asn Val Ile Asn Ala Ala Val Ser Val Ile Thr Pro Val 210 215 220			672
ggc atg gac cac gtg gat cgc ctg ggc aac acc att ggt gaa atc gct Gly Met Asp His Val Asp Arg Leu Gly Asn Thr Ile Gly Glu Ile Ala 225 230 235 240			720
ggt gaa aag gcc ggc atc atc aag gct cgt cct gca tct gag gat ggc Gly Glu Lys Ala Gly Ile Ile Lys Ala Arg Pro Ala Ser Glu Asp Gly 245 250 255			768
acc gag cct gag ggc aac gtt gtc atc gtg ggc aag cag gag cca gaa Thr Glu Pro Glu Gly Asn Val Val Ile Val Gly Lys Gln Glu Pro Glu 260 265 270			816
gca atg aac gtg att ctg cag caa gcc gtg gac gtg gac gca gct gtt Ala Met Asn Val Ile Leu Gln Gln Ala Val Asp Val Asp Ala Ala Val 275 280 285			864
gct cgt ttg aac atg gaa ttc ggc gtg gtg gaa tcc gcc att gcc gtt Ala Arg Leu Asn Met Glu Phe Gly Val Val Glu Ser Ala Ile Ala Val 290 295 300			912
ggt gga cag cag ctc acc ctg aag ggt ttg ggc ggc gaa tac acc gac Gly Gly Gln Gln Leu Thr Leu Lys Gly Leu Gly Gly Glu Tyr Thr Asp 305 310 315 320			960
atc ttc ctc cca ctg tct ggc gcg cac caa gca gat aat gcc gcg gtt 1008 Ile Phe Leu Pro Leu Ser Gly Ala His Gln Ala Asp Asn Ala Ala Val			

325	330	335
gct ctc gca gca gtg gaa gca ttt ttc ggt gca tcc gcc gga cgc cca		
1056		
Ala Leu Ala Ala Val Glu Ala Phe Phe Gly Ala Ser Ala Gly Arg Pro		
340	345	350
ttg gat atc gac acg gtg cgc gaa ggc ttc gca caa gtt cag tcc cca		
1104		
Leu Asp Ile Asp Thr Val Arg Glu Gly Phe Ala Gln Val Gln Ser Pro		
355	360	365
ggg cgc ctc gag cgc ctg cgc tct gca cca acc gtg ttc atc gac gca		
1152		
Gly Arg Leu Glu Arg Leu Arg Ser Ala Pro Thr Val Phe Ile Asp Ala		
370	375	380
gct cac aac cca cac ggt gcc gca gca ctt ggt gca gca cta gac cgt		
1200		
Ala His Asn Pro His Gly Ala Ala Ala Leu Gly Ala Ala Leu Asp Arg		
385	390	395
400		
gac ttt gag ttc cgt cgc ctc atc ggt gtc atc gga gtg ctc tgc gac		
1248		
Asp Phe Glu Phe Arg Arg Leu Ile Gly Val Ile Gly Val Leu Cys Asp		
405	410	415
aag gat gcc cgc ggc atc ttg gaa tca ctt gag cca tac ctg cat gaa		
1296		
Lys Asp Ala Arg Gly Ile Leu Glu Ser Leu Glu Pro Tyr Leu His Glu		
420	425	430
att gtg tgc acc cag act gcc tca gag cgc gca ttg gac gca tac gat		
1344		
Ile Val Cys Thr Gln Thr Ala Ser Glu Arg Ala Leu Asp Ala Tyr Asp		
435	440	445
tta gct gaa tat gct cga gag atc tac ggc gat gag cgt gtg cac gtc		
1392		
Leu Ala Glu Tyr Ala Arg Glu Ile Tyr Gly Asp Glu Arg Val His Val		
450	455	460
caa gaa gat ctt gct ggc gcg gta gaa ctc gct att gaa cta gca gaa		
1440		
Gln Glu Asp Leu Ala Gly Ala Val Glu Leu Ala Ile Glu Leu Ala Glu		
465	470	475
480		
gac acc gat gta cag tcc gga tca ggt gtt gtg atc acc ggt tca atc		
1488		
Asp Thr Asp Val Gln Ser Gly Ser Gly Val Val Ile Thr Gly Ser Ile		
485	490	495
gtg acc gcc ggc gat gcg cgc acg ctg ttt gga aag gaa cct gca		
1533		
Val Thr Ala Gly Asp Ala Arg Thr Leu Phe Gly Lys Glu Pro Ala		
500	505	510
tgagcaagcg tgaagaatca att		
1556		

<210> 698  
 <211> 511  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 698

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 Asp Asp Ile Thr Val Gly Asp Val Thr Leu Gly Glu Thr Gly Leu Ser  
 20 25 30  
 Leu Pro Ile Asp Leu Ala Gly Glu Val Glu Ala Pro Ala Ser Glu Glu  
 35 40 45  
 Ile Thr Gln Glu Asp Leu Leu Arg Leu Ala Gln Val Glu Ala Glu Leu  
 50 55 60  
 Asp Gln Arg Trp Leu Glu Thr Lys Ile Asp Pro Thr Phe Arg Arg Met  
 65 70 75 80  
 Ser Tyr Met Met Asp Leu Met Gly Gln Pro Gln Asn Ser Phe Pro Ala  
 85 90 95  
 Ile His Val Ala Gly Thr Asn Gly Lys Thr Ser Thr Thr Arg Met Ile  
 100 105 110  
 Glu Ser Leu Leu Arg Ala Phe His Arg Arg Thr Gly Arg Thr Thr Ser  
 115 120 125  
 Pro His Leu Gln Leu Val Thr Glu Arg Ile Ala Ile Asp Gly Lys Pro  
 130 135 140  
 Ile His Pro Arg Asp Phe Val Arg Ile Tyr Glu Glu Ile Lys Pro Tyr  
 145 150 155 160  
 Met Glu Met Thr Asp Ala Trp Ser Glu Ala Glu Gly Gly Pro Lys Met  
 165 170 175  
 Ser Lys Phe Glu Ala Leu Val Ala Leu Ala Tyr Ala Gly Phe Ala Asp  
 180 185 190  
 Ala Pro Val Asp Val Ala Val Val Glu Val Gly Leu Gly Gly Arg Trp  
 195 200 205  
 Asp Ala Thr Asn Val Ile Asn Ala Ala Val Ser Val Ile Thr Pro Val  
 210 215 220  
 Gly Met Asp His Val Asp Arg Leu Gly Asn Thr Ile Gly Glu Ile Ala  
 225 230 235 240  
 Gly Glu Lys Ala Gly Ile Ile Lys Ala Arg Pro Ala Ser Glu Asp Gly  
 245 250 255  
 Thr Glu Pro Glu Gly Asn Val Val Ile Val Gly Lys Gln Glu Pro Glu  
 260 265 270  
 Ala Met Asn Val Ile Leu Gln Gln Ala Val Asp Val Asp Ala Ala Val  
 275 280 285  
 Ala Arg Leu Asn Met Glu Phe Gly Val Val Glu Ser Ala Ile Ala Val

973

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atc gag gaa ttc aaa gat gag atc gtg gcg cag tct gcg atc tac tca				211
Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln Ser Ala Ile Tyr Ser	25	30	35	
acc cca ccg tgg ggc att gag gat cag gat gaa ttc ctc aac gca gtg				259
Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu Phe Leu Asn Ala Val	40	45	50	
ctc gtt gtt gag gtt gaa gaa acc ccc atc gag ttg ctg cgc cgt ggc				307
Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly	55	60	65	
caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg				355
Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg Val Arg Lys Trp Gly	70	75	80	85
cca cgc acc ctc gat gtg gat atc gtg cag atc att aaa gat ggg gaa				403
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Glu	90	95	100	
gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct				451
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala	105	110	115	
tgg cag cgt gcc ttc gtg ttg atc cct tgg ttg gaa gca gaa cct gat				499
Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp	120	125	130	
gcc gtc ctg cac ggc acg acc att gca gaa cat gtg gat aat ctt gat				547
Ala Val Leu His Gly Thr Thr Ile Ala Glu His Val Asp Asn Leu Asp	135	140	145	
ccc aca gac att gaa ggt gtc acc aag att taaggagtcg tggctttcat				597
Pro Thr Asp Ile Glu Gly Val Thr Lys Ile	150	155		
gca				600
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Met His Ala Val Leu Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala	1	5	10	15
Leu Leu Asn Thr Val Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln	20	25	30	
Ser Ala Ile Tyr Ser Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu	35	40	45	
Phe Leu Asn Ala Val Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu	50	55	60	
Leu Leu Arg Arg Gly Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg	65	70	75	80



Val Arg Lys Trp Gly Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile  
85 90 95

Ile Lys Asp Gly Glu Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu  
100 105 110

Pro His Pro Trp Ala Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu  
115 120 125

Glu Ala Glu Pro Asp Ala Val Leu His Gly Thr Thr Ile Ala Glu His  
130 135 140

Val Asp Asn Leu Asp Pro Thr Asp Ile Glu Gly Val Thr Lys Ile  
145 150 155

<210> 701

<211> 1983

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1960)

<223> RXA00579

<400> 701

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gtgcttttct cggtgttttg tggttttgtc agaggatgtc atg cgc gtt tta att 115  
Met Arg Val Leu Ile  
1 5  
att gat aat tat gat tct ttc acg ttt aat ctc gcc acc tat gtg gaa 163  
Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu  
10 15 20  
gag gtt acg ggt cag gca cct gtg gtg gtg cct aat gat caa gaa ata 211  
Glu Val Thr Gly Gln Ala Pro Val Val Val Pro Asn Asp Gln Glu Ile  
25 30 35  
gat gag atg ctt ttc gac gcc gtc atc ctc tca cct ggc ccg ggc cac 259  
Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His  
40 45 50  
gcc ggc gtt gcg gct gat ttt ggt atc tgt gca ggc gtc att gag cgt 307  
Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala Gly Val Ile Glu Arg  
55 60 65  
gca cgc gtt ccg att ttg ggt gtg tgt tta ggc cac cag ggc att gcg 355  
Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly His Gln Gly Ile Ala  
70 75 80 85  
ttg gcc tat ggc ggt gat gtt gat ttg gcg ccc agg ccg gtc cac ggt 403  
Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro Arg Pro Val His Gly  
90 95 100  
gag gtt tcg cag atc acc cat gat ggt tca ggt tta ttt gca ggc atc 451  
Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly Leu Phe Ala Gly Ile  
105 110 115

cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc 499  
 Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg  
 120 125 130

ttg ccg gag tca ttg aaa gct aca gct acc agc gat gat ggt ttg atc 547  
 Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile  
 135 140 145

atg gca ttg gca cat gaa gtg ctt ccg cag tgg ggt gtg caa ttt cat 595  
 Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His  
 150 155 160 165

ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc 643  
 Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe  
 170 175 180

ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att 691  
 Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile  
 185 190 195

ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat 739  
 Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His  
 200 205 210

tcc tcc cat gct ttt tgg ctc gat gat gcc caa gga acc agc tat ctt 787  
 Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln Gly Thr Ser Tyr Leu  
 215 220 225

ggt gat gcc agc ggt cct ctc gca gcg aca aaa acc cat aat gtc gcc 835  
 Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly  
 230 235 240 245

gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca 883  
 Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser  
 250 255 260

gtt gcg ccc ggt caa ggt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt 931  
 Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly  
 265 270 275

tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt 979  
 Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser  
 280 285 290

ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa 1027  
 Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu  
 295 300 305

tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt 1075  
 Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe  
 310 315 320 325

gaa gaa acc atc aag aag ctg cat aat ctt gtc gcc ccg cgg ata cct 1123  
 Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro  
 330 335 340

gcg tcc gga cac ctc gct ttg cag gtt cga gat tcc aaa gat gag tat  
 1171  
 Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr  
 345 350 355

ctc gac aaa att cgc aga gcc cag gag ctg att act cgc ggc gaa tcg  
 1219  
 Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser  
 360 365 370

tat gaa atc tgc ctg acc aca aaa ctt cag ggc acc act gat gtg gcc  
 1267  
 Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala  
 375 380 385

cct ctg gct gcc tat cta gca ctg cgt ggg gcc aat ccc acc gca tat  
 1315  
 Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala Asn Pro Thr Ala Tyr  
 390 395 400 405

ggt gcg tat ctt cag ctg ggg gat acc tct att ttg agt tcc tcg ccg  
 1363  
 Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro  
 410 415 420

gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc  
 1411  
 Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro  
 425 430 435

att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa  
 1459  
 Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu  
 440 445 450

atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg  
 1507  
 Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu  
 455 460 465

atg atc gtg gat ttg gtc cgc aac gac tta gcc cgc ggc gct ttg ccc  
 1555  
 Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro  
 470 475 480 485

acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca  
 1603  
 Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr  
 490 495 500

gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt  
 1651  
 Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser  
 505 510 515

ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt  
 1699  
 Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly  
 520 525 530

gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct  
1747

Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala  
535 540 545

cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc  
1795

Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly  
550 555 560 565

gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat  
1843

Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn  
570 575 580

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg  
1891

His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro  
585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat  
1939

Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn  
600 605 610

ttg ttt ggg gtt gaa ttc cca tgacgtacct cgtgtgggac ggt  
1983

Leu Phe Gly Val Glu Phe Pro  
615 620

<210> 702

<211> 620

<212> PRT

<213> Corynebacterium glutamicum

<400> 702

Met Arg Val Leu Ile Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu  
1 5 10 15

Ala Thr Tyr Val Glu Glu Val Thr Gly Gln Ala Pro Val Val Val Pro  
20 25 30

Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser  
35 40 45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala  
50 55 60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly  
65 70 75 80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro  
85 90 95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly  
100 105 110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser  
115 120 125

Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser  
 130 135 140  
 Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp  
 145 150 155 160  
 Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln  
 165 170 175  
 Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu  
 180 185 190  
 Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu  
 195 200 205  
 Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln  
 210 215 220  
 Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys  
 225 230 235 240  
 Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp  
 245 250 255  
 Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp  
 260 265 270  
 Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala  
 275 280 285  
 Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg  
 290 295 300  
 Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu  
 305 310 315 320  
 Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val  
 325 330 335  
 Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp  
 340 345 350  
 Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile  
 355 360 365  
 Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly  
 370 375 380  
 Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala  
 385 390 395 400  
 Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile  
 405 410 415  
 Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr  
 420 425 430  
 Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala  
 435 440 445  
 Gln Glu Asp Gln Glu Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp

450	455	460
Arg Ala Glu Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala 465 470 475 480		
Arg Gly Ala Leu Pro Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val 485 490 495		
Glu Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Glu 500 505 510		
Leu Gly Pro Arg Ser Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly 515 520 525		
Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp 530 535 540		
Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr 545 550 555 560		
Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu 565 570 575		
Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu 580 585 590		
Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser 595 600 605		
Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro 610 615 620		
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 <400> 703		
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ccattgcgct tgctgctggt tccacttttg aggtcatccg atg aca cac gtt gtt 115		
	Met Thr His Val Val	
	1 5	
ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163		
Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe		
10 15 20		
gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211		
Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val		
25 30 35		
gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259		
Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly		
40 45 50		

cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307  
 Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg  
 55 60 65  
 aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355  
 Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala  
 70 75 80 85  
 ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403  
 Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His  
 90 95 100  
 ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451  
 Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro  
 105 110 115  
 gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499  
 Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile  
 120 125 130  
 cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547  
 Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val  
 135 140 145  
 gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595  
 Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile  
 150 155 160 165  
 ggt gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643  
 Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly  
 170 175 180  
 ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691  
 Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile  
 185 190 195  
 ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744  
 Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn  
 200 205

tca

747

&lt;210&gt; 704

&lt;211&gt; 208

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 704

Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn  
 1 5 10 15

Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg  
 20 25 30

Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp L u Ile  
 35 40 45

Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met  
 50 55 60

Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys  
65 70 75 80

Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro  
85 90 95

Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala  
100 105 110

Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro  
115 120 125

Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His  
130 135 140

Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr  
145 150 155 160

Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp  
165 170 175

Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro  
180 185 190

Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn  
195 200 205

<210> 705  
<211> 1266  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1243)  
<223> RXA02790

<400> 705  
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agggaaattt cccaggatga accaaatccg aaaccgccgg atg gag ccc gtc tac 115  
Met Glu Pro Val Tyr  
1 5

gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163  
Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile  
10 15 20

ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211  
Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg  
25 30 35

acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259  
Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val  
40 45 50



gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu 55 60 65	307
gaa cga gat atc gtg gcc acc aac tca gcg ttc caa aca gcg gcc agc Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser 70 75 80 85	355
aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln 90 95 100	403
gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac Glu Gln Met Asn Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp 105 110 115	451
aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp 120 125 130	499
gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile 135 140 145	547
gca gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu 150 155 160 165	595
gat ttg cag cag gtt gcc tcc acc gtg tcg cct gca gaa ttg ggt gtc Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val 170 175 180	643
cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys 185 190 195	691
cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr Val Val Asp Pro Ser 200 205 210	739
aac gac gcc cag gga atc ctc acc gat ctg atc acg cga tca gca aac Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile Thr Arg Ser Ala Asn 215 220 225	787
cat ttc caa gaa acc gac atc acg ggc cgt gca gat gcc atc gga ctt His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala Asp Ala Ile Gly Leu 230 235 240 245	835
act cca tat gag ctg gtc acc gca gca tct tta atc gag cgc gaa gca Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu Ile Glu Arg Glu Ala 250 255 260	883
cca gca gga gat ttt gat aag gtc gcc cgc gtc atc ttg aac cgt ctc Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val Ile Leu Asn Arg Leu 265 270 275	931
gcc gag cca atg cag ctg caa ttc gac tcc acc gtc aac tac ggt ctg Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr Val Asn Tyr Gly Leu 280 285 290	979

tct gaa caa gaa gta gca acc acc gac gaa gac cgt cag acc gtc acc  
1027

Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp Arg Gln Thr Val Thr  
295 300 305

cca tgg aac act tac gcc atg gac ggc ctg cca caa acc ccc atc gcc  
1075

Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro Gln Thr Pro Ile Ala  
310 315 320 325

gca gta tcc acc gaa gca ctc caa gcc atg gaa aac cct gca gaa gga  
1123

Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu Asn Pro Ala Glu Gly  
330 335 340

aac tgg ctg tac ttt gtc acc atc gac acc gat gga acc acc gtg ttc  
1171

Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp Gly Thr Thr Val Phe  
345 350 355

aac gac acc ttc gaa gag cac gaa gcc gac att gag caa gct ttg aac  
1219

Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile Glu Gln Ala Leu Asn  
360 365 370

agt ggc gtt cta gac agc aac cga taaggatcag cgaataaaat tgg  
1266

Ser Gly Val Leu Asp Ser Asn Arg  
375 380

<210> 706

<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 706

Met Glu Pro Val Tyr Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr  
1 5 10 15

Ile Ala Ser Leu Ile Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val  
20 25 30

Ala Thr Ser Asn Arg Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly  
35 40 45

Val Val Gln Leu Val Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu  
50 55 60

Gly Pro Glu Leu Glu Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe  
65 70 75 80

Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly  
85 90 95

Phe Tyr Arg Leu Gln Glu Gln Met Asn Ala Ala Ala Val Ser Ala  
100 105 110

Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly  
115 120 125

Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly  
 130 135 140

Ile Tyr Ser Gln Ile Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn  
 145 150 155 160

Cys Ile Thr Ala Glu Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro  
 165 170 175

Ala Glu Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg  
 180 185 190

Gly Thr Asp Pro Lys Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr  
 195 200 205

Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile  
 210 215 220

Thr Arg Ser Ala Asn His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala  
 225 230 235 240

Asp Ala Ile Gly Leu Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu  
 245 250 255

Ile Glu Arg Glu Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val  
 260 265 270

Ile Leu Asn Arg Leu Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr  
 275 280 285

Val Asn Tyr Gly Leu Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp  
 290 295 300

Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro  
 305 310 315 320

Gln Thr Pro Ile Ala Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu  
 325 330 335

Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp  
 340 345 350

Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile  
 355 360 365

Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg  
 370 375 380

&lt;210&gt; 707

&lt;211&gt; 579

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(556)

&lt;223&gt; RXA00106

&lt;400&gt; 707

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gctacgatcc acacccattg atccgcggca aggtcgccgt atg atc ggt gcg att 115  
Met Ile Gly Ala Ile  
1 5

tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163  
Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro  
10 15 20

tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211  
Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly  
25 30 35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259  
Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys  
40 45 50

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307  
Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly  
55 60 65

gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355  
Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly  
70 75 80 85

tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403  
Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala  
90 95 100

gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451  
Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr  
105 110 115

ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499  
Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu  
120 125 130

tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547  
Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr  
135 140 145

atc aag gtt taaggagcaa acaacatgag caa 579  
Ile Lys Val  
150

&lt;210&gt; 708

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 708

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Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys  
20 25 30

Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu  
35 40 45

Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser  
50 55 60

Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu  
65 70 75 80

Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala  
85 90 95

Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr  
100 105 110

Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe  
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Met Ser Thr Ser Val  
1 5

act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163  
Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala  
10 15 20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211  
Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu  
25 30 35

caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259  
Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly  
40 45 50

tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att 307  
Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile  
55 60 65

cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act 355  
His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr  
70 75 80 85

ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt 403  
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg

	90	95	100	
tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct				451
Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala				
	105	110	115	
gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt				499
Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly				
	120	125	130	
tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat				547
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr				
	135	140	145	
gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac				595
Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp				
	150	155	160	165
ggt ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag				643
Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln				
	170	175	180	
gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat				691
Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp				
	185	190	195	
aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc				739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr				
	200	205	210	
atg ctc atg ggt tct gag atc ggt gcc gcg ttg aca gcg ctg cag cca				787
Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro				
	215	220	225	
ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag				835
Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu				
	230	235	240	245
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg				883
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val				
	250	255	260	
tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca				931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala				
	265	270	275	
gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc				979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe				
	280	285	290	
gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca				1027
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr				
	295	300	305	
cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag				1075
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu				
	310	315	320	325

cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag  
1123

Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln  
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gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc  
1171

Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr  
345 350 355

tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc  
1219

Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg  
360 365 370

acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc  
1267

Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly  
375 380 385

gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt  
1315

Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly  
390 395 400 405

gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc  
1363

Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr  
410 415 420

gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg  
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Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu  
425 430 435

cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt  
1459

Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu  
440 445 450

gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac  
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Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp  
455 460 465

ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag  
1555

Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys  
470 475 480 485

cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag  
1603

Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln  
490 495 500

gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac  
1651

Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp  
505 510 515

gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac  
 1699  
 Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp  
 520 525 530

tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat  
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 Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp  
 535 540 545

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 Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro  
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 Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile  
 585 590 595

gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg  
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 Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro  
 600 605 610

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 Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val  
 615 620 625

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 Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln  
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 Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu  
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cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc  
 2131  
 Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile  
 665 670 675

gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag  
 2179  
 Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys  
 680 685 690

gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg  
 2227  
 Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met  
 695 700 705



aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc  
2275

Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe  
710 715 720 725

gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa  
2323

Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu  
730 735 740

ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag  
2371

Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu  
745 750 755

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat  
2419

Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp  
760 765 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac  
2467

Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp  
775 780 785

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2515

Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala  
790 795 800 805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg  
2563

Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val  
810 815 820

aag tcc acc gtg gtg atg aag caa acc atc agc gac  
2599

Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser Asp  
825 830

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<213> Corynebacterium glutamicum

<400> 710

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20 25 30

Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe  
35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp  
50 55 60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu  
65 70 75 80

992

Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val  
 405 410 415  
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala  
 420 425 430  
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val  
 435 440 445  
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser  
 450 455 460  
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile  
 465 470 475 480  
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile  
 485 490 495  
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala  
 500 505 510  
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys  
 515 520 525  
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu  
 530 535 540  
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu  
 545 550 555 560  
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile  
 565 570 575  
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe  
 580 585 590  
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser  
 595 600 605  
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val  
 610 615 620  
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu  
 625 630 635 640  
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys  
 645 650 655  
 Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu  
 660 665 670  
 Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu  
 675 680 685  
 Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp  
 690 695 700  
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tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct 451  
 Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala  
                     105                                    110                                    115

gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt 499  
 Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly  
                     120                                    125                                    130

tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat 547  
 Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr  
                     135                                    140                                    145

gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac 595  
 Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp  
                     150                                    155                                    160                                    165

ggt ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag 643  
 Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln  
                     170                                    175                                    180

gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat 691  
 Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp  
                     185                                    190                                    195

aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc 739  
 Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr  
                     200                                    205                                    210

atg ctc atg ggt tct gag atc ggt gcc gcg ttg aca gcg ctg cag cca 787  
 Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro  
                     215                                    220                                    225

ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag 835  
 Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu  
                     230                                    235                                    240                                    245

atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg 883  
 Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val  
                     250                                    255                                    260

tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca 931  
 Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala  
                     265                                    270                                    275

gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc 979  
 Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe  
                     280                                    285                                    290

gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca 1027  
 Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr  
                     295                                    300                                    305

cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag 1075  
 Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu  
                     310                                    315                                    320                                    325

cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag  
 1123  
 Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln  
 330 335 340

gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc  
 1171  
 Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr  
 345 350 355

tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc  
 1219  
 Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg  
 360 365 370

acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc  
 1267  
 Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly  
 375 380 385

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 Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly  
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 1363  
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gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg  
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 Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu  
 425 430 435

cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt  
 1459  
 Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu  
 440 445 450

gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac  
 1507  
 Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp  
 455 460 465

ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag  
 1555  
 Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys  
 470 475 480 485

cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag  
 1603  
 Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln  
 490 495 500

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 1651  
 Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp  
 505 510 515

gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac  
 1699  
 Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp  
 520 525 530

tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat  
 1747  
 Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp  
 535 540 545

ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca  
 1795  
 Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro  
 550 555 560 565

gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac  
 1843  
 Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn  
 570 575 580

cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att  
 1891  
 Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile  
 585 590 595

gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg  
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 Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro  
 600 605 610

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 1987  
 Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val  
 615 620 625

tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag  
 2035  
 Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln  
 630 635 640 645

ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa  
 2083  
 Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu  
 650 655 660

cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc  
 2131  
 Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile  
 665 670 675

gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag  
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 680 685 690

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 695 700 705

aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc  
2275

Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe  
710 715 720 725

gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa  
2323

Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu  
730 735 740

ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag  
2371

Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu  
745 750 755

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat  
2419

Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp  
760 765 770

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2467

Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp  
775 780 785

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2515

Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala  
790 795 800 805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg  
2563

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Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe  
35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp  
50 55 60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu  
65 70 75 80



Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr  
 85 90 95  
 Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val  
 100 105 110  
 Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg  
 115 120 125  
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 130 135 140  
 Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala  
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 Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val  
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 Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu  
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 Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala  
 225 230 235 240  
 Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His  
 245 250 255  
 Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu  
 260 265 270  
 Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln  
 275 280 285  
 Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly  
 290 295 300  
 Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val  
 305 310 315 320  
 Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala  
 325 330 335  
 Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val  
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 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser  
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 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu  
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 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln  
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Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val  
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 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala  
 420 425 430  
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val  
 435 440 445  
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser  
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 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile  
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 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile  
 485 490 495  
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala  
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 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys  
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 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu  
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 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile  
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 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val  
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 625 630 635 640  
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Ser	Ala	Gln	Ala	Glu	Gly	Lys	Gly	Lys	Ile	Val	Val	Ala	Thr	Val	Lys
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Gly	Asp	Val	His	Asp	Ile	Gly	Lys	Asn	Leu	Val	Asp	Ile	Ile	Leu	Ser
	770					775					780				
Asn	Asn	Gly	Tyr	Asp	Val	Val	Asn	Leu	Gly	Ile	Lys	Gln	Pro	Leu	Ser
785					790					795					800
Ala	Met	Leu	Glu	Ala	Ala	Glu	Glu	His	Lys	Ala	Asp	Val	Ile	Gly	Met
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Ser	Gly	Leu	Leu	Val	Lys	Ser	Thr	Val	Val						
		820						825							

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 Met Thr Ser Asn Phe  
 1 5  
 tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163  
 Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu  
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 Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp  
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 gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc 403  
 Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg  
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 Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met  
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acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct 499  
 Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser  
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 Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys  
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 Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr  
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gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act 787  
 Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr  
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gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc 883  
 Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly  
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 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly  
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gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979  
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg  
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 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe  
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 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala  
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 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys

520	525	530
cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc 1747		
His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser 535	540	545
ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca 1795		
Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala 550	555	560 565
ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag 1843		
Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys 570	575	580
atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccg cta cga 1891		
Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg 585	590	595
gac gtc gat aag cct gcc tac ctg cag tgg tcc gtg gac tcc ttc cgc 1939		
Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg 600	605	610
ctg gcg act gcc ggc gca ccc gac gac gtc caa atc cac acc cac atg 1987		
Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met 615	620	625
tgc tac tcc gag ttc aac gaa gtg atc tcc tcg gtc atc gcg ttg gat 2035		
Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp 630	635	640 645
gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc 2083		
Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu 650	655	660
gct gct ctg aaa tct tcc ggc ttc gag ctc ggc gtc gga cct ggt gtg 2131		
Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val 665	670	675
tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt 2179		
Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly 680	685	690
ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc 2227		
Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val 695	700	705
aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gct 2275		
Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala 710	715	720 725

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2323

Ser L u Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile  
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2358

Gly Ala Thr Ile  
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<212> PRT

<213> Corynebacterium glutamicum

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Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr  
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu  
100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu  
115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala  
130 135 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg  
145 150 155 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr  
165 170 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr  
180 185 190

Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
195 200 205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg  
210 215 220

Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr

225	230	235	240
Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly	245	250	255
Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu	260	265	270
Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly	275	280	285
Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys	290	295	300
Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu	305	310	315
Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val	325	330	335
Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu	340	345	350
Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala	355	360	365
Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro	370	375	380
Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg	385	390	395
Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr	405	410	415
Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala	420	425	430
Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met	435	440	445
Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu	450	455	460
Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr	465	470	475
Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val	485	490	495
Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn	500	505	510
Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln	515	520	525
Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr	530	535	540
Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr	545	550	555
			560



1007

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Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu	40	45	50	
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Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala	55	60	65	
atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat				355
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp	70	75	80	85
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc				403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg	90	95	100	
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Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	105	110	115	
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct				499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	120	125	130	
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Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	135	140	145	
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Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	150	155	160	165
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct				643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro	170	175	180	
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag				691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	185	190	195	
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Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	200	205	210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act				787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	215	220	225	
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc				835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	230	235	240	245
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc				883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	250	255	260	
gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt				931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	265	270	275	

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979  
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 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc  
 1027  
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg  
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 1171  
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 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu  
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 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe  
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 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu  
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 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys  
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 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala  
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 1843  
 Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys  
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&lt;210&gt; 716

&lt;211&gt; 600

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 716

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 Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser  
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Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
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 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
 65 70 75 80  
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
 85 90 95  
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu  
 100 105 110  
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu  
 115 120 125  
 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala  
 130 135 140  
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg  
 145 150 155 160  
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr  
 165 170 175  
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr  
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 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
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 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg  
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 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr  
 225 230 235 240  
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly  
 245 250 255  
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu  
 260 265 270  
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly  
 275 280 285  
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys  
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 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu  
 305 310 315 320  
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val  
 325 330 335  
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu  
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 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro

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 385                      390                      395                      400  
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr  
                     405                      410                      415  
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala  
                     420                      425                      430  
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met  
                     435                      440                      445  
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu  
                     450                      455                      460  
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr  
 465                      470                      475                      480  
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val  
                     485                      490                      495  
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn  
                     500                      505                      510  
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln  
                     515                      520                      525  
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr  
                     530                      535                      540  
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr  
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 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile  
                     565                      570                      575  
 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu  
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 Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln  
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 Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp  
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gtc caa atc cac acc cac atg tgc tac tcc gag ttc\* aac gaa gtg atc 259  
 Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile  
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 Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala  
 55 60 65

cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag 355  
 Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu  
 70 75 80 85

ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403  
 Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro  
 90 95 100

tcc gcg cag aaa gtg gac ggt ctc ctc gag gct gca ctg cag tcc gtg 451  
 Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val  
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gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct 547  
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 Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu  
 35 40 45  
 Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr  
 50 55 60

Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys  
 65 70 75 80  
 Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His  
 85 90 95  
 Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala  
 100 105 110  
 Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys  
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 <223> RXN02648

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 Met Ser Gln Asn Arg  
 1 5  
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163  
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu  
 10 15 20  
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 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe  
 25 30 35  
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 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val  
 40 45 50  
 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307  
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr  
 55 60 65  
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355  
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg  
 70 75 80 85  
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403



Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu	
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Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp	
105 110 115	
cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct	499
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser	
120 125 130	
ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga	547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly	
135 140 145	
cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg	595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu	
150 155 160 165	
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Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala	
170 175 180	
gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac	691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp	
185 190 195	
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Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu	
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Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala Pro	
215 220 225	
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Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys	
230 235 240 245	
gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca	883
Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala	
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Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly	
265 270 275	
tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att	979
Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile	
280 285 290	
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1027	
Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala	
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1075	
Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu	
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cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac  
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 Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn  
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gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc  
 1171  
 Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala  
                     345                    350                    355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg  
 1219  
 Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu  
                     360                    365                    370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta  
 1267  
 Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu  
                     375                    380                    385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac  
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<210> 720

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 720

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Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
                     20                    25                    30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
                     35                    40                    45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu  
                     50                    55                    60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn  
                     65                    70                    75                    80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg  
                     85                    90                    95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu  
                     100                    105                    110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr  
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Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn  
                     130                    135                    140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln  
 145 150 155 160  
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr  
 165 170 175  
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr  
 180 185 190  
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp  
 195 200 205  
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val  
 210 215 220  
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro  
 225 230 235 240  
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp  
 245 250 255  
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu  
 260 265 270  
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro  
 275 280 285  
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe  
 290 295 300  
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp  
 305 310 315 320  
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val  
 325 330 335  
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg  
 340 345 350  
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser  
 355 360 365  
 Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala  
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 Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu  
 385 390 395 400

Phe

&lt;210&gt; 721

&lt;211&gt; 548

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(525)

&lt;223&gt; FRXA02648

&lt;400&gt; 721

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agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96  
 Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile  
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aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144  
 Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile  
 35 40 45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192  
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly  
 50 55 60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240  
 Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe  
 65 70 75 80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288  
 Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu  
 85 90 95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336  
 Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His  
 100 105 110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384  
 Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val  
 115 120 125

cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432  
 Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp  
 130 135 140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480  
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu  
 145 150 155 160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525  
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
 165 170 175

taagctagac aacgagggtt gct 548

&lt;210&gt; 722

&lt;211&gt; 175

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 722

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Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile  
 20 25 30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile  
 35 40 45  
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly  
 50 55 60  
 Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe  
 65 70 75 80  
 Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu  
 85 90 95  
 Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His  
 100 105 110  
 Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val  
 115 120 125  
 Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp  
 130 135 140  
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 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
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 <223> FRXA02658

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 Met Ser Gln Asn Arg  
 1 5  
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163  
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu  
 10 15 20  
 gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211  
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe  
 25 30 35  
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 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val  
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 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307  
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr  
 55 60 65

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355  
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg  
 70 75 80 85

ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403  
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu  
 90 95 100

gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451  
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp  
 105 110 115

cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499  
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser  
 120 125 130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547  
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly  
 135 140 145

cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595  
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu  
 150 155 160 165

ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643  
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala  
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gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691  
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp  
 185 190 195

act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739  
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu  
 200 205 210

tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784  
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 <213> Corynebacterium glutamicum

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 Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
 35 40 45  
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu  
 50 55 60  
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn

1021

Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala  
 65 70 75 80  
 gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt 288  
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly  
 85 90 95  
 gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac 336  
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp  
 100 105 110  
 ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct 384  
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro  
 115 120 125  
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 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg  
 130 135 140  
 atc ggc gtg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc 480  
 Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser  
 145 150 155 160  
 aca gac gcg ttt gtg ctc tac cac cca gag gca aag tac ttt aac gtc 528  
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 Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro  
 35 40 45  
 Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu  
 50 55 60  
 Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala  
 65 70 75 80  
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly  
 85 90 95  
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp  
 100 105 110  
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro  
 115 120 125  
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg



130 135 140

Ile Gly Val<sup>o</sup> Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser  
 145 150 155 160

Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val  
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 Met Ser Lys Arg Glu  
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gaa tca att gag tac gga cca tta ggc aaa ggc cac gat cca tta aag 163  
 Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly His Asp Pro Leu Lys  
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gat ccc atg aag ggt atc cga ggt gtc atg gcc ggc acc tta gtg atg 211  
 Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala Gly Thr Leu Val Met  
 25 30 35

gaa gca atc acc tta ggt ctt gtt ctc acc gtg att ctg cgc gtg gac 259  
 Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val Ile Leu Arg Val Asp  
 40 45 50

gac ggc atc tac tgg acc acc ttc aac tgg gtc tat gta tca gca gtc 307  
 Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val Tyr Val Ser Ala Val  
 55 60 65

gcg atc gca cac ttt gtt gct gca ttt ctg caa agg ttt agt tgg tcc 355  
 Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln Arg Phe Ser Trp Ser  
 70 75 80 85

atc ccg atg aac atc gtg ctg cag gtt ctt gca ctt gcc ggt ttc ttt 403  
 Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala Leu Ala Gly Phe Phe  
 90 95 100

gtt cac ccc gcg atg ggc ttc gcc gcc atc atc ttc atc atc gcg tgg 451  
 Val His Pro Ala Met Gly Phe Ala Ala Ile Ile Phe Ile Ile Ala Trp  
 105 110 115

gcg tac ctg ttc tac ctg cgc tct aat ctg att gat cgc atg aaa cgc 499  
 Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile Asp Arg Met Lys Arg  
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ggg ctg ctt acc acg cag cac agc taagctttaa ggccctccgg ggc 546  
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 35 40 45  
 Ile Leu Arg Val Asp Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val  
 50 55 60  
 Tyr Val Ser Ala Val Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln  
 65 70 75 80  
 Arg Phe Ser Trp Ser Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala  
 85 90 95  
 Leu Ala Gly Phe Phe Val His Pro Ala Met Gly Phe Ala Ala Ile Ile  
 100 105 110  
 Phe Ile Ile Ala Trp Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile  
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 Asp Arg Met Lys Arg Gly Leu Leu Thr Thr Gln His Ser  
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 Val Ala Phe Met Gln  
 1 5  
 aaa acg tca gcg ggt tgg ttg atc gca acg gga ggt ttc ctc gcc gct 163  
 Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly Gly Phe Leu Ala Ala  
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Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly Ser Met Thr Ser Ile  
                   25                                  30                                  35

tcc atc acg gta tcc atc act ttt tgg ttg ttg gcc gtg gtg tgt ggt 259  
 Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu Ala Val Val Cys Gly  
                   40                                  45                                  50

ttc gca ggt gtg aag gtc caa ggt cgc ctc gat gag ggg ctg atc ggc 307  
 Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp Glu Gly Leu Ile Gly  
                   55                                  60                                  65

cag gac aaa tcc caa atg aac ccc gtg acc att gcc tat ctg gcc atg 355  
 Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile Ala Tyr Leu Ala Met  
                   70                                  75                                  80                                  85

ctg ggt cga gcg tgt gcg tgg ggt ggc gca att ttc ggc ggc gtt tat 403  
 Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile Phe Gly Gly Val Tyr  
                                   90                                  95                                  100

gtg gga att ggc agt tat gta atc cca cgc gcc ggt gag ttg tcc gca 451  
 Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala Gly Glu Leu Ser Ala  
                                   105                                  110                                  115

gca tcg aat gat ctt ccg gga gtt att gcc tgt gcg ctg ggc gga atc 499  
 Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys Ala Leu Gly Gly Ile  
                                   120                                  125                                  130

gca ctc tca gct gcc gga ctt tat tta gag cga agc tgt gag gct ccg 547  
 Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg Ser Cys Glu Ala Pro  
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cct ccc caa tct ggc gaa gcg atc agc tagattggaa ttcattgaatc 594  
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aag 597

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                   20                                  25                                  30

Ser Met Thr Ser Ile Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu  
                   35                                  40                                  45

Ala Val Val Cys Gly Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp  
                   50                                  55                                  60

Glu Gly Leu Ile Gly Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile  
                   65                                  70                                  75                                  80

Ala Tyr Leu Ala Met Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile  
                   85                                  90                                  95

Phe Gly Gly Val Tyr Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala  
 100 105 110

Gly Glu Leu Ser Ala Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys  
 115 120 125

Ala Leu Gly Gly Ile Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg  
 130 135 140

Ser Cys Glu Ala Pro Pro Pro Gln Ser Gly Glu Ala Ile Ser  
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<211> 723

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXC01942

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 Met Leu Arg Ile Gly  
 1 5

cta aca gga ggg atc ggc agc ggt aaa tct acc gtt gcc gat ctt ttg 163  
 Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr Val Ala Asp Leu Leu  
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 Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp Gln Val Ala Arg Asp  
 25 30 35

atc gtc gaa ccc gga caa ccg gca tta gca gag cta gct gaa gct ttt 259  
 Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu Leu Ala Glu Ala Phe  
 40 45 50

ggc caa gac atc tta aaa ccc gac ggc act cta gac cgc gcg gga tta 307  
 Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu Asp Arg Ala Gly Leu  
 55 60 65

gca gcc aaa gca ttt gtc agc gaa gaa caa aca gcg ctg ctc aat gcc 355  
 Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr Ala Leu Leu Asn Ala  
 70 75 80 85

att acc cac cct cgt atc gcc gaa gag tca gct cgt cga ttc aac gaa 403  
 Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala Arg Arg Phe Asn Glu  
 90 95 100

gcc gaa gat caa ggc gcc aaa gtt gcg gtt tat gac atg cct ttg ctt 451  
 Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr Asp Met Pro Leu Leu  
 105 110 115

gta gaa aaa ggc ctt gac cgc aag atg gac ctt gtc gtc gta gtt gat 499  
 Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu Val Val Val Asp

120	125	130	
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aca gag gac gac gtg cgg cgt cga atc gct tct caa gtg ccc gac gac Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser Gln Val Pro Asp Asp 150 155 160 165			595
gtc aga ctt aaa gcc gct gac atc gtt gtg gac aat aac ggc acg cta Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp Asn Asn Gly Thr Leu 170 175 180			643
gag gac ctt cat gct gaa gca agc aag ctg att gct gag att ctt agt Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile Ala Glu Ile Leu Ser 185 190 195			691
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Gln Val Ala Arg Asp Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu 35 40 45			
Leu Ala Glu Ala Phe Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu 50 55 60			
Asp Arg Ala Gly Leu Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr 65 70 75 80			
Ala Leu Leu Asn Ala Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala 85 90 95			
Arg Arg Phe Asn Glu Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr 100 105 110			
Asp Met Pro Leu Leu Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu 115 120 125			
Val Val Val Val Asp Val Asp Val Glu Glu Arg Val Arg Arg Leu Val 130 135 140			
Glu Lys Arg Gly Leu Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser 145 150 155 160			
Gln Val Pro Asp Asp Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp 165 170 175			

Asn Asn Gly Thr Leu Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile  
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Ala Glu Ile Leu Ser Arg Val Asn  
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 Val Lys Asn Leu Asp  
 1 5  
 atc gcc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa 163  
 Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly Glu Ile Gly Gln Gln  
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 aaa caa caa tcg ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc 211  
 Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser Val Ile Gly Ala Gly  
 25 30 35  
 ggc ctc ggg tca ccc gcc ctg ctc tac ctt gct ggc gct ggc gtc ggc 259  
 Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala Gly Ala Gly Val Gly  
 40 45 50  
 cac atc cac atc att gac gat gac ctc gtc gac ctc tcc aac ctc cac 307  
 His Ile His Ile Ile Asp Asp Asp Leu Val Asp Leu Ser Asn Leu His  
 55 60 65  
 cgc cag gtc att cac acc acc gct ggc gtt gga aca ccc aag gcc gag 355  
 Arg Gln Val Ile His Thr Thr Ala Gly Val Gly Thr Pro Lys Ala Glu  
 70 75 80 85  
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 Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro Ser Val Lys Val Thr  
 90 95 100  
 gtt tct gtc agg cga ctg gac tgg tca aat gca ctt tct gag ctg gca 451  
 Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala Leu Ser Glu Leu Ala  
 105 110 115  
 gat tcc gat gtg att ttg gat ggc tcc gat aac ttc gac acc cga cac 499  
 Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn Phe Asp Thr Arg His  
 120 125 130  
 ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc cac gtc tgg gca 547  
 Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile Pro His Val Trp Ala  
 135 140 145

tcc atc ctg ggt ttc gac gcc caa ctc tcc gtc ttc cac gcc ggc cac 595  
 Ser Ile Leu Gly Phe Asp Ala Gln Leu Ser Val Phe His Ala Gly His  
 150 155 160 165

ggc ccc atc tac gaa gac ctc ttc ccc acc ccg cca cca ccc gga tcc 643  
 Gly Pro Ile Tyr Glu Asp Leu Phe Pro Thr Pro Pro Pro Pro Gly Ser  
 170 175 180

gtc cca tca tgt tcc caa gca ggc gtt ttg ggt cca gtt gtc ggc gta 691  
 Val Pro Ser Cys Ser Gln Ala Gly Val Leu Gly Pro Val Val Gly Val  
 185 190 195

atg ggc tcc gcg atg gcc atg gaa gcc ctg aaa atc atc acc ggc gtg 739  
 Met Gly Ser Ala Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val  
 200 205 210

ggc aca ccc ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc 787  
 Gly Thr Pro Leu Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly  
 215 220 225

acc tgg gaa tac atc ccc gtc gtc ggt tcg ccg gag gtg ctg gaa cgg 835  
 Thr Trp Glu Tyr Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg  
 230 235 240 245

gtg ctt ggg tct gct ggt gtt tcg ggg att tct ggc ggt ttt ggt gag 883  
 Val Leu Gly Ser Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu  
 250 255 260

gtg ctc gat gtt cct cga gtt tcc gcg ctg gtt gac ggc gtt tcg ctc 931  
 Val Leu Asp Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu  
 265 270 275

atc gac gtc cgc gaa ccc tcc gaa ttc tcc gcc tac tcc atc ccc ggc 979  
 Ile Asp Val Arg Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly  
 280 285 290

gcg cac aac acc cca ctg tcc gcc atc cgc gaa ggc gcc atc cca ccc  
 1027  
 Ala His Asn Thr Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro  
 295 300 305

tcc gtt tcc gca ggt aaa gag gtt atc gtc tac tgc gca gct ggt gtc  
 1075  
 Ser Val Ser Ala Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val  
 310 315 320 325

cgc tcc gca caa gcc atc gca att tta gaa tcc gca ggc tac acc gga  
 1123  
 Arg Ser Ala Gln Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly  
 330 335 340

atg agc agc ctc gac ggc gga atc gaa ggc tgg cta gat tcc cta ggg  
 1171  
 Met Ser Ser Leu Asp Gly Gly Ile Glu Gly Trp Leu Asp Ser Leu Gly  
 345 350 355

taaaaccaag gcgttggtgcc acc  
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&lt;210&gt; 734

&lt;211&gt; 357

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 734

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 Glu Ile Gly Gln Gln Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser  
 20 25 30  
 Val Ile Gly Ala Gly Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala  
 35 40 45  
 Gly Ala Gly Val Gly His Ile His Ile Ile Asp Asp Asp Leu Val Asp  
 50 55 60  
 Leu Ser Asn Leu His Arg Gln Val Ile His Thr Thr Ala Gly Val Gly  
 65 70 75 80  
 Thr Pro Lys Ala Glu Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro  
 85 90 95  
 Ser Val Lys Val Thr Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala  
 100 105 110  
 Leu Ser Glu Leu Ala Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn  
 115 120 125  
 Phe Asp Thr Arg His Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile  
 130 135 140  
 Pro His Val Trp Ala Ser Ile Leu Gly Phe Asp Ala Gln Leu Ser Val  
 145 150 155 160  
 Phe His Ala Gly His Gly Pro Ile Tyr Glu Asp Leu Phe Pro Thr Pro  
 165 170 175  
 Pro Pro Pro Gly Ser Val Pro Ser Cys Ser Gln Ala Gly Val Leu Gly  
 180 185 190  
 Pro Val Val Gly Val Met Gly Ser Ala Met Ala Met Glu Ala Leu Lys  
 195 200 205  
 Ile Ile Thr Gly Val Gly Thr Pro Leu Ile Gly Lys Leu Gly Tyr Tyr  
 210 215 220  
 Ser Ser Leu Asp Gly Thr Trp Glu Tyr Ile Pro Val Val Gly Ser Pro  
 225 230 235 240  
 Glu Val Leu Glu Arg Val Leu Gly Ser Ala Gly Val Ser Gly Ile Ser  
 245 250 255  
 Gly Gly Phe Gly Glu Val Leu Asp Val Pro Arg Val Ser Ala Leu Val  
 260 265 270  
 Asp Gly Val Ser Leu Ile Asp Val Arg Glu Pro Ser Glu Phe Ser Ala  
 275 280 285  
 Tyr Ser Ile Pro Gly Ala His Asn Thr Pro Leu Ser Ala Ile Arg Glu  
 290 295 300



Gly Ala Ile Pro Pro Ser Val Ser Ala Gly Lys Glu Val Ile Val Tyr  
305 310 315 320

Cys Ala Ala Gly Val Arg Ser Ala Gln Ala Ile Ala Ile Leu Glu Ser  
325 330 335

Ala Gly Tyr Thr Gly Met Ser Ser Leu Asp Gly Gly Ile Glu Gly Trp  
340 345 350

Leu Asp Ser Leu Gly  
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<211> 497

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (7)..(474)

<223> FRXA02802

<400> 735

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Leu Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly Thr Trp Glu
      20             25             30

tac atc ccc gtc gtc ggt tcg ccg gag gtg ctg gaa cgg gtg ctt ggg 147
Tyr Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg Val Leu Gly
      35             40             45

tct gct ggt gtt tcg ggg att tct ggc ggt ttt ggt gag gtg ctc gat 195
Ser Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu Val Leu Asp
      50             55             60

gtt cct cga gtt tcc gcg ctg gtt gac ggc gtt tcg ctc atc gac gtc 243
Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val
      65             70             75

cgc gaa ccc tcc gaa ttc tcc gcc tac tcc atc ccc ggc gcg cac aac 291
Arg Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly Ala His Asn
      80             85             90             95

acc cca ctg tcc gcc atc cgc gaa ggc gcc atc cca ccc tcc gtt tcc 339
Thr Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro Ser Val Ser
      100            105            110

gca ggt aaa gag gtt atc gtc tac tgc gca gct ggt gtc cgc tcc gca 387
Ala Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val Arg Ser Ala
      115            120            125

caa gcc atc gca att tta gaa tcc gca ggc tac acc gga atg agc agc 435
Gln Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly Met Ser Ser
      130            135            140

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ctc gac ggc gga atc gaa ggc tgg cta gat tcc cta ggg taaaaccaag 484  
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<213> Corynebacterium glutamicum
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                20                        25                30

Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg Val Leu Gly Ser
          35                        40                45

Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu Val Leu Asp Val
  50                        55                60

Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val Arg
  65                        70                75                80

Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly Ala His Asn Thr
                85                        90                95

Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro Ser Val Ser Ala
          100                        105                110

Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val Arg Ser Ala Gln
  115                        120                125

Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly Met Ser Ser Leu
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Asp Gly Gly Ile Glu Gly Trp Leu Asp Ser Leu Gly
  145                        150                155

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<211> 535
<212> DNA
<213> Corynebacterium glutamicum
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<223> FRXA00438
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                               Val Lys Asn Leu Asp
                               1           5

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atc gcc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa 163  
 Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly Glu Ile Gly Gln Gln  
                   10                  15                  20

aaa caa caa tcg ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc 211  
 Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser Val Ile Gly Ala Gly  
                   25                  30                  35

ggc ctc ggg tca ccc gcc ctg ctc tac ctt gct ggc gct ggc gtc ggc 259  
 Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala Gly Ala Gly Val Gly  
                   40                  45                  50

cac atc cac atc att gac gat gac ctc gtc gac ctc tcc aac ctc cac 307  
 His Ile His Ile Ile Asp Asp Asp Leu Val Asp Leu Ser Asn Leu His  
                   55                  60                  65

cgc cag gtc att cac acc acc gct ggc gtt gga aca ccc aag gcc gag 355  
 Arg Gln Val Ile His Thr Thr Ala Gly Val Gly Thr Pro Lys Ala Glu  
                   70                  75                  80                  85

tcc gcg cgc gaa gca atg ctg gca ctg aac cct tcc gtt aaa gtg acg 403  
 Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro Ser Val Lys Val Thr  
                   90                  95                  100

gtt tct gtc agg cga ctg gac tgg tca aat gca ctt tct gag ctg gca 451  
 Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala Leu Ser Glu Leu Ala  
                   105                  110                  115

gat tcc gat gtg att ttg gat ggc tcc gat aac ttc gac acc cga cac 499  
 Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn Phe Asp Thr Arg His  
                   120                  125                  130

ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc 535  
 Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile Pro  
                   135                  140                  145

&lt;210&gt; 738

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 738

Val Lys Asn Leu Asp Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly  
   1                  5                  10                  15

Glu Ile Gly Gln Gln Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser  
                   20                  25                  30

Val Ile Gly Ala Gly Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala  
                   35                  40                  45

Gly Ala Gly Val Gly His Ile His Ile Ile Asp Asp Asp Leu Val Asp  
                   50                  55                  60

Leu Ser Asn Leu His Arg Gln Val Ile His Thr Thr Ala Gly Val Gly  
                   65                  70                  75                  80

Thr Pro Lys Ala Glu Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro  
                   85                  90                  95

Ser Val Lys Val Thr Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala  
 100 105 110

Leu Ser Glu Leu Ala Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn  
 115 120 125

Phe Asp Thr Arg His Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile  
 130 135 140

Pro  
 145

<210> 739

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXN00437

<400> 739

ttcatcatgg cgctgcccgg ctccacgggt gcggcgcgcg atgccaccgc tgtcctcgac 60

ccactcattg atcacatcac tggaactctg caaggccacc atg aac act gac ccc 115  
 Met Asn Thr Asp Pro  
 1 5

gct tac gtc gcc gaa caa acc ggc aaa ctc atc gac gct ttc ctc acc 163  
 Ala Tyr Val Ala Glu Gln Thr Gly Lys Leu Ile Asp Ala Phe Leu Thr  
 10 15 20

acc gac ccc ctc gaa ccg ctg ctc gac gcc gcc aaa aac ggc gtc tgc 211  
 Thr Asp Pro Leu Glu Pro Leu Leu Asp Ala Ala Lys Asn Gly Val Cys  
 25 30 35

aca gag gcg atg ggc gcg ctg gtc acc ttc gaa ggc atc gtc cgc gac 259  
 Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu Gly Ile Val Arg Asp  
 40 45 50

cac gac ggc ggc gcc cgc gtg acc tcc ctg acc tac acc gcg cat ccc 307  
 His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr Tyr Thr Ala His Pro  
 55 60 65

acc gcg ccg cag gtc ctt tct gct gtc gcg gac tcc atc gtt gaa aaa 355  
 Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp Ser Ile Val Glu Lys  
 70 75 80 85

cac ccg cgc acc cgc ctc tgg acc gcg cac cgc acc ggc gcc ttg aaa 403  
 His Pro Arg Thr Arg Leu Trp Thr Ala His Arg Thr Gly Ala Leu Lys  
 90 95 100

atc ggt gac gcc gcc ttc ctc gtc gtc gcc gcc tcc gcc cac cgc gcc 451  
 Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala Ser Ala His Arg Ala  
 105 110 115

gac gcc ttc gcc gcc tgc tcc gac ctc gcc gac gcc gtc aaa gcc cag 499  
 Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp Ala Val Lys Ala Gln  
 120 125 130

gtc ccg atc tgg aaa gag caa acg cgc ctc gac ggc tcc acc gat tgg 547  
 Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp Gly Ser Thr Asp Trp  
           135                          140                          145

gtc ggc ctg tgaaaaacct cgacatcgcc cgc 579  
 Val Gly Leu  
 150

<210> 740  
 <211> 152  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 740  
 Met Asn Thr Asp Pro Ala Tyr Val Ala Glu Gln Thr Gly Lys Leu Ile  
   1                          5                          10                          15  
 Asp Ala Phe Leu Thr Thr Asp Pro Leu Glu Pro Leu Leu Asp Ala Ala  
                           20                          25                          30  
 Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu  
                           35                          40                          45  
 Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr  
           50                          55                          60  
 Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp  
   65                          70                          75                          80  
 Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg  
                           85                          90                          95  
 Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala  
                           100                          105                          110  
 Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp  
           115                          120                          125  
 Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp  
   130                          135                          140  
 Gly Ser Thr Asp Trp Val Gly Leu  
 145                          150

<210> 741  
 <211> 383  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(360)  
 <223> FRXA00437

<400> 741  
 aaa aac ggc gtc tgc aca gag gcg atg ggc gcg ctg gtc acc ttc gaa 48  
 Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu  
   1                          5                          10                          15

ggc atc gtc cgc gac cac gac ggc ggc gcc cgc gtg acc tcc ctg acc 96  
 Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr  
                   20                  25                  30  
 tac acc gcg cat ccc acc gcg ccg cag gtc ctt tct gct gtc gcg gac 144  
 Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp  
                   35                  40                  45  
 tcc atc gtt gaa aaa cac ccg cgc acc cgc ctc tgg acc gcg cac cgc 192  
 Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg  
                   50                  55                  60  
 acc ggc gcc ttg aaa atc ggt gac gcc gcc ttc ctc gtc gtc gcc gcc 240  
 Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala  
                   65                  70                  75                  80  
 tcc gcc cac cgc gcc gac gcc ttc gcc gcc tgc tcc gac ctc gcc gac 288  
 Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp  
                   85                  90                  95  
 gcc gtc aaa gcc cag gtc ccg atc tgg aaa gag caa acg cgc ctc gac 336  
 Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp  
                   100                  105                  110  
 ggc tcc acc gat tgg gtc ggc ctg tgaaaaacct cgacatcgcc cgc 383  
 Gly Ser Thr Asp Trp Val Gly Leu  
                   115                  120

&lt;210&gt; 742

&lt;211&gt; 120

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 742

Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu  
   1                  5                  10                  15  
 Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr  
                   20                  25                  30  
 Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp  
                   35                  40                  45  
 Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg  
                   50                  55                  60  
 Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala  
                   65                  70                  75                  80  
 Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp  
                   85                  90                  95  
 Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp  
                   100                  105                  110  
 Gly Ser Thr Asp Trp Val Gly Leu  
                   115                  120

<210> 743  
 <211> 591  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(568)  
 <223> RXN00439

<400> 743

ctgccaccgc agactgtctg atcaggatcc cggcgcggac tacggtggag gaaaacgaca 60

tcgttaagat ttacccattc aactaacagg agttaattta atg agc gag ctc acc 115  
 Met Ser Glu Leu Thr  
 1 5

cac gtt cga gca gac ggt tcc gca cat atg gtg gat gtg acg ggc aaa 163  
 His Val Arg Ala Asp Gly Ser Ala His Met Val Asp Val Thr Gly Lys  
 10 15 20

aat gaa aca tcg aga act gct gtt gcc gaa ggg ttt gtg aag atg agg 211  
 Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly Phe Val Lys Met Arg  
 25 30 35

ggg gac gtc gta aag cag ctt ttt agt gct ggt ctg cct aaa ggc gac 259  
 Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly Leu Pro Lys Gly Asp  
 40 45 50

gcg cta cct gtg gcg cgg att gcg ggt atc atg ggt gcg aag aag acg 307  
 Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met Gly Ala Lys Lys Thr  
 55 60 65

ccg gac att atc cct tta tgc cac ccg ttg ccg ctg ggc aaa att act 355  
 Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro Leu Gly Lys Ile Thr  
 70 75 80 85

gtg gat ttt ttt gag ctt act gat ggt gtt cgg att gag gct tcg gtg 403  
 Val Asp Phe Phe Glu Leu Thr Asp Gly Val Arg Ile Glu Ala Ser Val  
 90 95 100

aaa acg cgt ggg gtt act ggt gtg gaa atg gag gcg ttg acg gcc gtg 451  
 Lys Thr Arg Gly Val Thr Gly Val Glu Met Glu Ala Leu Thr Ala Val  
 105 110 115

agc act gcg gcg ctg acg gta tac gac atg atc aag gct gtg gat aag 499  
 Ser Thr Ala Ala Leu Thr Val Tyr Asp Met Ile Lys Ala Val Asp Lys  
 120 125 130

atg gcc gtg att gat ggc att cgt gtg ctg tcg aaa act ggc ggt aaa 547  
 Met Ala Val Ile Asp Gly Ile Arg Val Leu Ser Lys Thr Gly Gly Lys  
 135 140 145

tct ggg gat tgg tct gtt cag tgacagctct gggtatcggt gcg 591  
 Ser Gly Asp Trp Ser Val Gln  
 150 155

<210> 744  
 <211> 156  
 <212> PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 744

Met Ser Glu Leu Thr His Val Arg Ala Asp Gly Ser Ala His Met Val  
 1 5 10 15

Asp Val Thr Gly Lys Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly  
 20 25 30

Phe Val Lys Met Arg Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly  
 35 40 45

Leu Pro Lys Gly Asp Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met  
 50 55 60

Gly Ala Lys Lys Thr Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro  
 65 70 75 80

Leu Gly Lys Ile Thr Val Asp Phe Phe Glu Leu Thr Asp Gly Val Arg  
 85 90 95

Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr Gly Val Glu Met Glu  
 100 105 110

Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr Val Tyr Asp Met Ile  
 115 120 125

Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly Ile Arg Val Leu Ser  
 130 135 140

Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val Gln  
 145 150 155

&lt;210&gt; 745

&lt;211&gt; 218

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(195)

&lt;223&gt; FRXA00439

&lt;400&gt; 745

act gat ggt gtt cgg att gag gct tcg gtg aaa acg cgt ggg gtt act 48  
 Thr Asp Gly Val Arg Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr  
 1 5 10 15

ggt gtg gaa atg gag gcg ttg acg gcc gtg agc act gcg gcg ctg acg 96  
 Gly Val Glu Met Glu Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr  
 20 25 30

gta tac gac atg atc aag gct gtg gat aag atg gcc gtg att gat ggc 144  
 Val Tyr Asp Met Ile Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly  
 35 40 45

att cgt gtg ctg tcg aaa act ggc ggt aaa tct ggg gat tgg tct gtt 192  
 Ile Arg Val Leu Ser Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val  
 50 55 60



cag tgacagctct gggtatcggt gcg

Gln

65

218

&lt;210&gt; 746

&lt;211&gt; 65

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 746

Thr Asp Gly Val Arg Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr  
 1 5 10 15

Gly Val Glu Met Glu Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr  
 20 25 30

Val Tyr Asp Met Ile Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly  
 35 40 45

Ile Arg Val Leu Ser Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val  
 50 55 60

Gln

65

&lt;210&gt; 747

&lt;211&gt; 358

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(358)

&lt;223&gt; FRXA00442

&lt;400&gt; 747

ctgccaccgc agactgtctg atcaggatcc cggcgcggac tacggtggag gaaaacgaca 60

tcgttaagat ttaccatttc aactaacagg agttaattta atg agc gag ctc acc 115  
 Met Ser Glu Leu Thr  
 1 5

cac gtt cga gca gac ggt tcc gca cat atg gtg gat gtg acg ggc aaa 163  
 His Val Arg Ala Asp Gly Ser Ala His Met Val Asp Val Thr Gly Lys  
 10 15 20

aat gaa aca tcg aga act gct gtt gcc gaa ggg ttt gtg aag atg agg 211  
 Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly Phe Val Lys Met Arg  
 25 30 35

ggg gac gtc gta aag cag ctt ttt agt gct ggt ctg cct aaa ggg gac 259  
 Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly Leu Pro Lys Gly Asp  
 40 45 50

gcg cta cct gtg gcg cgg att gcg ggt atc atg ggt gcg aag aag acg 307  
 Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met Gly Ala Lys Lys Thr  
 55 60 65

ccg gac att atc cct tta tgc cac ccg ttg ccg ctg ggc aaa att act 355

Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro Leu Gly Lys Ile Thr  
 70 75 80 85

gtg  
 Val

358

<210> 748  
 <211> 86  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 748

Met Ser Glu Leu Thr His Val Arg Ala Asp Gly Ser Ala His Met Val  
 1 5 10 15

Asp Val Thr Gly Lys Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly  
 20 25 30

Phe Val Lys Met Arg Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly  
 35 40 45

Leu Pro Lys Gly Asp Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met  
 50 55 60

Gly Ala Lys Lys Thr Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro  
 65 70 75 80

Leu Gly Lys Ile Thr Val  
 85

<210> 749  
 <211> 582  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(559)  
 <223> RXA00440

<400> 749

cggtatacga catgatcaag gctgtggata agatggccgt gattgatggc attcgtgtgc 60

tgtcgaaaac tggcggtaaa tctgggggatt ggtctgttca gtg aca gct ctg gtt 115  
 Val Thr Ala Leu Val  
 1 5

atc gtt gcg tcc act cgc gcc gct gcc ggg gtg tat gag gat cgc tct 163  
 Ile Val Ala Ser Thr Arg Ala Ala Ala Gly Val Tyr Glu Asp Arg Ser  
 10 15 20

ggc cca att ttg gtg tcg tgg ctg cgt gca aaa ggt ttt gac aca ccc 211  
 Gly Pro Ile Leu Val Ser Trp Leu Arg Ala Lys Gly Phe Asp Thr Pro  
 25 30 35

gcc ccc gtg atc gtg gcg gac gcc aac ctg ccc gca ttc ctg gac gag 259  
 Ala Pro Val Ile Val Ala Asp Ala Asn Leu Pro Ala Phe Leu Asp Glu  
 40 45 50

ctg gaa ttt ccg cag gta gta ctt att tca ggc ggc acc gga ctc acg 307  
 Leu Glu Phe Pro Gln Val Val Leu Ile Ser Gly Gly Thr Gly Leu Thr  
 55 60 65  
 cct gat gac atc acc gtg gac act tta atc ccg cgc ctc gac aaa gaa 355  
 Pro Asp Asp Ile Thr Val Val Asp Thr Leu Ile Pro Arg Leu Asp Lys Glu  
 70 75 80 85  
 atc ccc ggc atc gcc cac gct ttt tgg aat tac agc atg gac gcc gtc 403  
 Ile Pro Gly Ile Ala His Ala Phe Trp Asn Tyr Ser Met Asp Ala Val  
 90 95 100  
 ccg acc gca gta ttg tcg cgc acc gtc gcg ggc acc atc ggc ggc agt 451  
 Pro Thr Ala Val Leu Ser Arg Thr Val Ala Gly Thr Ile Gly Gly Ser  
 105 110 115  
 ttc atc atg gcg ctg ccc ggc tcc acg ggt gcg gcg cgc gat gcc acc 499  
 Phe Ile Met Ala Leu Pro Gly Ser Thr Gly Ala Ala Arg Asp Ala Thr  
 120 125 130  
 gct gtc ctc gac cca ctc att gat cac atc act gga act ctg caa ggc 547  
 Ala Val Leu Asp Pro Leu Ile Asp His Ile Thr Gly Thr Leu Gln Gly  
 135 140 145  
 cac cat gaa cac tgaccccgct tacgtcgccg aac 582  
 His His Glu His  
 150

&lt;210&gt; 750

&lt;211&gt; 153

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 750

Val Thr Ala Leu Val Ile Val Ala Ser Thr Arg Ala Ala Ala Gly Val  
 1 5 10 15  
 Tyr Glu Asp Arg Ser Gly Pro Ile Leu Val Ser Trp Leu Arg Ala Lys  
 20 25 30  
 Gly Phe Asp Thr Pro Ala Pro Val Ile Val Ala Asp Ala Asn Leu Pro  
 35 40 45  
 Ala Phe Leu Asp Glu Leu Glu Phe Pro Gln Val Val Leu Ile Ser Gly  
 50 55 60  
 Gly Thr Gly Leu Thr Pro Asp Asp Ile Thr Val Asp Thr Leu Ile Pro  
 65 70 75 80  
 Arg Leu Asp Lys Glu Ile Pro Gly Ile Ala His Ala Phe Trp Asn Tyr  
 85 90 95  
 Ser Met Asp Ala Val Pro Thr Ala Val Leu Ser Arg Thr Val Ala Gly  
 100 105 110  
 Thr Ile Gly Gly Ser Phe Ile Met Ala Leu Pro Gly Ser Thr Gly Ala  
 115 120 125  
 Ala Arg Asp Ala Thr Ala Val Leu Asp Pro Leu Ile Asp His Ile Thr

130 135 140

Gly Thr Leu Gln Gly His His Glu His  
145 150

<210> 751  
<211> 1287  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1264)  
<223> RXN00441

<400> 751  
agccttgagg gagggtgatta tgctttttggc tgtctatgtc ctcatcattg gagccatcgg 60  
agcgttacga ttgtttttcca aggtgagaaa ggtttaattg atg tct cgt tcg ccg 115  
Met Ser Arg Ser Pro  
1 5

gag caa cat ttg gca gaa att tca gcg ctg ctt ccc cca caa aag tcc 163  
Glu Gln His Leu Ala Glu Ile Ser Ala Leu Leu Pro Pro Gln Lys Ser  
10 15 20

acg ttc gtg aat ctg cgc gaa gcg ttg gga cgc cgc acg ttt tca gcg 211  
Thr Phe Val Asn Leu Arg Glu Ala Leu Gly Arg Arg Thr Phe Ser Ala  
25 30 35

gtc act gcg cag tgg gat tcg cca cgt ttt gat aat tcc caa atg gat 259  
Val Thr Ala Gln Trp Asp Ser Pro Arg Phe Asp Asn Ser Gln Met Asp  
40 45 50

ggc ttc gcg ctt ggc ccc tca cat ctt aac ggt ggc acc ttc gca gtc 307  
Gly Phe Ala Leu Gly Pro Ser His Leu Asn Gly Gly Thr Phe Ala Val  
55 60 65

ggt cca acc att ccc gct ggt cat gat cct gat cag tgg tac cca cga 355  
Gly Pro Thr Ile Pro Ala Gly His Asp Pro Asp Gln Trp Tyr Pro Arg  
70 75 80 85

ggc atc gaa aaa gac atc gcg ccg att atg acg ggt gcg cgc ctt cct 403  
Gly Ile Glu Lys Asp Ile Ala Pro Ile Met Thr Gly Ala Arg Leu Pro  
90 95 100

aaa aac acc gcc gcg atc att cct gtg gag aaa acc aca ccg gga aat 451  
Lys Asn Thr Ala Ala Ile Ile Pro Val Glu Lys Thr Thr Pro Gly Asn  
105 110 115

ttc gac gcc cca cag gta gaa atc ccc gcc acc ccg caa ggt cag ttc 499  
Phe Asp Ala Pro Gln Val Glu Ile Pro Ala Thr Pro Gln Gly Gln Phe  
120 125 130

ata cgg ttg cag ggt tcg gat att act gcc ggc gac gag atc att cca 547  
Ile Arg Leu Gln Gly Ser Asp Ile Thr Ala Gly Asp Glu Ile Ile Pro  
135 140 145

gca ggt acg gag ctt aac tcg gtg cac atc ggg gtg ttg gct agt cag 595  
Ala Gly Thr Glu Leu Asn Ser Val His Ile Gly Val Leu Ala Ser Gln

150	155	160	165	
tcg atc aag agc att gaa gtc gca gca aag cca cgt gtc ctc atc atc				643
Ser Ile Lys Ser Ile Glu Val Ala Ala Lys Pro Arg Val Leu Ile Ile	170	175	180	
acc ggc ggg tct gaa att tca gaa cag cac gga ccc gcc acg atc cct				691
Thr Gly Gly Ser Glu Ile Ser Glu Gln His Gly Pro Ala Thr Ile Pro	185	190	195	
gat gcc aac ggc cct ctg ctt cgt tcc ctg tgc gcc cgc aac aat atc				739
Asp Ala Asn Gly Pro Leu Leu Arg Ser Leu Cys Ala Arg Asn Asn Ile	200	205	210	
gag gtc atc gcg gga ctg cac acc aac gac gat cct gaa cga ctc cgc				787
Glu Val Ile Ala Gly Leu His Thr Asn Asp Asp Pro Glu Arg Leu Arg	215	220	225	
ttt gaa ctg gaa aac gcc att gac cag tat caa ccg gat gtc atc atc				835
Phe Glu Leu Glu Asn Ala Ile Asp Gln Tyr Gln Pro Asp Val Ile Ile	230	235	240	245
acc tct ggc ggt atc agc cac ggt aaa ttt gag gtg ttt agg cag atc				883
Thr Ser Gly Gly Ile Ser His Gly Lys Phe Glu Val Phe Arg Gln Ile	250	255	260	
ctc gaa ggc acc ccg aac tcc tgg ttt gga cat gtc gat cag cag cct				931
Leu Glu Gly Thr Pro Asn Ser Trp Phe Gly His Val Asp Gln Gln Pro	265	270	275	
ggc ggt cct caa ggc atc tcc act ttt gct gaa act cct gtc att tca				979
Gly Gly Pro Gln Gly Ile Ser Thr Phe Ala Glu Thr Pro Val Ile Ser	280	285	290	
ctt ccc gga aat ccg att tcc acc ttg gtg agt ttc aca ctt ttg gtc				1027
Leu Pro Gly Asn Pro Ile Ser Thr Leu Val Ser Phe Thr Leu Leu Val	295	300	305	
gcg cca gcg ctc aac cgc cag ccg ctc cgc cac ctc gat gcc cgc atc				1075
Ala Pro Ala Leu Asn Arg Gln Pro Leu Arg His Leu Asp Ala Arg Ile	310	315	320	325
acc gct ccg gtc cag ggc ttg caa gac aat cgc gag caa ttc ctt cgc				1123
Thr Ala Pro Val Gln Gly Leu Gln Asp Asn Arg Glu Gln Phe Leu Arg	330	335	340	
ggc acc atc agt tac cgc aac ggg cca cgt cct cgc cac gcc tct cct				1171
Gly Thr Ile Ser Tyr Arg Asn Gly Pro Arg Pro Arg His Ala Ser Pro	345	350	355	
ggg cac cag ttc cca cct gct ggt tca agc tgc cac cgc aga ctg tct				1219
Gly His Gln Phe Pro Pro Ala Gly Ser Ser Cys His Arg Arg Leu Ser	360	365	370	
gat cag gat ccc ggc gcg gac tac ggt gga gga aaa cga cat cgt				1264

Asp Gln Asp Pro Gly Ala Asp Tyr Gly Gly Gly Lys Arg His Arg  
 375 380 385

taagatttac ccattcaact aac  
 1287

<210> 752

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 752

Met Ser Arg Ser Pro Glu Gln His Leu Ala Glu Ile Ser Ala Leu Leu  
 1 5 10 15

Pro Pro Gln Lys Ser Thr Phe Val Asn Leu Arg Glu Ala Leu Gly Arg  
 20 25 30

Arg Thr Phe Ser Ala Val Thr Ala Gln Trp Asp Ser Pro Arg Phe Asp  
 35 40 45

Asn Ser Gln Met Asp Gly Phe Ala Leu Gly Pro Ser His Leu Asn Gly  
 50 55 60

Gly Thr Phe Ala Val Gly Pro Thr Ile Pro Ala Gly His Asp Pro Asp  
 65 70 75 80

Gln Trp Tyr Pro Arg Gly Ile Glu Lys Asp Ile Ala Pro Ile Met Thr  
 85 90 95

Gly Ala Arg Leu Pro Lys Asn Thr Ala Ala Ile Ile Pro Val Glu Lys  
 100 105 110

Thr Thr Pro Gly Asn Phe Asp Ala Pro Gln Val Glu Ile Pro Ala Thr  
 115 120 125

Pro Gln Gly Gln Phe Ile Arg Leu Gln Gly Ser Asp Ile Thr Ala Gly  
 130 135 140

Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser Val His Ile Gly  
 145 150 155 160

Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val Ala Ala Lys Pro  
 165 170 175

Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser Glu Gln His Gly  
 180 185 190

Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu Arg Ser Leu Cys  
 195 200 205

Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His Thr Asn Asp Asp  
 210 215 220

Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile Asp Gln Tyr Gln  
 225 230 235 240

Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His Gly Lys Phe Glu  
 245 250 255

Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser Trp Phe Gly His  
260 265 270

Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser Thr Phe Ala Glu  
275 280 285

Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser Thr Leu Val Ser  
290 295 300

Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln Pro Leu Arg His  
305 310 315 320

Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu Gln Asp Asn Arg  
325 330 335

Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn Gly Pro Arg Pro  
340 345 350

Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala Gly Ser Ser Cys  
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His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp Tyr Gly Gly Gly  
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Lys Arg His Arg  
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<211> 815

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(792)

<223> FRXA00441

<400> 753

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att act gcc ggc gac gag atc att cca gca ggt acg gag ctt aac tcg 96  
Ile Thr Ala Gly Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser  
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gtg cac atc ggg gtg ttg gct agt cag tcg atc aag agc att gaa gtc 144  
Val His Ile Gly Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val  
35 40 45

gca gca aag cca cgt gtc ctc atc atc acc ggc ggg tct gaa att tca 192  
Ala Ala Lys Pro Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser  
50 55 60

gaa cag cac gga ccc gcc acg atc cct gat gcc aac ggc cct ctg ctt 240  
Glu Gln His Gly Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu  
65 70 75 80

cgt tcc ctg tgc gcc cgc aac aat atc gag gtc atc gcg gga ctg cac 288  
Arg Ser Leu Cys Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His

85								90								95								
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Thr Asn Asp Asp Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile																								
100 105 110																								
gac cag tat caa ccg gat gtc atc atc acc tct ggc ggt atc agc cac	384																							
Asp Gln Tyr Gln Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His																								
115 120 125																								
ggt aaa ttt gag gtg ttt agg cag atc ctc gaa ggc acc ccg aac tcc	432																							
Gly Lys Phe Glu Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser																								
130 135 140																								
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Trp Phe Gly His Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser																								
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Thr Phe Ala Glu Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser																								
165 170 175																								
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Thr Leu Val Ser Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln																								
180 185 190																								
ccg ctc cgc cac ctc gat gcc cgc atc acc gct ccg gtc cag ggc ttg	624																							
Pro Leu Arg His Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu																								
195 200 205																								
caa gac aat cgc gag caa ttc ctt cgc ggc acc atc agt tac cgc aac	672																							
Gln Asp Asn Arg Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn																								
210 215 220																								
ggg cca cgt cct cgc cac gcc tct cct ggg cac cag ttc cca cct gct	720																							
Gly Pro Arg Pro Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala																								
225 230 235 240																								
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Gly Ser Ser Cys His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp																								
245 250 255																								
tac ggt gga gga aaa cga cat cgt taagatttac ccattcaact aac	815																							
Tyr Gly Gly Gly Lys Arg His Arg																								
260																								

&lt;210&gt; 754

&lt;211&gt; 264

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 754

Ile Pro Ala Thr Pro Gln Gly Gln Phe Ile Arg Leu Gln Gly Ser Asp
1 5 10 15

Ile Thr Ala Gly Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser
20 25 30

Val His Ile Gly Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val
35 40 45



Ala Ala Lys Pro Arg Val Leu Ile Ile Thr Gly Gly S r Glu Ile Ser  
 50 55 60  
 Glu Gln His Gly Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu  
 65 70 75 80  
 Arg Ser Leu Cys Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His  
 85 90 95  
 Thr Asn Asp Asp Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile  
 100 105 110  
 Asp Gln Tyr Gln Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His  
 115 120 125  
 Gly Lys Phe Glu Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser  
 130 135 140  
 Trp Phe Gly His Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser  
 145 150 155 160  
 Thr Phe Ala Glu Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser  
 165 170 175  
 Thr Leu Val Ser Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln  
 180 185 190  
 Pro Leu Arg His Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu  
 195 200 205  
 Gln Asp Asn Arg Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn  
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 Gly Pro Arg Pro Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala  
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 Gly Ser Ser Cys His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp  
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 Tyr Gly Gly Gly Lys Arg His Arg  
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 <222> (101)..(2335)  
 <223> RXN02085

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 Met Thr Ser Asn Phe  
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Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu	
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aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa	211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu	
25 30 35	
ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg	259
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu	
40 45 50	
tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca	307
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala	
55 60 65	
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Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp	
70 75 80 85	
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc	403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg	
90 95 100	
tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg	451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
105 110 115	
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct	499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
120 125 130	
gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc	547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	
135 140 145	
cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt	595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	
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cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct	643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro	
170 175 180	
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag	691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
185 190 195	
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc	739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
200 205 210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
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Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc	883

Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly  
 250 255 260

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931  
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly  
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979  
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg  
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc  
 1027  
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg  
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac  
 1075  
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr  
 310 315 320 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc  
 1123  
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala  
 330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta  
 1171  
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu  
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att  
 1219  
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile  
 360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc  
 1267  
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu  
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag  
 1315  
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu  
 390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc  
 1363  
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe  
 410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa  
 1411  
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu  
 425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat  
 1459  
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp  
 440 445 450

ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag 691  
 Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys  
 185 190 195

tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc 739  
 Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr  
 200 205 210

gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act 787  
 Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr  
 215 220 225

ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc 835  
 Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly  
 230 235 240 245

gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc 883  
 Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly  
 250 255 260

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931  
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly  
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979  
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg  
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc  
 1027  
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg  
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac  
 1075  
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr  
 310 315 320 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc  
 1123  
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala  
 330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta  
 1171  
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu  
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att  
 1219  
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile  
 360 365 370

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 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag  
 1315

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2083

Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu  
650 655 660

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2131

Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val  
665 670 675

tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt  
2179

Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly  
680 685 690

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2227

Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val  
695 700 705

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2275

Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala  
710 715 720 725

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc  
2323

Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile  
730 735 740

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2358

Gly Ala Thr Ile  
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<210> 756

<211> 745

<212> PRT

<213> Corynebacterium glutamicum

<400> 756

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Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr  
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu

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Pro Ala Gln Ala Met Thr Lys	Trp Phe Asp Thr Asn Tyr His Tyr Leu	
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Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg		
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Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr		
165	170	175
Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr		
180	185	190
Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu		
195	200	205
Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg		
210	215	220
Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr		
225	230	235
Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly		
245	250	255
Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu		
260	265	270
Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly		
275	280	285
Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys		
290	295	300
Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu		
305	310	315
Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val		
325	330	335
Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu		
340	345	350
Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala		
355	360	365
Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro		
370	375	380
Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg		
385	390	395
Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr		
405	410	415
Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala		
420	425	430

Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met  
 435 440 445  
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu  
 450 455 460  
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr  
 465 470 475 480  
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val  
 485 490 495  
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn  
 500 505 510  
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln  
 515 520 525  
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr  
 530 535 540  
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr  
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 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile  
 565 570 575  
 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu  
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 595 600 605  
 Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln  
 610 615 620  
 Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser  
 625 630 635 640  
 Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser  
 645 650 655  
 Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly  
 660 665 670  
 Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala  
 675 680 685  
 Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro  
 690 695 700  
 Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1900)  
 <223> FRXA02085

<400> 757

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                                         Met Thr Ser Asn Phe
                                         1                               5

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Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu
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aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa 211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu
                        25                        30                        35

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Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu
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Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp
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Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg
                        90                        95                        100

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Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met
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acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct 499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser
                        120                        125                        130

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Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu
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cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt 595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly
                        150                        155                        160                        165

cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct 643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro
                        170                        175                        180

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ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag 691  
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 Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr  
 200 205 210

gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act 787  
 Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr  
 215 220 225

ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc 835  
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 230 235 240 245

gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc 883  
 Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly  
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gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931  
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly  
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979  
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg  
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc  
 1027  
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg  
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac  
 1075  
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr  
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 1123  
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala  
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ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta  
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 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu  
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gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att  
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 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile  
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gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc  
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 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu  
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag  
 1315

Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu  
 390 395 400 405  
 aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc  
 1363  
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe  
 410 415 420  
 cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa  
 1411  
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu  
 425 430 435  
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 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp  
 440 445 450  
 ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac  
 1507  
 Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His  
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 ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc  
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 Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu  
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 gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc  
 1603  
 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser  
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 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala  
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 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys  
 520 525 530  
 cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc  
 1747  
 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser  
 535 540 545  
 ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca  
 1795  
 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala  
 550 555 560 565  
 ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag  
 1843  
 Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys  
 570 575 580  
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 1891  
 Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr

585

590

595

aga cgt cga taagcctgcc tacctgcagt ggt

1923

Arg Arg Arg

600

&lt;210&gt; 758

&lt;211&gt; 600

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 758

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly  
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20 25 30Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr  
35 40 45Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
50 55 60Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
65 70 75 80Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
85 90 95Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu  
100 105 110Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu  
115 120 125Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala  
130 135 140Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg  
145 150 155 160Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr  
165 170 175Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr  
180 185 190Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
195 200 205Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg  
210 215 220Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr  
225 230 235 240Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly  
245 250 255

Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu  
 260 265 270  
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly  
 275 280 285  
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys  
 290 295 300  
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu  
 305 310 315 320  
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val  
 325 330 335  
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu  
 340 345 350  
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala  
 355 360 365  
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro  
 370 375 380  
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg  
 385 390 395 400  
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr  
 405 410 415  
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala  
 420 425 430  
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met  
 435 440 445  
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu  
 450 455 460  
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr  
 465 470 475 480  
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val  
 485 490 495  
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn  
 500 505 510  
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln  
 515 520 525  
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr  
 530 535 540  
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr  
 545 550 555 560  
 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile  
 565 570 575

Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu  
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Leu Leu Pro Ala Thr Arg Arg Arg  
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 <213> Corynebacterium glutamicum

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 <222> (101)..(580)  
 <223> FRXA02086

<400> 759

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 aacgatctca tcgaggctgg cgccaagatc atccaggtgg atg agc ctg cga ttc 115  
   Met Ser Leu Arg Phe  
   1                                  5  
 gtg aac tgt tgc ccg cta cga gac gtc gat aag cct gcc tac ctg cag 163  
 Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln  
                                   10                                  15                                  20  
 tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc gac gac 211  
 Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp  
                                   25                                  30                                  35  
 gtc caa atc cac acc cac atg tgc tac tcc gag ttc aac gaa gtg atc 259  
 Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile  
                                   40                                  45                                  50  
 tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca 307  
 Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala  
                                   55                                  60                                  65  
 cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag 355  
 Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu  
                                   70                                  75                                  80                                  85  
 ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403  
 Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro  
                                   90                                  95                                  100  
 tcc gcg cag aaa gtg gac ggt ctc ctc gag gct gca ctg cag tcc gtg 451  
 Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val  
                                   105                                  110                                  115  
 gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt 499  
 Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg  
                                   120                                  125                                  130  
 gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct 547  
 Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala  
                                   135                                  140                                  145  
 aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgctagg 600

Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile  
 150 155 160

aac

603

&lt;210&gt; 760

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 760

Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys  
 1 5 10 15

Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala  
 20 25 30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu  
 35 40 45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr  
 50 55 60

Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys  
 65 70 75 80

Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His  
 85 90 95

Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala  
 100 105 110

Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys  
 115 120 125

Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val  
 130 135 140

Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile  
 145 150 155 160

&lt;210&gt; 761

&lt;211&gt; 1326

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (1303)

&lt;223&gt; RXN02648

&lt;400&gt; 761

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gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115  
 Met Ser Gln Asn Arg

1																5
atc	agg	acc	act	cac	gtt	ggt	tcc	ttg	ccc	cgt	acc	cca	gag	cta	ctt	163
Ile	Arg	Thr	Thr	His	Val	Gly	Ser	L u	Pro	Arg	Thr	Pro	Glu	Leu	Leu	
				10					15					20		
gat	gca	aac	atc	aag	cgt	tct	aac	ggt	gag	att	ggg	gag	gag	gaa	ttc	211
Asp	Ala	Asn	Ile	Lys	Arg	Ser	Asn	Gly	Glu	Ile	Gly	Glu	Glu	Glu	Phe	
			25					30					35			
ttc	cag	att	ctg	cag	tct	tct	gta	gat	gac	gtg	atc	aag	cgc	cag	gtt	259
Phe	Gln	Ile	Leu	Gln	Ser	Ser	Val	Asp	Asp	Val	Ile	Lys	Arg	Gln	Val	
		40					45					50				
gac	ctg	ggt	atc	gac	atc	ctt	aac	gag	ggc	gaa	tac	ggc	cac	gtc	acc	307
Asp	Leu	Gly	Ile	Asp	Ile	Leu	Asn	Glu	Gly	Glu	Tyr	Gly	His	Val	Thr	
	55					60					65					
tcc	ggt	gca	gtt	gac	ttc	ggt	gca	tgg	tgg	aac	tac	tcc	ttc	acc	cgc	355
Ser	Gly	Ala	Val	Asp	Phe	Gly	Ala	Trp	Trp	Asn	Tyr	Ser	Phe	Thr	Arg	
70					75					80					85	
ctg	ggc	gga	ctg	acc	atg	acc	gat	acc	gac	cgt	tgg	gca	agc	cag	gaa	403
Leu	Gly	Gly	Leu	Thr	Met	Thr	Asp	Thr	Asp	Arg	Trp	Ala	Ser	Gln	Glu	
				90					95					100		
gca	gtg	cgt	tcc	acc	cct	ggc	aac	atc	gag	ctg	acc	agc	ttc	tct	gat	451
Ala	Val	Arg	Ser	Thr	Pro	Gly	Asn	Ile	Glu	Leu	Thr	Ser	Phe	Ser	Asp	
			105					110					115			
cgt	cgc	gac	cgc	gca	ttg	ttc	agc	gaa	gca	tac	gag	gat	cca	gta	tct	499
Arg	Arg	Asp	Arg	Ala	Leu	Phe	Ser	Glu	Ala	Tyr	Glu	Asp	Pro	Val	Ser	
		120					125					130				
ggc	atc	ttc	acc	ggt	cgc	gct	tct	gtg	ggc	aac	cca	gag	ttc	acc	gga	547
Gly	Ile	Phe	Thr	Gly	Arg	Ala	Ser	Val	Gly	Asn	Pro	Glu	Phe	Thr	Gly	
	135					140					145					
cct	att	acc	tac	att	ggc	cag	gaa	gaa	act	cag	acg	gat	gtt	gat	ctg	595
Pro	Ile	Thr	Tyr	Ile	Gly	Gln	Glu	Glu	Thr	Gln	Thr	Asp	Val	Asp	Leu	
150					155					160					165	
ctg	aag	aag	ggc	atg	aac	gca	gcg	gga	gct	acc	gac	ggc	ttc	gtt	gca	643
Leu	Lys	Lys	Gly	Met	Asn	Ala	Ala	Gly	Ala	Thr	Asp	Gly	Phe	Val	Ala	
				170					175					180		
gca	cta	tcc	cca	gga	tct	gca	gct	cga	ttg	acc	aac	aag	ttc	tac	gac	691
Ala	Leu	Ser	Pro	Gly	Ser	Ala	Ala	Arg	Leu	Thr	Asn	Lys	Phe	Tyr	Asp	
			185					190					195			
act	gat	gaa	gaa	gtc	gtc	gca	gca	tgt	gct	gat	gcg	ctt	tcc	cag	gaa	739
Thr	Asp	Glu	Glu	Val	Val	Ala	Ala	Cys	Ala	Asp	Ala	Leu	Ser	Gln	Glu	
		200				205						210				
tac	aag	atc	atc	acc	gat	gca	ggt	ctg	acc	gtt	cag	ctc	gac	gca	ccg	787
Tyr	Lys	Ile	Ile	Thr	Asp	Ala	Gly	Leu	Thr	Val	Gln	Leu	Asp	Ala	Pro	
	215					220					225					
gac	ttg	gca	gaa	gca	tgg	gat	cag	atc	aac	cca	gag	cca	agc	gtg	aag	835
Asp	Leu	Ala	Glu	Ala	Trp	Asp	Gln	Ile	Asn	Pro	Glu	Pro	Ser	Val	Lys	
230					235					240					245	

gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca 883  
 Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala  
                   250                                  255                                  260

gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc 931  
 Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly  
                   265                                  270                                  275

tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att 979  
 Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile  
                   280                                  285                                  290

ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca  
 1027  
 Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala  
           295                                  300                                  305

tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt  
 1075  
 Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu  
 310                                  315                                  320                                  325

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac  
 1123  
 Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn  
                   330                                  335                                  340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc  
 1171  
 Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala  
                   345                                  350                                  355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg  
 1219  
 Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu  
           360                                  365                                  370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta  
 1267  
 Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu  
           375                                  380                                  385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac  
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 Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
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 1326

<210> 762

<211> 401

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 762

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Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
                   20                                  25                                  30  
 Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
                   35                                  40                                  45  
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu  
                   50                                  55                                  60  
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn  
                   65                                  70                                  75                                  80  
 Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg  
                                   85                                  90                                  95  
 Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu  
                                   100                                  105                                  110  
 Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr  
                   115                                  120                                  125  
 Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn  
                   130                                  135                                  140  
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln  
                   145                                  150                                  155                                  160  
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr  
                                   165                                  170                                  175  
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr  
                                   180                                  185                                  190  
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp  
                   195                                  200                                  205  
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val  
                   210                                  215                                  220  
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro  
                   225                                  230                                  235                                  240  
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp  
                                   245                                  250                                  255  
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu  
                                   260                                  265                                  270  
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro  
                   275                                  280                                  285  
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe  
                   290                                  295                                  300  
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp  
                   305                                  310                                  315                                  320  
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val  
                                   325                                  330                                  335  
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg

340							345					350				
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Thr	Asp	Cys	Gly	Leu	Gly	Gly	Arg	Leu	His	Ser	Gln	Ile	Ala	Trp	Ala	
	370					375					380					
Lys	Leu	Glu	Ser	Leu	Val	Glu	Gly	Ala	Arg	Ile	Ala	Ser	Lys	Glu	Leu	
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Phe																

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<211> 548
<212> DNA
<213> Corynebacterium glutamicum
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Ser	Val	Lys	Asp	Tyr	Leu	Asp	Trp	Ile	Gly	Thr	Arg	Ile	Asp	Ala	Ile	
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Asn	Ser	Ala	Val	Lys	Gly	Leu	Pro	Lys	Glu	Gln	Thr	Arg	Leu	His	Ile	
		35					40					45				
tgc	tgg	ggc	tct	tgg	cac	gga	cca	cac	gtc	act	gac	atc	cca	ttc	ggc	192
Cys	Trp	Gly	Ser	Trp	His	Gly	Pro	His	Val	Thr	Asp	Ile	Pro	Phe	Gly	
	50					55					60					
gac	atc	att	ggc	gag	atc	ctg	cgc	gca	gag	gtc	ggc	ggc	ttc	tcc	ttc	240
Asp	Ile	Ile	Gly	Glu	Ile	Leu	Arg	Ala	Glu	Val	Gly	Gly	Phe	Ser	Phe	
65					70					75					80	
gaa	ggc	gca	tct	cct	cgt	cac	gca	cac	gag	tgg	cgt	gta	tgg	gaa	gaa	288
Glu	Gly	Ala	Ser	Pro	Arg	His	Ala	His	Glu	Trp	Arg	Val	Trp	Glu	Glu	
				85					90					95		
aac	aag	ctt	cct	gaa	ggc	tct	gtt	atc	tac	cct	ggc	gtt	gtg	tct	cac	336
Asn	Lys	Leu	Pro	Glu	Gly	Ser	Val	Ile	Tyr	Pro	Gly	Val	Val	Ser	His	
			100					105					110			
tcc	atc	aac	gct	gtg	gag	cac	cca	cgc	ctg	gtt	gct	gat	cgt	atc	gtt	384
Ser	Ile	Asn	Ala	Val	Glu	His	Pro	Arg	Leu	Val	Ala	Asp	Arg	Ile	Val	
		115					120					125				
cag	ttc	gcc	aag	ctt	gtt	ggc	cct	gag	aac	gtc	att	gcg	tcc	act	gac	432
Gln	Phe	Ala	Lys	Leu	Val	Gly	Pro	Glu	Asn	Val	Ile	Ala	Ser	Thr	Asp	
	130					135					140					

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480  
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu  
 145 150 155 160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525  
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
 165 170 175

taagctagac aacgagggtt gct 548

<210> 764

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 764

Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro  
 1 5 10 15

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile  
 20 25 30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile  
 35 40 45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly  
 50 55 60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe  
 65 70 75 80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu  
 85 90 95

Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His  
 100 105 110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val  
 115 120 125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp  
 130 135 140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu  
 145 150 155 160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
 165 170 175

<210> 765

<211> 784

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(784)

<223> FRXA02658



Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala  
 215 220 225

<210> 766

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 766

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg  
 1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu  
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn  
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg  
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu  
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr  
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn  
 130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln  
 145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr  
 165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr  
 180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp  
 195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val  
 210 215 220

Gln Leu Asp Ala  
 225

<210> 767

<211> 513

<212> DNA

<213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(490)

&lt;223&gt; RXA01516

&lt;400&gt; 767

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gttgatgttg ccgcattgtg gcgaagtgga ggaactcacc atg gct gat cgt att 115  
Met Ala Asp Arg Ile  
1 5

gaa ctt aaa ggc ctt gaa tgc ttc gga cac cac ggt gtg ttc gac ttt 163  
Glu Leu Lys Gly Leu Glu Cys Phe Gly His His Gly Val Phe Asp Phe  
10 15 20

gaa aaa gag caa ggc cag ccc ttc att gtg gat gtc acc tgc tgg atg 211  
Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp Val Thr Cys Trp Met  
25 30 35

gat ttc gat gcc gca ggt gcc agc gat gac ctt tcc gac acc gta gat 259  
Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu Ser Asp Thr Val Asp  
40 45 50

tac ggc gcg ttg gca ttg ttg gtt gct gaa atc gtg gaa ggc cca tcc 307  
Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile Val Glu Gly Pro Ser  
55 60 65

agg gat ttg atc gag acg gtg gcc acg gaa tct gcg gat gct gtg atg 355  
Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser Ala Asp Ala Val Met  
70 75 80 85

gct aaa ttt gat gcg ctt cat gcg gtg gaa gta acc atc cat aag ccc 403  
Ala Lys Phe Asp Ala Leu His Ala Val Glu Val Thr Ile His Lys Pro  
90 95 100

aaa gca ccg atc cca cgt act ttt gct gac gtc gcg gtg gtt gcc cga 451  
Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val Ala Val Val Ala Arg  
105 110 115

cgt tcc agg aaa tcc atg gct gct gga agg agc aac gcc taatgcatgc 500  
Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser Asn Ala  
120 125 130

agttttgtcc atc 513

&lt;210&gt; 768

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 768

Met Ala Asp Arg Ile Glu Leu Lys Gly Leu Glu Cys Phe Gly His His  
1 5 10 15

Gly Val Phe Asp Phe Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp  
20 25 30

Val Thr Cys Trp Met Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu  
35 40 45

Ser Asp Thr Val Asp Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile  
 50 55 60

Val Glu Gly Pro Ser Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser  
 65 70 75 80

Ala Asp Ala Val Met Ala Lys Phe Asp Ala Leu His Ala Val Glu Val  
 85 90 95

Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val  
 100 105 110

Ala Val Val Ala Arg Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser  
 115 120 125

Asn Ala  
 130

<210> 769

<211> 975

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(952)

<223> RXA01515

<400> 769

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ctcccgcgct gaggtgttct ccttgattcg ggggcactaa atg aac gta tcc tct 115  
 Met Asn Val Ser Ser  
 1 5

ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163  
 Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr  
 10 15 20

gag gat tcc ttt tcg gac ggt ggc aag tac att gac gtt gat cag gcg 211  
 Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala  
 25 30 35

atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat 259  
 Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp  
 40 45 50

gtc ggc ggc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc 307  
 Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser  
 55 60 65

gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355  
 Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala  
 70 75 80 85

ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct 403  
 Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala  
 90 95 100

gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg 451  
 Ala Ala Gly Ala Gly Val Ser Met Il Asn Asp Val S r Gly Gly Leu  
 105 110 115

gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg 499  
 Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val  
 120 125 130

tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag 547  
 Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln  
 135 140 145

gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat 595  
 Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp  
 150 155 160 165

gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc 643  
 Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile  
 170 175 180

gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg 691  
 Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp  
 185 190 195

cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc 739  
 Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile  
 200 205 210

ctg gtg gga gca tcc cgg aag cga ttc ctg gct ggc gtg cgc aaa gac 787  
 Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp  
 215 220 225

cgt ggc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835  
 Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala  
 230 235 240 245

gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883  
 Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His  
 250 255 260

gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931  
 Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg  
 265 270 275

agt gga gga act cac cat ggc tgatcgtatt gaacttaaag gcc 975  
 Ser Gly Gly Thr His His Gly  
 280

&lt;210&gt; 770

&lt;211&gt; 284

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 770

Met Asn Val Ser Ser Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly  
 1 5 10 15

Ile Val Asn Val Thr Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile  
 20 25 30



Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly  
 35 40 45  
 Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val  
 50 55 60  
 Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys  
 65 70 75 80  
 Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala  
 85 90 95  
 Ser Val Ala Gln Ala Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp  
 100 105 110  
 Val Ser Gly Gly Leu Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu  
 115 120 125  
 Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly  
 130 135 140  
 Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val  
 145 150 155 160  
 His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val  
 165 170 175  
 Ala Glu Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser  
 180 185 190  
 Arg Glu Asp Asn Trp Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser  
 195 200 205  
 Gly Pro Phe Pro Ile Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala  
 210 215 220  
 Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp  
 225 230 235 240  
 Pro Ala Thr Ala Ala Val Thr Ala Val Ser Ala His Met Gly Ala Trp  
 245 250 255  
 Gly Val Arg Val His Asp Val Pro Val Ser Arg Asp Ala Val Asp Val  
 260 265 270  
 Ala Ala Leu Trp Arg Ser Gly Gly Thr His His Gly  
 275 280

&lt;210&gt; 771

&lt;211&gt; 859

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (859)

&lt;223&gt; RXA02024

&lt;400&gt; 771

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agcgcgtctc cacaattaag cagtggctac attaggtgtt atg agt tct ttg ccg	115
Met Ser Ser Leu Pro	
1 5	
gtc atc atg gcc atc gtc aat cgc acc ccg gat tct ttc tat gac aag	163
Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys	
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ggc ggc aca ttt gag gac acc gct gcg cta aac agg gca gcg gag gtc	211
Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn Arg Ala Ala Glu Val	
25 30 35	
att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc	259
Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly	
40 45 50	
ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac cgc gtg gtg cca	307
Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile Asp Arg Val Val Pro	
55 60 65	
atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat att tct gtt	355
Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val	
70 75 80 85	
gat acc tgg cgg gcg tcg gtg gct gat gtc gca gtg gcg cat gga gca	403
Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala	
90 95 100	
acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag	451
Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Leu Val Gln	
105 110 115	
gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggc	499
Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly	
120 125 130	
gtg att cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtg	547
Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Asp Ile Val	
135 140 145	
gcc gat gta att acg gag acc acc aaa ttg gca gag caa gct gtt cgt	595
Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala Glu Gln Ala Val Arg	
150 155 160 165	
gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc	643
Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp Pro Thr His Asp Phe	
170 175 180	
ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag	691
Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu Arg Arg Ile Asp Glu	
185 190 195	
gtg gtt gcc acg ggc tgg ccg gtg ctg atg gcc ttg agt aat aag gat	739
Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp	
200 205 210	
ttc att ggg gaa act ttg gaa agg ggc gtc gat aag cgt gtt gct ggc	787
Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp Lys Arg Val Ala Gly	
215 220 225	

acg ctt gct gcc act gcc tgg gcg gcg gcg cgc ggc gtt gcg gct ttt 835  
 Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg Gly Val Ala Ala Phe  
 230 235 240 245

cgc gtg cat gaa gtt gcg gaa acc 859  
 Arg Val His Glu Val Ala Glu Thr  
 250

<210> 772

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 772

Met Ser Ser Leu Pro Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp  
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Ser Phe Tyr Asp Lys Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn  
 20 25 30

Arg Ala Ala Glu Val Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly  
 35 40 45

Gly Val Lys Ala Gly Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile  
 50 55 60

Asp Arg Val Val Pro Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp  
 65 70 75 80

Ile Asp Ile Ser Val Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala  
 85 90 95

Val Ala His Gly Ala Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp  
 100 105 110

His Glu Leu Val Gln Val Ala Gly Gln His Lys Val Gly Tyr Val Cys  
 115 120 125

Ser His Thr Gly Gly Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His  
 130 135 140

Phe Asp Asp Ile Val Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala  
 145 150 155 160

Glu Gln Ala Val Arg Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp  
 165 170 175

Pro Thr His Asp Phe Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu  
 180 185 190

Arg Arg Ile Asp Glu Val Val Ala Thr Gly Trp Pro Val Leu Met Ala  
 195 200 205

Leu Ser Asn Lys Asp Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp  
 210 215 220

Lys Arg Val Ala Gly Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg  
 225 230 235 240

Gly Val Ala Ala Phe Arg Val His Glu Val Ala Glu Thr

245

250

<210> 773  
 <211> 684  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101) .. (661)  
 <223> RXA01719

<400> 773

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cgaggacggg ctgggtgatg ttgtgctggg gagaatgtaa atg aat atc atc att 115
                                         Met Asn Ile Ile Ile
                                         1           5

ctt gct ggt ggc gag ggt aaa cgc atg ggt ggg gtg gat aag gct gct 163
Leu Ala Gly Gly Glu Gly Lys Arg Met Gly Gly Val Asp Lys Ala Ala
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gtg gcg gtg gat ggt cgc acg ctg ctg gat atc ctg ctt tca cag ctg 211
Val Ala Val Asp Gly Arg Thr Leu Leu Asp Ile Leu Leu Ser Gln Leu
              25              30              35

gat cca gaa gat gac gtc gtg gtg gtt tcc ccc gcg atc atc gac gga 259
Asp Pro Glu Asp Asp Val Val Val Val Ser Pro Ala Ile Ile Asp Gly
              40              45              50

atc acg act gtc tgc gag gaa cct ccg ctt ggc ggg ccg gtc gcg gga 307
Ile Thr Thr Val Cys Glu Glu Pro Pro Leu Gly Gly Pro Val Ala Gly
              55              60              65

atc gag gca ggg ctg aat tct ttt gag cac gcc cat gaa ttc act gcg 355
Ile Glu Ala Gly Leu Asn Ser Phe Glu His Ala His Glu Phe Thr Ala
              70              75              80              85

att ctt gcc gtg gac gcg cct tat tct gca gcg atg ctg ccc cta ctt 403
Ile Leu Ala Val Asp Ala Pro Tyr Ser Ala Ala Met Leu Pro Leu Leu
              90              95              100

cag gca cag att ggc aaa gcc gat gtg gcc gta acc ctt gct gcc gat 451
Gln Ala Gln Ile Gly Lys Ala Asp Val Ala Val Thr Leu Ala Ala Asp
              105              110              115

ggc tgg gta caa ccg ttg tgc gcg ctg tgg aga agt ggc agc cta gaa 499
Gly Trp Val Gln Pro Leu Cys Ala Leu Trp Arg Ser Gly Ser Leu Glu
              120              125              130

gcg gtg att cac agc ctg ggc gag act aga aat cga ccg gca aaa gcg 547
Ala Val Ile His Ser Leu Gly Glu Thr Arg Asn Arg Pro Ala Lys Ala
              135              140              145

tta ctg aag caa gcg gga cac att gtg gaa gtg ggt ggc gat ggc act 595
Leu Leu Lys Gln Ala Gly His Ile Val Glu Val Gly Gly Asp Gly Thr
              150              155              160              165

gaa aaa gac tac gat acg gtg gct gaa ctg gag gta ttg ggc aac gta 643

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Glu Lys Asp Tyr Asp Thr Val Ala Glu Leu Glu Val Leu Gly Asn Val  
 170 175 180

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 Thr Leu Pro Lys Ala His  
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684

<210> 774  
 <211> 187  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 774  
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 20 25 30  
 Leu Leu Ser Gln Leu Asp Pro Glu Asp Asp Val Val Val Val Ser Pro  
 35 40 45  
 Ala Ile Ile Asp Gly Ile Thr Thr Val Cys Glu Glu Pro Pro Leu Gly  
 50 55 60  
 Gly Pro Val Ala Gly Ile Glu Ala Gly Leu Asn Ser Phe Glu His Ala  
 65 70 75 80  
 His Glu Phe Thr Ala Ile Leu Ala Val Asp Ala Pro Tyr Ser Ala Ala  
 85 90 95  
 Met Leu Pro Leu Leu Gln Ala Gln Ile Gly Lys Ala Asp Val Ala Val  
 100 105 110  
 Thr Leu Ala Ala Asp Gly Trp Val Gln Pro Leu Cys Ala Leu Trp Arg  
 115 120 125  
 Ser Gly Ser Leu Glu Ala Val Ile His Ser Leu Gly Glu Thr Arg Asn  
 130 135 140  
 Arg Pro Ala Lys Ala Leu Leu Lys Gln Ala Gly His Ile Val Glu Val  
 145 150 155 160  
 Gly Gly Asp Gly Thr Glu Lys Asp Tyr Asp Thr Val Ala Glu Leu Glu  
 165 170 175  
 Val Leu Gly Asn Val Thr Leu Pro Lys Ala His  
 180 185

<210> 775  
 <211> 1332  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA01720

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ctatatattt gagtgtttat tgtcgaaaaa ggggttttcaa gtg gca cag caa cgc 115  
 Val Ala Gln Gln Arg  
 1 5

agc gtc gat gac tat ctt tcc att ttg ata gac agc gtc gca ccg ctt 163  
 Ser Val Asp Asp Tyr Leu Ser Ile Leu Ile Asp Ser Val Ala Pro Leu  
 10 15 20

ccg cca gta aaa acc cct atc ctc ggc gcg cat ccg tta agt cac ctt 211  
 Pro Pro Val Lys Thr Pro Ile Leu Gly Ala His Pro Leu Ser His Leu  
 25 30 35

gca gag gat gtt gtc gcg aca att cct atc ccg aaa ttt act aat tct 259  
 Ala Glu Asp Val Val Ala Thr Ile Pro Ile Pro Lys Phe Thr Asn Ser  
 40 45 50

gct gtt gat ggt tac gcc att ttg aaa gaa gac atc cat ggc agc ggg 307  
 Ala Val Asp Gly Tyr Ala Ile Leu Lys Glu Asp Ile His Gly Ser Gly  
 55 60 65

ccg tgg aca ttt ctt gtg ggc ggt gat act ccg gcg ggt tct gcg ccg 355  
 Pro Trp Thr Phe Leu Val Gly Gly Asp Thr Pro Ala Gly Ser Ala Pro  
 70 75 80 85

gcg agc att aat aat gga aaa gcc atc cgt gtg atg aca ggt gga ccc 403  
 Ala Ser Ile Asn Asn Gly Lys Ala Ile Arg Val Met Thr Gly Gly Pro  
 90 95 100

gtc cca tcc acc aac aag gac atg atc gtg gtt cca gtg gag ctc acc 451  
 Val Pro Ser Thr Asn Lys Asp Met Ile Val Val Pro Val Glu Leu Thr  
 105 110 115

aat gct ccg gtg gat cac tcg ctt cct aca gaa atc acg atc aat gag 499  
 Asn Ala Pro Val Asp His Ser Leu Pro Thr Glu Ile Thr Ile Asn Glu  
 120 125 130

cta cca ggt gag agg aat aat att cgc cat gct ggt gag cat ctt aaa 547  
 Leu Pro Gly Glu Arg Asn Asn Ile Arg His Ala Gly Glu His Leu Lys  
 135 140 145

gaa ggc gaa att gcg gtt gct gcg ggg acg gca ttt gat gcg ggt act 595  
 Glu Gly Glu Ile Ala Val Ala Ala Gly Thr Ala Phe Asp Ala Gly Thr  
 150 155 160 165

gtg tcg acg gtg att tca gtt ggc cat gac act gta aaa gcc cat cct 643  
 Val Ser Thr Val Ile Ser Val Gly His Asp Thr Val Lys Ala His Pro  
 170 175 180

tgc cct cgg gtt gcg gtg atc act acc ggt gat gag cta aac cag gga 691  
 Cys Pro Arg Val Ala Val Ile Thr Thr Gly Asp Glu Leu Asn Gln Gly  
 185 190 195

aat ccc tgg ggt atc cct aat tcc aat ggg ccg atg ctg gtt gcg gag 739  
 Asn Pro Trp Gly Ile Pro Asn Ser Asn Gly Pro Met Leu Val Ala Glu  
 200 205 210

cta aaa cgc gtg ggg att aag gat ccg cag cat ttc cat tcc gat gat 787  
 Leu Lys Arg Val Gly Ile Lys Asp Pro Gln His Phe His Ser Asp Asp

215	220	225	
tct gag act gca ttg agg gag acg ctc gat aag cct gca gag gtt gcg			835
Ser Glu Thr Ala Leu Arg Glu Thr Leu Asp Lys Pro Ala Glu Val Ala			
230	235	240	245
gat gtg atc atc act gtg ggt ggg atc tcg gcg ggc gcg ttc gat gtg			883
Asp Val Ile Ile Thr Val Gly Gly Ile Ser Ala Gly Ala Phe Asp Val			
	250	255	260
gtc aaa gcc gtg gga act aag act ggt ggt ttt gaa ttc ttc ccc att			931
Val Lys Ala Val Gly Thr Lys Thr Gly Gly Phe Glu Phe Phe Pro Ile			
	265	270	275
gcg atg aag ccg ggt aaa ccg caa ggt cat ggg cag tgg ggc gac gca			979
Ala Met Lys Pro Gly Lys Pro Gln Gly His Gly Gln Trp Gly Asp Ala			
	280	285	290
aaa gtg gtg tgt ctg ccg gga aac ccg gtg gcg gcg tgg gtt agt ttt			
1027			
Lys Val Val Cys Leu Pro Gly Asn Pro Val Ala Ala Trp Val Ser Phe			
	295	300	305
agg ctc ttt gtt gtt ccg gta att gag aga tta ggg ggt gga aag agg			
1075			
Arg Leu Phe Val Val Pro Val Ile Glu Arg Leu Gly Gly Gly Lys Arg			
310	315	320	325
ctg gcg tcg ata agc gaa ctc cct gtg gtg gcg ctg cgc tcg aac cgg			
1123			
Leu Ala Ser Ile Ser Glu Leu Pro Val Val Ala Leu Arg Ser Asn Arg			
	330	335	340
gcg ctg aag gcg cgg gag ggc ccc gta ttg gcg ata ccg gtg gcg att			
1171			
Ala Leu Lys Ala Arg Glu Gly Pro Val Leu Ala Ile Pro Val Ala Ile			
	345	350	355
gat tgg gag aaa aga atg gca aat tct cag gca cat cga tcc cat atg			
1219			
Asp Trp Glu Lys Arg Met Ala Asn Ser Gln Ala His Arg Ser His Met			
	360	365	370
gtc ggt gca ctg gct gga agt ggc ggt att gca ctg gtg act tcg tcg			
1267			
Val Gly Ala Leu Ala Gly Ser Gly Gly Ile Ala Leu Val Thr Ser Ser			
	375	380	385
att gcc gag gac ggt ctg gtt gat gtt gtg ctg ggg aga atg			
1309			
Ile Ala Glu Asp Gly Leu Val Asp Val Val Leu Gly Arg Met			
390	395	400	
taaataaata tcatcattct tgc			
1332			

&lt;210&gt; 776

&lt;211&gt; 403

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 776

Val	Ala	Gln	Gln	Arg	Ser	Val	Asp	Asp	Tyr	Leu	Ser	Ile	Leu	Ile	Asp
1				5					10					15	
Ser	Val	Ala	Pro	Leu	Pro	Pro	Val	Lys	Thr	Pro	Ile	Leu	Gly	Ala	His
			20					25					30		
Pro	Leu	Ser	His	Leu	Ala	Glu	Asp	Val	Val	Ala	Thr	Ile	Pro	Ile	Pro
		35					40					45			
Lys	Phe	Thr	Asn	Ser	Ala	Val	Asp	Gly	Tyr	Ala	Ile	Leu	Lys	Glu	Asp
	50					55					60				
Ile	His	Gly	Ser	Gly	Pro	Trp	Thr	Phe	Leu	Val	Gly	Gly	Asp	Thr	Pro
65					70					75					80
Ala	Gly	Ser	Ala	Pro	Ala	Ser	Ile	Asn	Asn	Gly	Lys	Ala	Ile	Arg	Val
				85					90					95	
Met	Thr	Gly	Gly	Pro	Val	Pro	Ser	Thr	Asn	Lys	Asp	Met	Ile	Val	Val
			100					105					110		
Pro	Val	Glu	Leu	Thr	Asn	Ala	Pro	Val	Asp	His	Ser	Leu	Pro	Thr	Glu
		115					120					125			
Ile	Thr	Ile	Asn	Glu	Leu	Pro	Gly	Glu	Arg	Asn	Asn	Ile	Arg	His	Ala
	130					135					140				
Gly	Glu	His	Leu	Lys	Glu	Gly	Glu	Ile	Ala	Val	Ala	Ala	Gly	Thr	Ala
145					150					155					160
Phe	Asp	Ala	Gly	Thr	Val	Ser	Thr	Val	Ile	Ser	Val	Gly	His	Asp	Thr
				165					170					175	
Val	Lys	Ala	His	Pro	Cys	Pro	Arg	Val	Ala	Val	Ile	Thr	Thr	Gly	Asp
			180					185					190		
Glu	Leu	Asn	Gln	Gly	Asn	Pro	Trp	Gly	Ile	Pro	Asn	Ser	Asn	Gly	Pro
		195					200					205			
Met	Leu	Val	Ala	Glu	Leu	Lys	Arg	Val	Gly	Ile	Lys	Asp	Pro	Gln	His
	210					215					220				
Phe	His	Ser	Asp	Asp	Ser	Glu	Thr	Ala	Leu	Arg	Glu	Thr	Leu	Asp	Lys
225					230					235					240
Pro	Ala	Glu	Val	Ala	Asp	Val	Ile	Ile	Thr	Val	Gly	Gly	Ile	Ser	Ala
				245					250					255	
Gly	Ala	Phe	Asp	Val	Val	Lys	Ala	Val	Gly	Thr	Lys	Thr	Gly	Gly	Phe
			260					265					270		
Glu	Phe	Phe	Pro	Ile	Ala	Met	Lys	Pro	Gly	Lys	Pro	Gln	Gly	His	Gly
		275					280					285			
Gln	Trp	Gly	Asp	Ala	Lys	Val	Val	Cys	Leu	Pro	Gly	Asn	Pro	Val	Ala
	290					295					300				
Ala	Trp	Val	Ser	Phe	Arg	Leu	Phe	Val	Val	Pro	Val	Ile	Glu	Arg	Leu
305					310					315					320



Gly Gly Gly Lys Arg Leu Ala Ser Ile Ser Glu Leu Pro Val Val Ala  
                   325                  330                  335  
 Leu Arg Ser Asn Arg Ala Leu Lys Ala Arg Glu Gly Pro Val Leu Ala  
                   340                  345                  350  
 Ile Pro Val Ala Ile Asp Trp Glu Lys Arg Met Ala Asn Ser Gln Ala  
                   355                  360                  365  
 His Arg Ser His Met Val Gly Ala Leu Ala Gly Ser Gly Gly Ile Ala  
                   370                  375                  380  
 Leu Val Thr Ser Ser Ile Ala Glu Asp Gly Leu Val Asp Val Val Leu  
 385                  390                  395                  400  
 Gly Arg Met

<210> 777  
 <211> 1237  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (2)..(1207)  
 <223> RXS03223

<400> 777  
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 Pro Glu Pro Val Arg Ile Ala Ile Ala Glu Ala Leu Gly Leu Met Cys  
   1                  5                  10                  15  
 gcg gaa gag gtt caa gct agt cgt gct ttg ccg ggt ttc gcg caa gca 97  
 Ala Glu Glu Val Gln Ala Ser Arg Ala Leu Pro Gly Phe Ala Gln Ala  
                   20                  25                  30  
 gcg att gat ggt tat gcg gtt cga gca gtc gat gtc ggc ggc gag aag 145  
 Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys  
                   35                  40                  45  
 tcg ttt agc cag caa ctg ccg gtt gct cct ccg gaa aaa tcc ctg ccc 193  
 Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro  
                   50                  55                  60  
 gtg gtg ggt gaa gta gct gcg ggt tct cag cag ccg ttg cgc ctg cag 241  
 Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln  
   65                  70                  75                  80  
 cct aaa caa gca gtc atg gtc cac acc ggt gcg cca ctg ccg atg ctt 289  
 Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu  
                   85                  90                  95  
 gcg gat gcg gtg ctg ccc atg gcg tgg tca gat cgt ggc cgc aaa cga 337  
 Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg  
                   100                  105                  110  
 gta acc gcg cag cga cct gtg cgc tct ggc gag ttt gtg cgc aaa gaa 385  
 Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu

115	120	125	
ggc gat gac atc caa ccg gga gac atc gca gtc agc gcc ggc gcg gtc Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val 130 135 140			433
tta ggc cct gcc caa att ggt ttg ctc gca gct gtt ggt cgc tcc aaa Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys 145 150 155 160			481
gtg ttg gtg tac cca cgc cca cgc atg tcg gtt atc tcc gta ggc gct Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala 165 170 175			529
gaa ctt gtt gat att gat cgc cag cca ggc ctc ggc cag gtt tat gat Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp 180 185 190			577
gtc aat tcc tat tct ctg gct gcc gcc ggt agg gaa gcg ggc gca gat Val Asn Ser Tyr Ser Leu Ala Ala Ala Gly Arg Glu Ala Gly Ala Asp 195 200 205			625
gtg tac cgc tac ggc att gct gcc ggt gaa cct cgt cgc atc aaa gag Val Tyr Arg Tyr Gly Ile Ala Ala Gly Glu Pro Arg Arg Ile Lys Glu 210 215 220			673
atc att gaa tcc cag atg ctg cgc tcg gaa atc atc gtc atc acc gga Ile Ile Glu Ser Gln Met Leu Arg Ser Glu Ile Ile Val Ile Thr Gly 225 230 235 240			721
gct gtt ggc ggt gct ggt tca gct ggc gtg cgc cag gtt ctc aac gag Ala Val Gly Gly Ala Gly Ser Ala Gly Val Arg Gln Val Leu Asn Glu 245 250 255			769
cta ggc gat atc gac acc gaa cgc gtc gca atg cac ccc ggt tct gtc Leu Gly Asp Ile Asp Thr Glu Arg Val Ala Met His Pro Gly Ser Val 260 265 270			817
caa gga ttc ggt ctg ctc ggc gag aac aag att cca tgc ttc ctt ctg Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu 275 280 285			865
cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg 290 295 300			913
ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val 305 310 315 320			961
gtt cga gct cga gcg ctc aac cac gtt gtg tct gtg gcg ggt cga aaa 1009 Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys 325 330 335			
ggc ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac 1057 Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr 340 345 350			

ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg  
 1105  
 Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu  
           355                                  360                                  365

gca gga ttg tcc gaa gca aac ggt atg atc cgc att cca gaa gat gtc  
 1153  
 Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val  
           370                                  375                                  380

aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa  
 1201  
 Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln  
 385                                  390                                  395                                  400

ggt cga tagttcgatg cgtaatgcac cgtcagggtcc  
 1237  
 Gly Arg

<210> 778  
 <211> 402  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 778  
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 Ala Glu Glu Val Gln Ala Ser Arg Ala Leu Pro Gly Phe Ala Gln Ala  
                                   20                                  25                                  30  
 Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys  
                                   35                                  40                                  45  
 Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro  
           50                                  55                                  60  
 Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln  
   65                                  70                                  75                                  80  
 Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu  
                                   85                                  90                                  95  
 Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg  
                                   100                                  105                                  110  
 Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu  
                                   115                                  120                                  125  
 Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val  
           130                                  135                                  140  
 Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys  
   145                                  150                                  155                                  160  
 Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala  
                                   165                                  170                                  175  
 Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp

180						185						190					
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp		
195						200						205					
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu		
210						215						220					
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly		
225						230						235					
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu		
245						250						255					
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val		
260						265						270					
Gln	Gly	Phe	Gly	Leu	Leu	Gly	Glu	Asn	Lys	Ile	Pro	Cys	Phe	Leu	Leu		
275						280						285					
Pro	Ser	Asn	Pro	Val	Ala	Ser	Leu	Val	Ile	Phe	Glu	Thr	Phe	Val	Arg		
290						295						300					
Pro	Val	Val	Arg	Met	Ser	Leu	Gly	Lys	Ser	Asn	Ala	Ala	Arg	Arg	Val		
305						310						315					
Val	Arg	Ala	Arg	Ala	Leu	Asn	His	Val	Val	Ser	Val	Ala	Gly	Arg	Lys		
325						330						335					
Gly	Phe	Ile	Arg	Ser	Arg	Leu	Met	Arg	Asp	Ala	Glu	Thr	Gln	Asp	Tyr		
340						345						350					
Leu	Val	Glu	Ala	Leu	Gly	Gly	Ala	Thr	Gly	Ala	Pro	Ser	His	Leu	Leu		
355						360						365					
Ala	Gly	Leu	Ser	Glu	Ala	Asn	Gly	Met	Ile	Arg	Ile	Pro	Glu	Asp	Val		
370						375						380					
Thr	Glu	Ile	Arg	Pro	Gly	Asp	Val	Val	Asp	Val	Ile	Phe	Leu	Ala	Gln		
385						390						395					

Gly Arg

&lt;210&gt; 779

&lt;211&gt; 1229

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1206)

&lt;223&gt; FRXA01970

&lt;400&gt; 779

cca	gag	cca	gtg	cgt	att	gct	att	gca	gag	gca	ctg	ggt	ttg	atg	tgc	48
Pro	Glu	Pro	Val	Arg	Ile	Ala	Ile	Ala	Glu	Ala	Leu	Gly	Leu	Met	Cys	
1				5				10					15			

gcg	gaa	gag	gtt	caa	gct	agt	cgt	gct	ttg	ccg	ggt	ttc	gcg	caa	gca	96
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Ala	Glu	Glu	Val	Gln	Ala	Ser	Arg	Ala	Leu	Pro	Gly	Phe	Ala	Gln	Ala		
			20					25					30				
gcg	att	gat	ggt	tat	gcg	ggt	cga	gca	gtc	gat	gtc	ggc	ggc	gag	aag	144	
Ala	Ile	Asp	Gly	Tyr	Ala	Val	Arg	Ala	Val	Asp	Val	Gly	Gly	Glu	Lys		
		35					40					45					
tcg	ttt	agc	cag	caa	ctg	ccg	ggt	gct	cct	ccg	gaa	aaa	tcc	ctg	ccc	192	
Ser	Phe	Ser	Gln	Gln	Leu	Pro	Val	Ala	Pro	Pro	Glu	Lys	Ser	Leu	Pro		
	50					55					60						
gtg	gtg	ggt	gaa	gta	gct	gcg	ggt	tct	cag	cag	ccg	ttg	cgc	ctg	cag	240	
Val	Val	Gly	Glu	Val	Ala	Ala	Gly	Ser	Gln	Gln	Pro	Leu	Arg	Leu	Gln		
65					70				75						80		
cct	aaa	caa	gca	gtc	atg	gtc	cac	acc	ggt	gcg	cca	ctg	ccg	atg	ctt	288	
Pro	Lys	Gln	Ala	Val	Met	Val	His	Thr	Gly	Ala	Pro	Leu	Pro	Met	Leu		
			85					90						95			
gcg	gat	gcg	gtg	ctg	ccc	atg	gcg	tgg	tca	gat	cgt	ggc	cgc	aaa	cga	336	
Ala	Asp	Ala	Val	Leu	Pro	Met	Ala	Trp	Ser	Asp	Arg	Gly	Arg	Lys	Arg		
			100					105					110				
gta	acc	gcg	cag	cga	cct	gtg	cgc	tct	ggc	gag	ttt	gtg	cgc	aaa	gaa	384	
Val	Thr	Ala	Gln	Arg	Pro	Val	Arg	Ser	Gly	Glu	Phe	Val	Arg	Lys	Glu		
		115					120					125					
ggc	gat	gac	atc	caa	ccg	gga	gac	atc	gca	gtc	agc	gcc	ggc	gcg	gtc	432	
Gly	Asp	Asp	Ile	Gln	Pro	Gly	Asp	Ile	Ala	Val	Ser	Ala	Gly	Ala	Val		
	130					135					140						
tta	ggc	cct	gcc	caa	att	ggt	ttg	ctc	gca	gct	gtt	ggt	cgc	tcc	aaa	480	
Leu	Gly	Pro	Ala	Gln	Ile	Gly	Leu	Leu	Ala	Ala	Val	Gly	Arg	Ser	Lys		
145					150				155						160		
gtg	ttg	gtg	tac	cca	cgc	cca	cgc	atg	tcg	gtt	atc	tcc	gta	ggc	gct	528	
Val	Leu	Val	Tyr	Pro	Arg	Pro	Arg	Met	Ser	Val	Ile	Ser	Val	Gly	Ala		
				165				170					175				
gaa	ctt	gtt	gat	att	gat	cgc	cag	cca	ggc	ctc	ggc	cag	gtt	tat	gat	576	
Glu	Leu	Val	Asp	Ile	Asp	Arg	Gln	Pro	Gly	Leu	Gly	Gln	Val	Tyr	Asp		
			180				185					190					
gtc	aat	tcc	tat	tct	ctg	gct	gcc	gcc	ggt	agg	gaa	gcg	ggc	gca	gat	624	
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp		
		195				200						205					
gtg	tac	cgc	tac	ggc	att	gct	gcc	ggt	gaa	cct	cgt	cgc	atc	aaa	gag	672	
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu		
	210					215					220						
atc	att	gaa	tcc	cag	atg	ctg	cgc	tcg	gaa	atc	atc	gtc	atc	acc	gga	720	
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly		
225					230				235						240		
gct	gtt	ggc	ggt	gct	ggt	tca	gct	ggc	gtg	cgc	cag	gtt	ctc	aac	gag	768	
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu		
				245				250						255			
cta	ggc	gat	atc	gac	acc	gaa	cgc	gtc	gca	atg	cac	ccc	ggt	tct	gtc	816	
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val		

260	265	270	
caa gga ttc ggt ctg ctc ggc gag aac aag att cca tgc ttc ctt ctg			864
Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu			
275	280	285	
cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc			912
Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg			
290	295	300	
ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt			960
Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val			
305	310	315	320
ggt cga gct cga gcg ctc aac cac gtt gtg tct gtg gcg ggt cga aaa			
1008			
Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys			
	325	330	335
ggt ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac			
1056			
Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr			
	340	345	350
ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg			
1104			
Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu			
	355	360	365
gca gga ttg tcc gaa gca aac ggt atg atc cgc att cca gaa gat gtc			
1152			
Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val			
	370	375	380
aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa			
1200			
Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln			
385	390	395	400
ggt cga tagttcgatg cgtaatgcac cgt			
1229			
Gly Arg			

&lt;210&gt; 780

&lt;211&gt; 402

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 780

Pro	Glu	Pro	Val	Arg	Ile	Ala	Ile	Ala	Glu	Ala	Leu	Gly	Leu	Met	Cys
1				5					10					15	

Ala	Glu	Glu	Val	Gln	Ala	Ser	Arg	Ala	Leu	Pro	Gly	Phe	Ala	Gln	Ala
			20					25					30		

Ala	Ile	Asp	Gly	Tyr	Ala	Val	Arg	Ala	Val	Asp	Val	Gly	Gly	Glu	Lys
		35					40					45			

Ser	Phe	Ser	Gln	Gln	Leu	Pro	Val	Ala	Pro	Pro	Glu	Lys	Ser	Leu	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50					55					60					
Val	Val	Gly	Glu	Val	Ala	Ala	Gly	Ser	Gln	Gln	Pro	Leu	Arg	Leu	Gln
65					70					75					80
Pro	Lys	Gln	Ala	Val	Met	Val	His	Thr	Gly	Ala	Pro	Leu	Pro	Met	Leu
				85					90					95	
Ala	Asp	Ala	Val	Leu	Pro	Met	Ala	Trp	Ser	Asp	Arg	Gly	Arg	Lys	Arg
			100					105					110		
Val	Thr	Ala	Gln	Arg	Pro	Val	Arg	Ser	Gly	Glu	Phe	Val	Arg	Lys	Glu
		115					120					125			
Gly	Asp	Asp	Ile	Gln	Pro	Gly	Asp	Ile	Ala	Val	Ser	Ala	Gly	Ala	Val
	130					135					140				
Leu	Gly	Pro	Ala	Gln	Ile	Gly	Leu	Leu	Ala	Ala	Val	Gly	Arg	Ser	Lys
145					150					155					160
Val	Leu	Val	Tyr	Pro	Arg	Pro	Arg	Met	Ser	Val	Ile	Ser	Val	Gly	Ala
				165					170					175	
Glu	Leu	Val	Asp	Ile	Asp	Arg	Gln	Pro	Gly	Leu	Gly	Gln	Val	Tyr	Asp
			180					185					190		
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp
		195					200					205			
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu
	210					215					220				
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly
225					230					235					240
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu
				245					250					255	
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val
			260					265					270		
Gln	Gly	Phe	Gly	Leu	Leu	Gly	Glu	Asn	Lys	Ile	Pro	Cys	Phe	Leu	Leu
		275					280					285			
Pro	Ser	Asn	Pro	Val	Ala	Ser	Leu	Val	Ile	Phe	Glu	Thr	Phe	Val	Arg
	290					295					300				
Pro	Val	Val	Arg	Met	Ser	Leu	Gly	Lys	Ser	Asn	Ala	Ala	Arg	Arg	Val
305					310					315					320
Val	Arg	Ala	Arg	Ala	Leu	Asn	His	Val	Val	Ser	Val	Ala	Gly	Arg	Lys
				325					330					335	
Gly	Phe	Ile	Arg	Ser	Arg	Leu	Met	Arg	Asp	Ala	Glu	Thr	Gln	Asp	Tyr
			340					345					350		
Leu	Val	Glu	Ala	Leu	Gly	Gly	Ala	Thr	Gly	Ala	Pro	Ser	His	Leu	Leu
		355					360					365			
Ala	Gly	Leu	Ser	Glu	Ala	Asn	Gly	Met	Ile	Arg	Ile	Pro	Glu	Asp	Val
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Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln  
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Gly Arg

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 <223> RXA02629

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 Met Ser Lys Asp Pro  
 1 5  
 ttg gga agt ctt acc gat gtt gta gac aca cga gtt ccg ctt ccg gat 163  
 Leu Gly Ser Leu Thr Asp Val Val Asp Thr Arg Val Pro Leu Pro Asp  
 10 15 20  
 gtt gaa ccg gat ccg gag ttc ctg aag gct acg gaa aaa gaa ttc cac 211  
 Val Glu Pro Asp Pro Glu Phe Leu Lys Ala Thr Glu Lys Glu Phe His  
 25 30 35  
 atg gca tcc cag aag cgc gct ctt gtt gtc ctg gtg ggc gat cat gtc 259  
 Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu Val Gly Asp His Val  
 40 45 50  
 gct gag gca gat ggg act ggc cgt ttg gtt acg gag ctg ctc tta gag 307  
 Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr Glu Leu Leu Leu Glu  
 55 60 65  
 tct ggc ttc aac gtg gac gct gtg gtc agc gtg aag tct aag aag tct 355  
 Ser Gly Phe Asn Val Asp Ala Val Val Ser Val Lys Ser Lys Lys Ser  
 70 75 80 85  
 cag att agg caa gct att gaa acc gca gtt gtt ggc ggc gct gac ctt 403  
 Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val Gly Gly Ala Asp Leu  
 90 95 100  
 gtg ctg acc atc ggc gga gtg ggc gtt ggt cct cgg gat aaa act cct 451  
 Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro Arg Asp Lys Thr Pro  
 105 110 115  
 gag gca acc agc gct gtg ttg gac cag gac gtc cca gga atc gcg cag 499  
 Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val Pro Gly Ile Ala Gln  
 120 125 130  
 gcg ctt cgt tcc tcc ggt ttg gcc tgt ggc gcg gtg gat gca agt gtt 547  
 Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala Val Asp Ala Ser Val  
 135 140 145



tcc cga ggc gta gcg ggc gta tcc ggc tca acc gtg gtg gtc aac ctc 595  
 Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr Val Val Val Asn Leu  
 150 155 160 165

gct gag tct cgt tcg gca att cgt gat ggc atg gca act ctg aca ccg 643  
 Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met Ala Thr Leu Thr Pro  
 170 175 180

ttg gtt gat ttt gtt gta gat cag ctt cgc act tcc gtg gtt 685  
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<210> 782

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<212> PRT

<213> Corynebacterium glutamicum

<400> 782

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Glu Lys Glu Phe His Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu  
 35 40 45

Val Gly Asp His Val Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr  
 50 55 60

Glu Leu Leu Leu Glu Ser Gly Phe Asn Val Asp Ala Val Val Ser Val  
 65 70 75 80

Lys Ser Lys Lys Ser Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val  
 85 90 95

Gly Gly Ala Asp Leu Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro  
 100 105 110

Arg Asp Lys Thr Pro Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val  
 115 120 125

Pro Gly Ile Ala Gln Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala  
 130 135 140

Val Asp Ala Ser Val Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr  
 145 150 155 160

Val Val Val Asn Leu Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met  
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Ala Thr Leu Thr Pro Leu Val Asp Phe Val Val Asp Gln Leu Arg Thr  
 180 185 190

Ser Val Val  
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 Met Asn Ser Leu Phe  
 1 5  
 gac gtc tcc cca cac tgg tcc tcc gcc aac gcc aag ctc acc gca cat 163  
 Asp Val Ser Pro His Trp Ser Ser Ala Asn Ala Lys Leu Thr Ala His  
 10 15 20  
 ttt aac acc gga aaa ttc tcc act ggc atg aaa ttt gtc aac ctc att 211  
 Phe Asn Thr Gly Lys Phe Ser Thr Gly Met Lys Phe Val Asn Leu Ile  
 25 30 35  
 gcc gac tcc gca gaa gaa gcc aac cac cac ccc gat atc ctt ctc acc 259  
 Ala Asp Ser Ala Glu Glu Ala Asn His His Pro Asp Ile Leu Leu Thr  
 40 45 50  
 tat ggt ttt gtg gaa atc acc ctc acc agc cac gat gtg ggt gag ata 307  
 Tyr Gly Phe Val Glu Ile Thr Leu Thr Ser His Asp Val Gly Glu Ile  
 55 60 65  
 acc gac cgt gat gtc gcc cta gca aaa gtc atc gac gcc cac gcc aag 355  
 Thr Asp Arg Asp Val Ala Leu Ala Lys Val Ile Asp Ala His Ala Lys  
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 Thr Leu Ala Ile Ser Ala Glu Ala  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Phe Val Asn Leu Ile Ala Asp Ser Ala Glu Glu Ala Asn His His Pro  
 35 40 45  
 Asp Ile Leu Leu Thr Tyr Gly Phe Val Glu Ile Thr Leu Thr Ser His  
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 Asp Val Gly Glu Ile Thr Asp Arg Asp Val Ala Leu Ala Lys Val Ile

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Asp Ala His Ala Lys Thr Leu Ala Ile Ser Ala Glu Ala			
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	Met His Ala Val Leu		
	1		5
tcc atc ggt tcc aac atg gat gat cgc tac gcg ctg ctc aac aca gtg	163		
Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala Leu Leu Asn Thr Val			
	10	15	20
atc gag gaa ttc aaa gat gag atc gtg gcg cag tct gcg atc tac tca	211		
Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln Ser Ala Ile Tyr Ser			
	25	30	35
acc cca ccg tgg ggc att gag gat cag gat gaa ttc ctc aac gca gtg	259		
Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu Phe Leu Asn Ala Val			
	40	45	50
ctc gtt gtt gag gtt gaa gaa acc ccc atc gag ttg ctg cgc cgt ggc	307		
Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly			
	55	60	65
caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg	355		
Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg Val Arg Lys Trp Gly			
	70	75	85
cca cgc acc ctc gat gtg gat atc gtg cag atc att aaa gat ggg gaa	403		
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Glu			
	90	95	100
gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct	451		
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala			
	105	110	115
tgg cag cgt gcc ttc gtg ttg atc cct tgg ttg gaa gca gaa cct gat	499		
Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp			
	120	125	130
gcc gtc ctg cac ggc acg acc att gca gaa cat gtg gat aat ctt gat	547		
Ala Val Leu His Gly Thr Thr Ile Ala Glu His Val Asp Asn Leu Asp			
	135	140	145
ccc aca gac att gaa ggt gtc acc aag att taaggagtcg tggctttcat	597		
Pro Thr Asp Ile Glu Gly Val Thr Lys Ile			

150

155

gca

600

&lt;210&gt; 786

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 786

Met His Ala Val Leu Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala  
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Leu Leu Asn Thr Val Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln  
 20 25 30

Ser Ala Ile Tyr Ser Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu  
 35 40 45

Phe Leu Asn Ala Val Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu  
 50 55 60

Leu Leu Arg Arg Gly Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg  
 65 70 75 80

Val Arg Lys Trp Gly Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile  
 85 90 95

Ile Lys Asp Gly Glu Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu  
 100 105 110

Pro His Pro Trp Ala Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu  
 115 120 125

Glu Ala Glu Pro Asp Ala Val Leu His Gly Thr Thr Ile Ala Glu His  
 130 135 140

Val Asp Asn Leu Asp Pro Thr Asp Ile Glu Gly Val Thr Lys Ile  
 145 150 155

&lt;210&gt; 787

&lt;211&gt; 609

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(586)

&lt;223&gt; RXN01304

&lt;400&gt; 787

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 Met Pro Ala Gln Asn  
 1 5

aaa aac ctc cca gga tcc gtc atc gtt gtg tct gat cgg att aaa tcg 163  
 Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser Asp Arg Ile Lys Ser

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Gly	Glu	Arg	Ile	Asp	Lys	Ala	Gly	Pro	Val	Ala	Val	Asp	Leu	Leu	Gln					
			25					30					35							
gaa	tca	ggc	gtg	gag	att	tcc	aca	ttc	acc	gtc	gtg	gag	gag	ggc	ttt	259				
Glu	Ser	Gly	Val	Glu	Ile	Ser	Thr	Phe	Thr	Val	Val	Glu	Glu	Gly	Phe					
		40					45					50								
gaa	cct	gtc	cat	caa	gaa	ttg	gtt	aag	gcg	ttg	gcg	cgc	cgg	gat	cgc	307				
Glu	Pro	Val	His	Gln	Glu	Leu	Val	Lys	Ala	Leu	Ala	Arg	Arg	Asp	Arg					
	55					60				65										
gtc	atc	atc	acc	atc	ggc	gga	acg	ggc	gtg	ggg	cct	aga	aat	cgg	acg	355				
Val	Ile	Ile	Thr	Ile	Gly	Gly	Thr	Gly	Val	Gly	Pro	Arg	Asn	Arg	Thr					
70					75				80						85					
ccg	gag	gcc	aca	gaa	ccg	cac	atc	gat	acg	cta	ctg	ccg	ggt	ctg	atg	403				
Pro	Glu	Ala	Thr	Glu	Pro	His	Ile	Asp	Thr	Leu	Leu	Pro	Gly	Leu	Met					
			90					95					100							
acg	cag	att	ttg	ttc	tct	gga	ctg	tcc	aat	acc	gcg	cag	gcg	ggg	tta	451				
Thr	Gln	Ile	Leu	Phe	Ser	Gly	Leu	Ser	Asn	Thr	Ala	Gln	Ala	Gly	Leu					
		105					110					115								
tct	cgg	ggg	ctg	gtg	ggc	ttg	agt	gct	cgc	gat	tcc	acg	gcc	gcg	ctc	499				
Ser	Arg	Gly	Leu	Val	Gly	Leu	Ser	Ala	Arg	Asp	Ser	Thr	Ala	Ala	Leu					
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atc	gtc	aac	gcg	ccg	agt	tct	tcc	ggg	ggc	gtg	cgc	gac	gcg	ctc	ggg	547				
Ile	Val	Asn	Ala	Pro	Ser	Ser	Ser	Gly	Gly	Val	Arg	Asp	Ala	Leu	Gly					
	135					140				145										
gtg	gtc	tgc	ccg	ctt	ttc	ggt	tcc	att	ttt	gag	cgt	ctt	taaaagattt			596				
Val	Val	Cys	Pro	Leu	Phe	Gly	Ser	Ile	Phe	Glu	Arg	Leu								
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&lt;210&gt; 788

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 788

Met	Pro	Ala	Gln	Asn	Lys	Asn	Leu	Pro	Gly	Ser	Val	Ile	Val	Val	Ser
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Asp	Arg	Ile	Lys	Ser	Gly	Glu	Arg	Ile	Asp	Lys	Ala	Gly	Pro	Val	Ala
		20						25					30		

Val	Asp	Leu	Leu	Gln	Glu	Ser	Gly	Val	Glu	Ile	Ser	Thr	Phe	Thr	Val
		35					40					45			

Val	Glu	Glu	Gly	Phe	Glu	Pro	Val	His	Gln	Glu	Leu	Val	Lys	Ala	Leu
	50					55					60				

Ala	Arg	Arg	Asp	Arg	Val	Ile	Ile	Thr	Ile	Gly	Gly	Thr	Gly	Val	Gly
65					70					75					80

Pro Arg Asn Arg Thr Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu  
85 90 95

Leu Pro Gly Leu Met Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr  
100 105 110

Ala Gln Ala Gly Leu Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp  
115 120 125

Ser Thr Ala Ala Leu Ile Val Asn Ala Pro Ser Ser Ser Gly Gly Val  
130 135 140

Arg Asp Ala Leu Gly Val Val Cys Pro Leu Phe Gly Ser Ile Phe Glu  
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Arg Leu

**<210> 789**

**<211> 1281**

**<212> DNA**

<213> Corynebacterium glutamicum

**<220>**

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<223> RXS02556

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Leu Ile Val Ser Thr  
1 5

cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg 163  
Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val  
10 15 20

atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg 211  
Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr  
25 30 35

ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct 259  
Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala  
40 45 50

aac acc ttc aac cgt ggc aat cag aag caa ggc gat cag cag aag gcg 307  
Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala  
55 60 65

ctg	gcg	gct	tcg	att	gca	acg	ttt	gcc	acc	atg	ctc	gtt	act	cct	gat	355
Leu	Ala	Ala	Ser	Ile	Ala	Thr	Phe	Ala	Thr	Met	Leu	Val	Thr	Pro	Asp	
70					75					80					85	

gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg 403  
Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val  
90 95 100

tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg 451  
 Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu  
 105 110 115

ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct 499  
 Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro  
 120 125 130

gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg 547  
 Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu  
 135 140 145

atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc 595  
 Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly  
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 Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala  
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acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca 691  
 Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro  
 185 190 195

ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag 739  
 Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln  
 200 205 210

ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att 787  
 Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile  
 215 220 225

gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta 835  
 Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val  
 230 235 240 245

tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt 883  
 Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val  
 250 255 260

ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc 931  
 Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly  
 265 270 275

tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac 979  
 Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp  
 280 285 290

gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg  
 1027  
 Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val  
 295 300 305

gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa  
 1075  
 Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu  
 310 315 320 325

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 1123  
 Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile

330 335 340  
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 1171  
 Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys  
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 aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta  
 1219  
 Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val  
 360 365 370  
 aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca  
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 Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His  
 35 40 45  
 Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly  
 50 55 60  
 Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met  
 65 70 75 80  
 Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile  
 85 90 95  
 Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile  
 100 105 110  
 Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu  
 115 120 125  
 Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile  
 130 135 140  
 Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn  
 145 150 155 160  
 Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys  
 165 170 175  
 Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu



180										185					190						
Val	Ala	Pro	Glu	Pro	Gly	Gln	Tyr	Thr	Ser	Ile	Gly	Val	Val	Leu	Asp						
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Asp	Gly	Ala	Arg	Gln	Leu	Arg	Gln	Tyr	Ser	Leu	Leu	Gly	Gly	Ser	Asp						
	210					215					220										
Thr	Glu	Tyr	Arg	Ile	Ala	Val	Glu	Asp	Asn	Gly	Glu	Val	Ser	Gly	Phe						
225					230					235					240						
Leu	Arg	Asp	Arg	Val	Ser	Val	Gly	Asp	Lys	Ile	Glu	Ala	Thr	Ile	Ala						
				245					250					255							
Ala	Gly	Asp	Leu	Val	Leu	Asn	Lys	Asp	Thr	Asn	Pro	Val	Val	Leu	Ile						
			260					265					270								
Ser	Gln	Gly	Ile	Gly	Ser	Thr	Pro	Met	Val	Gly	Met	Leu	Ala	Gly	Met						
		275					280					285									
Asn	Pro	Glu	Arg	Asp	Val	Val	Val	Leu	His	Ala	Asp	Gln	Ala	Glu	Ser						
	290					295					300										
Thr	Tyr	Ala	Gln	Val	Glu	Glu	Val	Gln	Gly	Leu	Val	Glu	Lys	Leu	Pro						
305					310					315					320						
Lys	Ala	Ala	Phe	Glu	Ile	Phe	Tyr	Arg	Asp	Asn	Asp	Gln	Trp	Leu	Glu						
			325						330					335							
Val	Ala	Gly	Arg	Ile	Pro	Ser	Gly	Ala	Ser	Val	Tyr	Leu	Cys	Gly	Gly						
			340					345					350								
Val	Glu	Phe	Leu	Lys	Asn	Val	Arg	Glu	Gln	Ile	Glu	Ala	Leu	Asp	Glu						
		355					360					365									
Gln	Pro	Arg	Asp	Val	Asn	Phe	Glu	Leu	Phe	Ala	Pro	Asn	Asp	Trp	Leu						
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Ile	Ser																				
385																					

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 <213> Corynebacterium glutamicum

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 <223> RXS02560

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 Met Gln Gly Asn Ser  
 1 5  
 ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca 163  
 Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro

10								15					20				
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Gly	Glu	Leu	Leu	Ala	Ala	Arg	Tyr	Gly	Gln	Pro	Ala	Thr	Trp	Thr	Pro		
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ccg	cag	tgg	aat	gag	acg	ctt	gat	gtc	att	cac	cag	cat	cga	tca	gtt		259
Pro	Gln	Trp	Asn	Glu	Thr	Leu	Asp	Val	Ile	His	Gln	His	Arg	Ser	Val		
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cgc	agg	tgg	ttg	gat	aaa	ccg	gtt	gat	gat	gac	acc	atc	cgc	acc	att		307
Arg	Arg	Trp	Leu	Asp	Lys	Pro	Val	Asp	Asp	Asp	Thr	Ile	Arg	Thr	Ile		
	55					60					65						
att	tcc	gcc	gca	caa	tcg	gct	gga	acc	tct	tcc	aat	aag	cag	gtc	att		355
Ile	Ser	Ala	Ala	Gln	Ser	Ala	Gly	Thr	Ser	Ser	Asn	Lys	Gln	Val	Ile		
70					75					80					85		
tct	gtc	atc	gtg	gtt	aaa	gat	cct	gag	ctg	agg	aaa	ggc	ctc	gcg	ggg		403
Ser	Val	Ile	Val	Val	Lys	Asp	Pro	Glu	Leu	Arg	Lys	Gly	Leu	Ala	Gly		
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atc	act	cgc	cag	atg	ttt	ccg	cac	ctt	gag	cag	gtt	ccc	gcg	gtg	ctg		451
Ile	Thr	Arg	Gln	Met	Phe	Pro	His	Leu	Glu	Gln	Val	Pro	Ala	Val	Leu		
			105					110					115				
att	tgg	ttg	att	gat	tat	tcc	cga	atc	agt	gcg	gtg	gca	gcc	aga	gaa		499
Ile	Trp	Leu	Ile	Asp	Tyr	Ser	Arg	Ile	Ser	Ala	Val	Ala	Ala	Arg	Glu		
		120					125					130					
gat	ctc	cca	aca	ggg	gct	ctt	gat	tat	ctc	gat	gag	gcc	gcg	tgg	ggg		547
Asp	Leu	Pro	Thr	Gly	Ala	Leu	Asp	Tyr	Leu	Asp	Glu	Ala	Ala	Trp	Gly		
	135					140					145						
ttc	ctc	gac	gcc	gga	atc	gca	gct	caa	aac	gct	gca	att	gct	gcg	gag		595
Phe	Leu	Asp	Ala	Gly	Ile	Ala	Ala	Gln	Asn	Ala	Ala	Ile	Ala	Ala	Glu		
150					155				160						165		
tca	ctt	gga	ttg	gga	acg	ctc	tat	ttg	ggt	tcg	gtg	cgc	aac	gat	gcg		643
Ser	Leu	Gly	Leu	Gly	Thr	Leu	Tyr	Leu	Gly	Ser	Val	Arg	Asn	Asp	Ala		
				170				175						180			
gaa	gcc	gtg	cac	aaa	ttg	ctt	ggc	ctt	cca	cct	gag	atc	gtg	cct	gtc		691
Glu	Ala	Val	His	Lys	Leu	Leu	Gly	Leu	Pro	Pro	Glu	Ile	Val	Pro	Val		
			185					190					195				
gtg	ggc	ttg	gaa	atg	ggg	cat	gcg	gat	ccg	cct	gaa	cct	gcc	gga	att		739
Val	Gly	Leu	Glu	Met	Gly	His	Ala	Asp	Pro	Pro	Glu	Pro	Ala	Gly	Ile		
		200					205					210					
aaa	cct	ccc	ctg	cca	caa	gaa	gcc	att	gtt	cac	tgg	gat	acc	tac	acc		787
Lys	Pro	Pro	Leu	Pro	Gln	Glu	Ala	Ile	Val	His	Trp	Asp	Thr	Tyr	Thr		
	215					220					225						
gag	aaa	aac	ctc	gaa	ctt	atc	gat	tcc	tac	gac	cgc	gcc	ctc	gac	act		835
Glu	Lys	Asn	Leu	Glu	Leu	Ile	Asp	Ser	Tyr	Asp	Arg	Ala	Leu	Asp	Thr		
230					235					240					245		
tac	tat	tct	cgc	tac	ggc	cag	cac	cag	ctc	tgg	tcg	aag	cag	acg	gcg		883
Tyr	Tyr	Ser	Arg	Tyr	Gly	Gln	His	Gln	Leu	Trp	Ser	Lys	Gln	Thr	Ala		
				250				255						260			

cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt 931  
 His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu  
                   265                                  270                                  275

agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg 977  
 Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg  
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Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro  
                   20                                  25                                  30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His  
                   35                                  40                                  45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp  
                   50                                  55                                  60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser  
   65                                  70                                  75                                  80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg  
                                   85                                  90                                  95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln  
                   100                                  105                                  110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala  
                   115                                  120                                  125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp  
                   130                                  135                                  140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala  
   145                                  150                                  155                                  160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser  
                   165                                  170                                  175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro  
                   180                                  185                                  190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro  
                   195                                  200                                  205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His  
                   210                                  215                                  220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp

225		230		235		240									
Arg	Ala	Leu	Asp	Thr	Tyr	Tyr	Ser	Arg	Tyr	Gly	Gln	His	Gln	Leu	Trp
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Ser	Lys	Gln	Thr	Ala	His	Arg	Ala	Ala	Ser	Lys	Ser	Phe	Ser	Lys	Thr
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 Met Thr Ser Ser Asn  
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 Thr Ala Arg Ser Ala Glu Trp Phe Glu Lys Ala Gln Lys Leu Thr Pro  
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 Gly Gly Val Asn Ser Pro Val Arg Ala Phe Gly Ser Val Gly Gly Gln  
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 Ala Arg Phe Ile Glu Lys Ala His Gly Ser Thr Leu Ile Asp Val Asp  
 40 45 50  
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 Gly Asn Glu Tyr Val Asp Leu Val Cys Ser Trp Gly Pro Met Leu Met  
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 Asp Gly Leu Ser Phe Gly Ala Pro Thr Ile Gly Glu Val Glu Leu Ala  
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 Gln Asp Ile Val Lys Arg Thr Ser Val Glu Glu Val Arg Leu Val Asn  
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Thr	Gln	Arg	Ser	Lys	Ile	Leu	Lys	Phe	Glu	Gly	Cys	Tyr	His	Gly	His		
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Val	Asp	Ala	Leu	Leu	Ala	Ser	Ala	Gly	Ser	Gly	Val	Ala	Thr	Phe	Ala		
	150				155					160					165		
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Leu	Pro	Asp	Ser	Pro	Gly	Ile	Thr	Gly	Ala	Gln	Thr	Ser	Asp	Thr	Ile		
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Val	Val	Pro	Tyr	Asn	Asp	Ile	Glu	Ala	Val	Arg	Asn	Ala	Phe	Ala	Glu		
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Tyr	Pro	Gly	Glu	Ile	Ala	Cys	Ile	Ile	Ala	Glu	Ala	Ala	Gly	Gly	Asn		
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atg	ggc	acc	gtc	gct	cca	aag	gac	aac	ttt	aac	gac	aag	ctt	ctc	gcg	787	
Met	Gly	Thr	Val	Ala	Pro	Lys	Asp	Asn	Phe	Asn	Asp	Lys	Leu	Leu	Ala		
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Ile	Ala	His	Ala	Asp	Gly	Ala	Leu	Leu	Ile	Leu	Asp	Glu	Val	Met	Thr		
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Gly	Phe	Arg	Thr	Ser	Tyr	Arg	Gly	Trp	Phe	Gly	Val	Asp	Lys	Val	Ala		
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gct	gac	ctg	gtc	acc	ttc	ggc	aag	gtc	gtc	tcc	ggc	ggc	cta	cct	gcc	931	
Ala	Asp	Leu	Val	Thr	Phe	Gly	Lys	Val	Val	Ser	Gly	Gly	Leu	Pro	Ala		
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Ala	Ala	Phe	Gly	Gly	Lys	Ala	Glu	Ile	Met	Asn	Met	Leu	Ala	Pro	Gln		
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1171																	
Leu	Thr	His	Glu	Gly	Val	Ala	His	His	Ile	Gln	Arg	Ala	Ser	Asn	Met		

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 Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe Phe His Thr Leu Leu  
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 Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe Glu Thr Trp Phe Val  
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 Ser Ser Ala Leu Thr Asp Asp Asp Phe Ser Lys Ile Glu Gln Ala Leu  
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 Gly Pro Met Leu Met Gly His Ala His Pro Ala Val Val Glu Ala Val  
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 Gln Lys Ala Val Val Asp Gly Leu Ser Phe Gly Ala Pro Thr Ile Gly  
 85 90 95  
 Glu Val Glu Leu Ala Gln Asp Ile Val Lys Arg Thr Ser Val Glu Glu  
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 Val Arg Leu Val Asn Ser Gly Thr Glu Ala Thr Met Ser Ala Val Arg  
 115 120 125

Leu Ala Arg Gly Tyr Thr Gln Arg Ser Lys Ile Leu Lys Phe Glu Gly  
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 Cys Tyr His Gly His Val Asp Ala Leu Leu Ala Ser Ala Gly Ser Gly  
 145 150 155 160  
 Val Ala Thr Phe Ala Leu Pro Asp Ser Pro Gly Ile Thr Gly Ala Gln  
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 Thr Ser Asp Thr Ile Val Val Pro Tyr Asn Asp Ile Glu Ala Val Arg  
 180 185 190  
 Asn Ala Phe Ala Glu Tyr Pro Gly Glu Ile Ala Cys Ile Ile Ala Glu  
 195 200 205  
 Ala Ala Gly Gly Asn Met Gly Thr Val Ala Pro Lys Asp Asn Phe Asn  
 210 215 220  
 Asp Lys Leu Leu Ala Ile Ala His Ala Asp Gly Ala Leu Leu Ile Leu  
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 Asp Glu Val Met Thr Gly Phe Arg Thr Ser Tyr Arg Gly Trp Phe Gly  
 245 250 255  
 Val Asp Lys Val Ala Ala Asp Leu Val Thr Phe Gly Lys Val Val Ser  
 260 265 270  
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 275 280 285  
 Met Leu Ala Pro Gln Gly Pro Val Tyr Gln Ala Gly Thr Leu Ser Gly  
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 Asn Pro Val Ala Val Ala Ala Gly Arg Ala Ser Leu Lys Leu Ala Asp  
 305 310 315 320  
 Glu Ser Leu Tyr Thr Thr Ile Asn Ala Asn Ala Asp Arg Leu His Gly  
 325 330 335  
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 Asn Phe Ser Asp Met Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe  
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 Phe His Thr Leu Leu Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe  
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 Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn Val Thr His Gly Arg  
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ggg att ccg ccg gaa cgt cta gat gaa gtg gcg gtt cat tac cac cac 259  
 Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala Val His Tyr His His  
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aat gtg gaa aaa gaa ttg gcg tct cgc gat cac aag ctg cct gtt tat 355  
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 Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn Glu Ala Ala Glu Gln  
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 Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser Ile Thr Phe Thr Lys  
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 Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp Glu Leu Arg Asp Glu  
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gct gcg gga acc cct gag gat ggc tcc ttg tat tcc aca cag gtc aag 739  
 Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr Ser Thr Gln Val Lys  
 200 205 210

gaa gcg tca gca ctg att gct gag gct gtt ggt gtg tca gat ttt gat 787  
 Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly Val Ser Asp Phe Asp  
 215 220 225

gtg gtg tgg cag tcc cgc tcg ggt agc ccg cac act ccg tgg ctg gag 835  
 Val Val Trp Gln Ser Arg Ser Gly Ser Pro His Thr Pro Trp Leu Glu  
 230 235 240 245

cct gac atc gtg gat cac gca gtg gag ctc aac gag aag ggt caa aaa 883  
 Pro Asp Ile Val Asp His Ala Val Glu Leu Asn Glu Lys Gly Gln Lys  
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gcg ctc gtt gtc tgc cct gta ggc ttt att tct gat cat atg gaa gtc 931  
 Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser Asp His Met Glu Val  
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&lt;210&gt; 796

&lt;211&gt; 370

&lt;212&gt; PRT

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&lt;400&gt; 796

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Lys	Leu	Pro	Val	Tyr	Phe	Gly	Asn	Arg	Asn	Trp	Lys	Pro	Phe	Asp	Asn
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Ser	Thr	Gln	Val	Lys	Glu	Ala	Ser	Ala	Leu	Ile	Ala	Glu	Ala	Val	Gly
	210					215					220				
Val	Ser	Asp	Phe	Asp	Val	Val	Trp	Gln	Ser	Arg	Ser	Gly	Ser	Pro	His
225					230					235					240
Thr	Pro	Trp	Leu	Glu	Pro	Asp	Ile	Val	Asp	His	Ala	Val	Glu	Leu	Asn
				245					250					255	
Glu	Lys	Gly	Gln	Lys	Ala	Leu	Val	Val	Cys	Pro	Val	Gly	Phe	Ile	Ser
			260					265					270		
Asp	His	Met	Glu	Val	Ile	Trp	Asp	Leu	Asp	Ser	Glu	Leu	Met	Glu	Glu
		275					280					285			
Ala	Glu	Lys	Arg	Asn	Met	Val	Val	Glu	Arg	Val	Ala	Thr	Val	Gly	Pro
						295					300				
Thr	Asp	Glu	Phe	Ala	Ala	Leu	Val	Val	Asp	Leu	Ile	Glu	Glu	Ala	Glu
305					310					315					320

[illegible]

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<212> DNA
<213> Corynebacterium glutamicum
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<220>
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<222> (101) .. (787)
<223> RXA00624
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caacaggacg acaacggccg gacatgcgac aatacaatgc atg tcc ggc cgt ctt 115  
Met Ser Gly Arg Leu  
1 5

ctt gtt tca gtt tct agt att ttc gac cag acc cga tcg gcg gct gac 163  
 Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr Arg Ser Ala Ala Asp  
 10 15 20

agg ctc att tca gac ctg cga gcc gac ggc atc gag gtc tca tta ctt 211  
Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile Glu Val Ser Leu Leu  
25 30 35

gtc gca ccc cgc atc gat ggg gac tgg cgt ctc gcc aaa gac aaa ggg 259  
Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu Ala Lys Asp Lys Gly  
40 45 50

acc ctc gcg tgg atg gaa caa caa cgc gaa cgc ggc cac gaa ctc atc 307  
Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg Gly His Glu Leu Ile  
55 60 65

ctc aac ggt ttc gac caa gca gtt cag gga cgt cgc tca gaa ttc gcc 355  
Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg Arg Ser Glu Phe Ala  
70 75 80 85

aac ctt gaa cgg cac gaa gca cgt ctt cgc ctt acc ggt gcc att agg 403  
Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu Thr Gly Ala Ile Arg  
90 95 100

caa atg cag aaa att ggc ttc gaa ttc caa atc ttt gcc cca cct cgt 451  
Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile Phe Ala Pro Pro Arg  
105 110 115

tgg aga atg tca gaa ggc acc ttc gcg gta ctc cca gaa ttt gat ttc 499  
Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu Pro Glu Phe Asp Phe

120	125	130	
aac gtc gcc gcc tcg acc agg gga tta cat aac ctc gac acc ggc gaa			547
Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn Leu Asp Thr Gly Glu			
135	140	145	
ttc ttg gcg tgt aga aac ctc tcc gtg ggt gaa ggt ttt ggt gct gca			595
Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu Gly Phe Gly Ala Ala			
150	155	160	165
aaa tgg tgg cgc aag aat gtc atc aag gct gtc act cgt gga gcg gaa			643
Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val Thr Arg Gly Ala Glu			
	170	175	180
aaa gga aat aca gtg cgc ttg tcc gca tcg gcg cga aat ctc acc aac			691
Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala Arg Asn Leu Thr Asn			
	185	190	195
cct aaa gtc gca gct gac ttc cgg gaa gct gca tta gct gcc ttg gat			739
Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala Leu Ala Ala Leu Asp			
	200	205	210
ttg ggt gct cag gtg caa acc tat tct cag gcg gcc gca caa ctg gcc			787
Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala Ala Ala Gln Leu Ala			
215	220	225	
tagttgggga gggtcggggc acc			810

&lt;210&gt; 798

&lt;211&gt; 229

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 798

Met Ser Gly Arg Leu Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr			
1	5	10	15
Arg Ser Ala Ala Asp Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile			
	20	25	30
Glu Val Ser Leu Leu Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu			
	35	40	45
Ala Lys Asp Lys Gly Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg			
	50	55	60
Gly His Glu Leu Ile Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg			
65	70	75	80
Arg Ser Glu Phe Ala Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu			
	85	90	95
Thr Gly Ala Ile Arg Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile			
	100	105	110
Phe Ala Pro Pro Arg Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu			
	115	120	125
Pro Glu Phe Asp Phe Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn			
130	135	140	

Leu Asp Thr Gly Glu Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu  
 145 150 155 160  
 Gly Phe Gly Ala Ala Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val  
 165 170 175  
 Thr Arg Gly Ala Glu Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala  
 180 185 190  
 Arg Asn Leu Thr Asn Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala  
 195 200 205  
 Leu Ala Ala Leu Asp Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala  
 210 215 220  
 Ala Ala Gln Leu Ala  
 225

<210> 799  
 <211> 956  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(933)  
 <223> RXA00306

<400> 799  
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 1 5 10 15  
 gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg 96  
 Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val  
 20 25 30  
 gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat 144  
 Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp  
 35 40 45  
 cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc 192  
 Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu  
 50 55 60  
 aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg 240  
 Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala  
 65 70 75 80  
 gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt 288  
 Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly  
 85 90 95  
 tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat 336  
 Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr  
 100 105 110  
 gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag 384  
 Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu

115	120	125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag			432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys			
130	135	140	
gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa			480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu			
145	150	155	160
gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag			528
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln			
	165	170	175
tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc			576
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg			
	180	185	190
acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc			624
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg			
	195	200	205
ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat			672
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp			
210	215	220	
gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc			720
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg			
225	230	235	240
acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc			768
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser			
	245	250	255
atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg			816
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu			
	260	265	270
gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac			864
Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn			
275	280	285	
ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg			912
Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu			
290	295	300	
ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aag			956
Pro Ala Asp Leu Leu Asp Ser			
305	310		

&lt;210&gt; 800

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 800

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro  
 1 5 10 15

Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val

20								25				30			
Val	Gly	Pro	Pro	Glu	Ile	Gly	His	Val	Tyr	Arg	Asp	Ser	Gly	Met	Asp
		35					40					45			
Leu	Asp	Gly	Ala	Thr	Ala	Leu	Val	Val	Lys	Glu	Ala	Cys	Ala	His	Leu
	50					55					60				
Asn	Pro	Gly	Gly	Thr	Ala	His	Leu	Leu	Gly	Ala	Trp	Val	His	Ser	Ala
	65				70				75						80
Asp	Gln	Ser	Trp	Gln	Gln	Arg	Val	Ala	Glu	Trp	Leu	Pro	Asp	Asn	Gly
				85					90					95	
Tyr	Val	Ala	Trp	Val	Ile	Glu	Arg	Asp	Ala	Val	Ser	Pro	Ala	Gln	Tyr
			100						105					110	
Val	Gly	Thr	Trp	Leu	Ser	Asp	Glu	Ser	Leu	Asp	Leu	Arg	Ser	Pro	Glu
			115				120					125			
Ala	Ala	Ala	Arg	Thr	Thr	Ala	Trp	Leu	Asn	His	Phe	Glu	Lys	Ala	Lys
						135					140				
Val	Gln	Gly	Val	Gly	Phe	Gly	Phe	Ile	Ala	Ile	Gln	Arg	Leu	Glu	Glu
	145				150					155					160
Asp	Glu	Ala	Asp	Glu	Lys	Ser	Asp	Ile	Leu	Ala	Glu	Ser	Met	Thr	Gln
				165					170					175	
Tyr	Phe	Glu	Asp	Pro	Leu	Gly	Pro	Glu	Ile	Glu	Glu	Tyr	Phe	Thr	Arg
			180						185					190	
Thr	Ala	Trp	Leu	Arg	Glu	Gln	Thr	Arg	Asp	Ser	Ile	Leu	Ser	Ser	Arg
			195				200					205			
Phe	Lys	Val	Arg	Pro	Gly	Val	Ala	Arg	Glu	Gln	Ile	Ser	Leu	Ala	Asp
						215					220				
Ala	Glu	Glu	Gly	Met	Gly	Phe	Ser	Pro	Val	Thr	Leu	Arg	Leu	Thr	Arg
	225				230					235					240
Thr	Asp	Gly	Pro	Arg	Trp	Ser	His	Asp	Val	Asp	Glu	His	Val	Ala	Ser
				245					250					255	
Ile	Val	Ala	Gly	Leu	Asn	Pro	His	Gly	Leu	Pro	Phe	Glu	Glu	Ile	Leu
			260						265				270		
Glu	Met	Tyr	Ala	Met	Ala	Gln	Gly	Ile	Glu	Gly	Glu	Ser	Leu	His	Asn
		275					280					285			
Gly	Ala	Ile	Ala	Ala	Leu	Val	Asp	Leu	Ile	Arg	His	Gly	Leu	Val	Leu
	290					295					300				
Pro	Ala	Asp	Leu	Leu	Asp	Ser									
	305				310										

&lt;210&gt; 801

&lt;211&gt; 1263

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1240)

&lt;223&gt; RXA00884

&lt;400&gt; 801

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caattaatca tgtatagggg gcaggcacta ggcttggggc atg tca gtt ttt ggt 115  
 Met Ser Val Phe Gly  
 1 5

gtg tat att cat gtg ccg ttt tgt tca act cgg tgc ggt tat tgc gat 163  
 Val Tyr Ile His Val Pro Phe Cys Ser Thr Arg Cys Gly Tyr Cys Asp  
 10 15 20

ttc aac acc tat act gct ggg gaa tta ggt agt act gca ggc ccg gac 211  
 Phe Asn Thr Tyr Thr Ala Gly Glu Leu Gly Ser Thr Ala Gly Pro Asp  
 25 30 35

acc tat ctt gac tcg ttg gaa gtt gag ttg gag atg gct gtg gct tcg 259  
 Thr Tyr Leu Asp Ser Leu Glu Val Glu Leu Glu Met Ala Val Ala Ser  
 40 45 50

ctg gat aat cct cgg cag gcg gaa act atc ttt att ggc ggg ggt acc 307  
 Leu Asp Asn Pro Arg Gln Ala Glu Thr Ile Phe Ile Gly Gly Gly Thr  
 55 60 65

ccg tcg ttg att ggt gcg gac ggt ttg gcc agg gtt ttg ggg gct gtg 355  
 Pro Ser Leu Ile Gly Ala Asp Gly Leu Ala Arg Val Leu Gly Ala Val  
 70 75 80 85

cgc aat act ttt ggc att gcg gat ggt gcg gaa gtc acc acg gag tcc 403  
 Arg Asn Thr Phe Gly Ile Ala Asp Gly Ala Glu Val Thr Thr Glu Ser  
 90 95 100

aat ccg gag tct acc tcg cct gag ttt ttt gat ggc ctg cgt gag gcg 451  
 Asn Pro Glu Ser Thr Ser Pro Glu Phe Phe Asp Gly Leu Arg Glu Ala  
 105 110 115

ggc tac aac agg att tcg tta ggg atg cag tcg gcg tcg tca agc gtt 499  
 Gly Tyr Asn Arg Ile Ser Leu Gly Met Gln Ser Ala Ser Ser Ser Val  
 120 125 130

ttg aag gtg ctg gac cgc acg cac acc cca ggg cgc ccg gtg gcg gcg 547  
 Leu Lys Val Leu Asp Arg Thr His Thr Pro Gly Arg Pro Val Ala Ala  
 135 140 145

gcc aag gag gca cgt gag gcg ggg ttt gag cat gtc aat ttg gac atg 595  
 Ala Lys Glu Ala Arg Glu Ala Gly Phe Glu His Val Asn Leu Asp Met  
 150 155 160 165

att tat ggc acg ccg aca gag acc gat gat gat gtc cgc aag acg ctg 643  
 Ile Tyr Gly Thr Pro Thr Glu Thr Asp Asp Asp Val Arg Lys Thr Leu  
 170 175 180

aat gcg gtg ctc gaa gcg aac gtg gat cac gtg tct gcc tat tcc ttg 691  
 Asn Ala Val Leu Glu Ala Asn Val Asp His Val Ser Ala Tyr Ser Leu  
 185 190 195



atc gtg aaa gat ggc acg gcg atg gcg cgc aag gtg cac aag ggc gag 739  
 Ile Val Lys Asp Gly Thr Ala Met Ala Arg Lys Val His Lys Gly Glu  
 200 205 210

ctg cca gcg ccg gac gag gat gtc tac gct gat cgt ttt gag ctt atc 787  
 Leu Pro Ala Pro Asp Glu Asp Val Tyr Ala Asp Arg Phe Glu Leu Ile  
 215 220 225

gac gct cgc ctg cgc tca gct ggt ttc gat tgg tac gag gtg tcc aac 835  
 Asp Ala Arg Leu Arg Ser Ala Gly Phe Asp Trp Tyr Glu Val Ser Asn  
 230 235 240 245

tgg gcg aaa ccc ggc gga gaa tgc aag cac aac atg ggc tat tgg gtc 883  
 Trp Ala Lys Pro Gly Gly Glu Cys Lys His Asn Met Gly Tyr Trp Val  
 250 255 260

gac ggc gac tgg tgg ggc gcg ggc ccg ggc gcg cac tcg cac atc ggc 931  
 Asp Gly Asp Trp Trp Gly Ala Gly Pro Gly Ala His Ser His Ile Gly  
 265 270 275

gac cgc cgc ttc tac aac atc aag cac cca gcg cgt tac tcc gcg cag 979  
 Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala Arg Tyr Ser Ala Gln  
 280 285 290

att gcg gcc ggc gag ctg ccc att aag gaa aca gag cgg ctg acg gcg  
 1027  
 Ile Ala Ala Gly Glu Leu Pro Ile Lys Glu Thr Glu Arg Leu Thr Ala  
 295 300 305

gaa gat cac cac acc gag cgc gtc atg ctt ggt ttg cgc ctg aaa caa  
 1075  
 Glu Asp His His Thr Glu Arg Val Met Leu Gly Leu Arg Leu Lys Gln  
 310 315 320 325

ggc gtg ccg ctg aac ctt ttc gca ccc gca gcg cgc ccg gtc atc gac  
 1123  
 Gly Val Pro Leu Asn Leu Phe Ala Pro Ala Ala Arg Pro Val Ile Asp  
 330 335 340

cgt cat atc gca ggg ggc ctg ctg cac gtc aat gcg ctg ggc aac ctg  
 1171  
 Arg His Ile Ala Gly Gly Leu Leu His Val Asn Ala Leu Gly Asn Leu  
 345 350 355

gcg gtg acc gat gcg gga cgt ttg ctt gcc gac ggc atc atc gcc gac  
 1219  
 Ala Val Thr Asp Ala Gly Arg Leu Leu Ala Asp Gly Ile Ile Ala Asp  
 360 365 370

att ttg ctt agt gaa gaa gac taaatattta gtaggggttac aga  
 1263  
 Ile Leu Leu Ser Glu Glu Asp  
 375 380

&lt;210&gt; 802

&lt;211&gt; 380

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 802

Met	Ser	Val	Phe	Gly	Val	Tyr	Ile	His	Val	Pro	Phe	Cys	Ser	Thr	Arg			
1				5					10					15				
Cys	Gly	Tyr	Cys	Asp	Phe	Asn	Thr	Tyr	Thr	Ala	Gly	Glu	Leu	Gly	Ser			
			20					25					30					
Thr	Ala	Gly	Pro	Asp	Thr	Tyr	Leu	Asp	Ser	Leu	Glu	Val	Glu	Leu	Glu			
		35					40					45						
Met	Ala	Val	Ala	Ser	Leu	Asp	Asn	Pro	Arg	Gln	Ala	Glu	Thr	Ile	Phe			
	50					55					60							
Ile	Gly	Gly	Gly	Thr	Pro	Ser	Leu	Ile	Gly	Ala	Asp	Gly	Leu	Ala	Arg			
65					70					75					80			
Val	Leu	Gly	Ala	Val	Arg	Asn	Thr	Phe	Gly	Ile	Ala	Asp	Gly	Ala	Glu			
				85					90					95				
Val	Thr	Thr	Glu	Ser	Asn	Pro	Glu	Ser	Thr	Ser	Pro	Glu	Phe	Phe	Asp			
			100					105					110					
Gly	Leu	Arg	Glu	Ala	Gly	Tyr	Asn	Arg	Ile	Ser	Leu	Gly	Met	Gln	Ser			
		115					120					125						
Ala	Ser	Ser	Ser	Val	Leu	Lys	Val	Leu	Asp	Arg	Thr	His	Thr	Pro	Gly			
	130					135				140								
Arg	Pro	Val	Ala	Ala	Ala	Lys	Glu	Ala	Arg	Glu	Ala	Gly	Phe	Glu	His			
145					150					155					160			
Val	Asn	Leu	Asp	Met	Ile	Tyr	Gly	Thr	Pro	Thr	Glu	Thr	Asp	Asp	Asp			
				165					170					175				
Val	Arg	Lys	Thr	Leu	Asn	Ala	Val	Leu	Glu	Ala	Asn	Val	Asp	His	Val			
			180					185					190					
Ser	Ala	Tyr	Ser	Leu	Ile	Val	Lys	Asp	Gly	Thr	Ala	Met	Ala	Arg	Lys			
		195					200					205						
Val	His	Lys	Gly	Glu	Leu	Pro	Ala	Pro	Asp	Glu	Asp	Val	Tyr	Ala	Asp			
	210					215					220							
Arg	Phe	Glu	Leu	Ile	Asp	Ala	Arg	Leu	Arg	Ser	Ala	Gly	Phe	Asp	Trp			
225					230					235					240			
Tyr	Glu	Val	Ser	Asn	Trp	Ala	Lys	Pro	Gly	Gly	Glu	Cys	Lys	His	Asn			
				245					250					255				
Met	Gly	Tyr	Trp	Val	Asp	Gly	Asp	Trp	Trp	Gly	Ala	Gly	Pro	Gly	Ala			
			260					265					270					
His	Ser	His	Ile	Gly	Asp	Arg	Arg	Phe	Tyr	Asn	Ile	Lys	His	Pro	Ala			
		275					280					285						
Arg	Tyr	Ser	Ala	Gln	Ile	Ala	Ala	Gly	Glu	Leu	Pro	Ile	Lys	Glu	Thr			
	290					295					300							
Glu	Arg	Leu	Thr	Ala	Glu	Asp	His	His	Thr	Glu	Arg	Val	Met	Leu	Gly			
305					310					315					320			
Leu	Arg	Leu	Lys	Gln	Gly	Val	Pro	Leu	Asn	Leu	Phe	Ala	Pro	Ala	Ala			

	325		330		335
Arg Pro Val Ile Asp Arg His Ile Ala Gly Gly Leu Leu His Val Asn					
	340		345		350
Ala Leu Gly Asn Leu Ala Val Thr Asp Ala Gly Arg Leu Leu Ala Asp					
	355		360		365
Gly Ile Ile Ala Asp Ile Leu Leu Ser Glu Glu Asp					
	370		375		380

&lt;210&gt; 803

&lt;211&gt; 522

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(499)

&lt;223&gt; RXN02503

&lt;400&gt; 803

gcagcaccgg caaccacgtc cgtcaacgcg tcagaactgc cggatgcggg tatcgtcgca 60

ttcgtgaacg caccttctgc cacacaaacg agggagtaac	atg acc tta aaa att	115
	Met Thr Leu Lys Ile	
	1 5	

ggt acc cga gga tcc aaa ctt gcc acc acc caa gct ggc acc atc cgc	163
Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln Ala Gly Thr Ile Arg	
10 15 20	

gac cag ctg aaa cac tac gga cgc gac gct gaa ctg cac atc gtg acc	211
Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu Leu His Ile Val Thr	
25 30 35	

acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc	259
Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly	
40 45 50	

gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat	307
Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp	
55 60 65	

gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga	355
Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg	
70 75 80 85	

ttc cac ctg gtc gtg cca act cgt gcg gac tcg cgc gag gcc ctt atc	403
Phe His Leu Val Val Pro Thr Arg Ala Asp Ser Arg Glu Ala Leu Ile	
90 95 100	

gcc cgc gac ggc ctg act ctg gct gag ctt cca gaa agg cgc aaa ggt	451
Ala Arg Asp Gly Leu Thr Leu Ala Glu Leu Pro Glu Arg Arg Lys Gly	
105 110 115	

ggg aac ttc cgc tcc tcg acg cat ctc cca gct caa ggc aat ccg ccc	499
Gly Asn Phe Arg Ser Ser Thr His Leu Pro Ala Gln Gly Asn Pro Pro	
120 125 130	

tgacctggag attctccac tgc

522

&lt;210&gt; 804

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 804

Met	Thr	Leu	Lys	Ile	Gly	Thr	Arg	Gly	Ser	Lys	Leu	Ala	Thr	Thr	Gln
1				5					10					15	

Ala	Gly	Thr	Ile	Arg	Asp	Gln	Leu	Lys	His	Tyr	Gly	Arg	Asp	Ala	Glu
			20					25					30		

Leu	His	Ile	Val	Thr	Thr	Pro	Gly	Asp	Val	Asn	Met	Ser	Pro	Val	Glu
		35					40					45			

Arg	Ile	Gly	Val	Gly	Val	Phe	Thr	Gln	Ala	Leu	Arg	Asp	Val	Leu	His
	50					55					60				

Ser	Gly	Glu	Cys	Asp	Val	Ala	Val	His	Ser	Met	Lys	Asp	Leu	Pro	Thr
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Ala	Thr	Asp	Pro	Arg	Phe	His	Leu	Val	Val	Pro	Thr	Arg	Ala	Asp	Ser
				85					90					95	

Arg	Glu	Ala	Leu	Ile	Ala	Arg	Asp	Gly	Leu	Thr	Leu	Ala	Glu	Leu	Pro
			100					105					110		

Glu	Arg	Arg	Lys	Gly	Gly	Asn	Phe	Arg	Ser	Ser	Thr	His	Leu	Pro	Ala
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Gln	Gly	Asn	Pro	Pro
	130			

&lt;210&gt; 805

&lt;211&gt; 558

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(535)

&lt;223&gt; FRXA02503

&lt;400&gt; 805

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				Met	Thr	Leu	Lys	Ile		
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ggt	acc	cga	gga	tcc	aaa	ctt	gcc	acc	acc	caa	gct	ggc	acc	atc	cgc	163
Gly	Thr	Arg	Gly	Ser	Lys	Leu	Ala	Thr	Thr	Gln	Ala	Gly	Thr	Ile	Arg	
				10					15					20		

gac	cag	ctg	aaa	cac	tac	gga	cgc	gac	gct	gaa	ctg	cac	atc	gtg	acc	211
Asp	Gln	Leu	Lys	His	Tyr	Gly	Arg	Asp	Ala	Glu	Leu	His	Ile	Val	Thr	
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acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc 259  
 Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly  
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 Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp  
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gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga 355  
 Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg  
           70                          75                          80                          85

ttc cac ctg gtc gtg cca act cgt gcg gac tck cgc cga ggs cct tat 403  
 Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa Arg Arg Xaa Pro Tyr  
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cgc ccn cga cgg sct gan ttt kgg ttr agc tty caa aar gsg saa agg 451  
 Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa Gln Xaa Xaa Xaa Arg  
                           105                          110                          115

tgg gaa ctt tcc gct cct cga cgc atc tcc cag ctc aag gca atc cgc 499  
 Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg  
           120                          125                          130

cct gac ctg gag att ctc cca ctt gcg cgg aaa cat tgacaccggc 545  
 Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys His  
           135                          140                          145

atgggcaagg tca 558

&lt;210&gt; 806

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 806

Met Thr Leu Lys Ile Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln  
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Ala Gly Thr Ile Arg Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu  
                           20                          25                          30

Leu His Ile Val Thr Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu  
                           35                          40                          45

Arg Ile Gly Val Gly Val Phe Thr Gln Ala Leu Arg Asp Val Leu His  
           50                          55                          60

Ser Gly Glu Cys Asp Val Ala Val His Ser Met Lys Asp Leu Pro Thr  
           65                          70                          75                          80

Ala Thr Asp Pro Arg Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa  
                           85                          90                          95

Arg Arg Xaa Pro Tyr Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa  
                           100                          105                          110

Gln Xaa Xaa Xaa Arg Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln  
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His  
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 <223> RXA00377

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 Val Trp Leu Leu Phe  
 1 5

cta aat tgg gat aaa tgg ggc aag att gag cgc atg tct gct ctt act 163  
 Leu Asn Trp Asp Lys Trp Gly Lys Ile Glu Arg Met Ser Ala Leu Thr  
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 Ile Pro Ala Ala Arg Arg Thr Leu Asn Asn Ala Pro Ile Ile Asp Ala  
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gct aat ggc aag acc ccg act cgc act ccg gtg tgg ttt atg cgc cag 259  
 Ala Asn Gly Lys Thr Pro Thr Arg Thr Pro Val Trp Phe Met Arg Gln  
 40 45 50

gcg ggt agg tcg ttg cct gag tac aag aag gtc cgt gag gga atc agc 307  
 Ala Gly Arg Ser Leu Pro Glu Tyr Lys Lys Val Arg Glu Gly Ile Ser  
 55 60 65

atg ttg gat tcc tgt ttc atg ccg gag ttg ttg gcg gag att act ttg 355  
 Met Leu Asp Ser Cys Phe Met Pro Glu Leu Leu Ala Glu Ile Thr Leu  
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cag ccg gtt cgt cgt cat gat gtg gat gct gcg att ttg ttc tct gac 403  
 Gln Pro Val Arg Arg His Asp Val Asp Ala Ala Ile Leu Phe Ser Asp  
 90 95 100

att gtg gtg ccg ttg cgt gct gcg ggt gtt ggt gtg gaa atc gtg gcg 451  
 Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly Val Glu Ile Val Ala  
 105 110 115

ggt cgt gga cct gtg ttg gat gcg ccg gtg cgg agc cgt ggg gat gtg 499  
 Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg Ser Arg Gly Asp Val  
 120 125 130

ttg aat ctt cct att ttg gag ggc aac gtt ccg gag gtg gag cag ggt 547  
 Leu Asn Leu Pro Il Leu Glu Gly Asn Val Pro Glu Val Glu Gln Gly  
 135 140 145

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Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser Gln Ala Leu Ile Gly	
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Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr Leu Val Glu Gly Gly	
170 175 180	
cct tcc aag aat cat gag aag acc aaa gca atg atg cat ggt gat cct	691
Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met Met His Gly Asp Pro	
185 190 195	
gag acg tgg cat gcg ttg atg gct cgt ttg gtg ccg acg att gtg aat	739
Glu Thr Trp His Ala Leu Met Ala Arg Leu Val Pro Thr Ile Val Asn	
200 205 210	
tct ttg aag tcg cag atc gat gcg ggt atc gat gcg gtg cag ttg ttt	787
Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp Ala Val Gln Leu Phe	
215 220 225	
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Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp Tyr Thr Glu Phe Val	
230 235 240 245	
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Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val Gly Lys Tyr Gln Leu	
250 255 260	
cct cgt att cac ttt ggt gtg ggt act ggt gag ttg ctt ggt gcg atg	931
Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu Leu Leu Gly Ala Met	
265 270 275	
agc aag gct ggc tca gag gtc atg ggt gtg gat tgg cgg gtg ccg ttg	979
Ser Lys Ala Gly Ser Glu Val Met Gly Val Asp Trp Arg Val Pro Leu	
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1171 Ala Gly His Ala Thr Gly His Ile Phe Asn Leu Gly His Gly Val Leu	
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 Ser

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                   20                  25                  30  
 Pro Ile Ile Asp Ala Ala Asn Gly Lys Thr Pro Thr Arg Thr Pro Val  
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 Trp Phe Met Arg Gln Ala Gly Arg Ser Leu Pro Glu Tyr Lys Lys Val  
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 Arg Glu Gly Ile Ser Met Leu Asp Ser Cys Phe Met Pro Glu Leu Leu  
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 Ala Glu Ile Thr Leu Gln Pro Val Arg Arg His Asp Val Asp Ala Ala  
                   85                  90                  95  
 Ile Leu Phe Ser Asp Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly  
                   100                  105                  110  
 Val Glu Ile Val Ala Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg  
       115                  120                  125  
 Ser Arg Gly Asp Val Leu Asn Leu Pro Ile Leu Glu Gly Asn Val Pro  
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 Glu Val Glu Gln Gly Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser  
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 Gln Ala Leu Ile Gly Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr  
                   165                  170                  175  
 Leu Val Glu Gly Gly Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met  
                   180                  185                  190  
 Met His Gly Asp Pro Glu Thr Trp His Ala Leu Met Ala Arg Leu Val  
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 Pro Thr Ile Val Asn Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp  
       210                  215                  220  
 Ala Val Gln Leu Phe Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp  
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 Tyr Thr Glu Phe Val Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val  
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				Val	Gly	Thr	Ser	Ala									
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cct	cga	cgc	atc	tcc	cag	ctc	aag	gca	atc	cgc	cct	gac	ctg	gag	att	163	
Pro	Arg	Arg	Ile	Ser	Gln	Leu	Lys	Ala	Ile	Arg	Pro	Asp	Leu	Glu	Ile		
				10					15					20			
ctc	cca	ctg	cgc	gga	aac	att	gac	acc	ggc	atg	ggc	aag	gtc	acc	tcc	211	
Leu	Pro	Leu	Arg	Gly	Asn	Ile	Asp	Thr	Gly	Met	Gly	Lys	Val	Thr	Ser		
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Gly	Met	Gln	Asp	Arg	Ala	Thr	Glu	Val	Phe	Asp	Ala	Asp	Ile	Ile	Met		
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ccc	gcc	ccc	gca	cag	ggc	gca	ctt	gcg	atc	gaa	tgc	cgc	gcc	gac	gac	355	
Pro	Ala	Pro	Ala	Gln	Gly	Ala	Leu	Ala	Ile	Glu	Cys	Arg	Ala	Asp	Asp		
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 Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe  
                   90                  95                  100

gtt tcc gcg gtt gca gaa cgc acc gtg ctc aac cgc ctc gaa gct ggc 451  
 Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly  
                   105                  110                  115

tgt acc gcg cct gtc gca gcg cac gcc acc ttg gac ggc tac tcc ggc 499  
 Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly  
                   120                  125                  130

gac acc atg act ctc acc gcc ggc gtc tac gca ctt gac ggc tct gac 547  
 Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp  
                   135                  140                  145

cag ctg gta ttc tcc gcc gaa ggt gac ggc gcc cgc cca gaa gag ctc 595  
 Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu  
                   150                  155                  160                  165

ggc gag ctc gtt gca caa cag ctt atc gac gcc gga gcc gcc aat ttg 643  
 Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala Gly Ala Ala Asn Leu  
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ctc ggc gac cgc agc taattagggc ccgaaatttc cat 681  
 Leu Gly Asp Arg Ser  
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                   20                  25                  30

Gly Lys Val Thr Ser Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala  
                   35                  40                  45

Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp  
                   50                  55                  60

Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu  
   65                  70                  75                  80

Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met  
                   85                  90                  95

His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn  
                   100                  105                  110

Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu  
                   115                  120                  125

Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala  
                   130                  135                  140

Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala  
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Met Leu Val Met Leu  
1 5

gcc tac gca ggc ctc acc cgc gtc ggc atg cag gac cgc gca acg gaa 163  
Ala Tyr Ala Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu  
10 15 20

gtt ttc gac gcc gac atc atc atg ccc gcc ccc gca cag ggc gca ctt 211  
Val Phe Asp Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu  
25 30 35

gcg atc gaa tgc cgc gcc gac gac act gaa acc gtc cgc gcg ctc aac 259  
Ala Ile Glu Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn  
40 45 50

atg ctg atg cac gcc gac acg ttt gtt tcc gcg gtt gca gaa cgc acc 307  
Met Leu Met His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr  
55 60 65

gtg ctc aac cgc ctc gaa gct ggc tgt acc gcg cct gtc gca gcg cac 355  
Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His  
70 75 80 85

gcc acc ttg gac ggc tac tcc ggc gac acc atg act ctc acc gcc ggc 403  
Ala Thr Leu Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly  
90 95 100

gtc tac gca ctt gac ggc tct gac cag ctg gta ttc tcc gcc gaa ggt 451  
Val Tyr Ala Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly  
105 110 115

gac ggc gcc cgc cca gaa gag ctc ggc gag ctc gtt gca caa cag ctt 499  
Asp Gly Ala Arg Pro Glu Glu Leu Gly Glu Leu Val Ala Gln Gln Leu  
120 125 130

atc gac gcc gga gcc gcc aat ttg ctc ggc gac cgc agc taattagggc 548

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561

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 35 40 45

Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe Val Ser Ala  
 50 55 60

Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala  
 65 70 75 80

Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly Asp Thr Met  
 85 90 95

Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp Gln Leu Val  
 100 105 110

Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu Gly Glu Leu  
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Arg Ser  
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 <223> RXN01162

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 Met Tyr Ile Val Gly  
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att tgt cta caa tta gtg gtt atg agc caa ccg atg tca gca ccc gac 163

Ile	Cys	Leu	Gln	Leu	Val	Val	Met	Ser	Gln	Pro	Met	Ser	Ala	Pro	Asp	
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Ser	Ala	Pro	Gly	Thr	Glu	Arg	Gly	His	Glu	Arg	Thr	His	Phe	Ala	Val	
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gtc	ggt	gac	tcc	cag	gat	cca	gca	cag	gca	aca	gct	cct	aga	gcg	cca	259
Val	Gly	Asp	Ser	Gln	Asp	Pro	Ala	Gln	Ala	Thr	Ala	Pro	Arg	Ala	Pro	
		40					45					50				
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Ala	Glu	Ser	Ile	Thr	Leu	Ile	Gly	Ile	Gly	Thr	Asp	Gly	Phe	Glu	Gly	
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Leu	Gly	Leu	Lys	Ala	Gln	Gln	Ala	Leu	Gln	Arg	Ala	Ser	Val	Val	Ile	
	70				75					80					85	
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Gly	Ser	Trp	Arg	Gln	Leu	Asn	Leu	Val	Pro	Asp	Ala	Ile	Lys	Ala	Glu	
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Arg	Arg	Pro	Trp	Pro	Gly	Asn	Thr	Lys	His	Pro	Asp	Leu	Asp	Ala	Leu	
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ttt	aaa	gag	ttc	ctc	ggt	cgg	cat	gtt	gct	gtt	ctg	gcc	tct	ggc	gat	499
Phe	Lys	Glu	Phe	Leu	Gly	Arg	His	Val	Ala	Val	Leu	Ala	Ser	Gly	Asp	
		120					125					130				
cca	ctg	ttt	tac	ggc	gtg	ggc	acc	gca	atg	gtc	cat	gtg	ctg	ggg	atg	547
Pro	Leu	Phe	Tyr	Gly	Val	Gly	Thr	Ala	Met	Val	His	Val	Leu	Gly	Met	
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gat	aga	ctc	acg	gtt	att	ccg	gga	cca	tca	tcc	gcg	tcg	ctt	gct	tgc	595
Asp	Arg	Leu	Thr	Val	Ile	Pro	Gly	Pro	Ser	Ser	Ala	Ser	Leu	Ala	Cys	
	150				155					160					165	
gcc	cgc	ttg	ggt	tgg	aca	gtc	aac	cgc	aca	cgg	gtg	gtg	tac	cta	gga	643
Ala	Arg	Leu	Gly	Trp	Thr	Val	Asn	Arg	Thr	Arg	Val	Val	Tyr	Leu	Gly	
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caa	gaa	ccc	att	gag	aca	ctc	atc	ccg	att	att	gaa	tca	ggc	gct	caa	691
Gln	Glu	Pro	Ile	Glu	Thr	Leu	Ile	Pro	Ile	Ile	Glu	Ser	Gly	Ala	Gln	
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Phe	Leu	Val	Leu	Gly	Lys	Asp	Glu	Phe	Ser	Thr	Ala	Gln	Val	Ala	Thr	
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Leu	Leu	Asn	Glu	Leu	Gly	Leu	Gly	Glu	Thr	Pro	Leu	Thr	Val	Leu	Ser	
		215				220					225					
gat	ttg	ggc	agt	act	gat	gag	gag	atc	acc	caa	ggc	aca	gct	tca	cat	835
Asp	Leu	Gly	Ser	Thr	Asp	Glu	Glu	Ile	Thr	Gln	Gly	Thr	Ala	Ser	His	
	230				235					240					245	
cca	cca	gct	gca	gtg	tct	gtt	ctc	aac	gtg	att	gct	gtg	gga	gct	cgc	883
Pro	Pro	Ala	Ala	Val	Ser	Val	Leu	Asn	Val	Ile	Ala	Val	Gly	Ala	Arg	

250								255					260					
acc gca atg ccg aaa ccc cac ttt gaa ggc gac gta tca aac gaa gac	931																	
Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp																		
265	270	275																
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg	979																	
Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met																		
280	285	290																
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta																		
1027																		
Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu																		
295	300	305																
cgc gca gcc ggc aac aag gcg cac gcc att agt ttt gcc tcc atg gtt																		
1075																		
Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val																		
310	315	320	325															
gag caa agc caa agg aat gct cgc aaa cta ggt gta tcc acc ctc agt																		
1123																		
Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser																		
330	335	340																
gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta																		
1171																		
Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val																		
345	350	355																
caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc																		
1219																		
Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly																		
360	365	370																
cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct																		
1267																		
Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro																		
375	380	385																
gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag																		
1315																		
Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys																		
390	395	400	405															
ctt cac aca ctc caa gaa caa cac ggc gga atc atc aaa cac atc cgc																		
1363																		
Leu His Thr Leu Gln Glu Gln His Gly Gly Ile Ile Lys His Ile Arg																		
410	415	420																
atc gac gac aca gac gtg cac caa tgg cga gtt aca aag ccg gtg act																		
1411																		
Ile Asp Asp Thr Asp Val His Gln Trp Arg Val Thr Lys Pro Val Thr																		
425	430	435																
cca gaa gcg gtg aat tagcatcaaa aaccaacccc atg																		
1449																		
Pro Glu Ala Val Asn																		
440																		

<210> 814  
 <211> 442  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 814

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Met	Ser	Ala	Pro	Asp	Ser	Ala	Pro	Gly	Thr	Glu	Arg	Gly	His	Glu	Arg	20	25	30	
Thr	His	Phe	Ala	Val	Val	Gly	Asp	Ser	Gln	Asp	Pro	Ala	Gln	Ala	Thr	35	40	45	
Ala	Pro	Arg	Ala	Pro	Ala	Glu	Ser	Ile	Thr	Leu	Ile	Gly	Ile	Gly	Thr	50	55	60	
Asp	Gly	Phe	Glu	Gly	Leu	Gly	Leu	Lys	Ala	Gln	Gln	Ala	Leu	Gln	Arg	65	70	75	80
Ala	Ser	Val	Val	Ile	Gly	Ser	Trp	Arg	Gln	Leu	Asn	Leu	Val	Pro	Asp	85	90	95	
Ala	Ile	Lys	Ala	Glu	Arg	Arg	Pro	Trp	Pro	Gly	Asn	Thr	Lys	His	Pro	100	105	110	
Asp	Leu	Asp	Ala	Leu	Phe	Lys	Glu	Phe	Leu	Gly	Arg	His	Val	Ala	Val	115	120	125	
Leu	Ala	Ser	Gly	Asp	Pro	Leu	Phe	Tyr	Gly	Val	Gly	Thr	Ala	Met	Val	130	135	140	
His	Val	Leu	Gly	Met	Asp	Arg	Leu	Thr	Val	Ile	Pro	Gly	Pro	Ser	Ser	145	150	155	160
Ala	Ser	Leu	Ala	Cys	Ala	Arg	Leu	Gly	Trp	Thr	Val	Asn	Arg	Thr	Arg	165	170	175	
Val	Val	Tyr	Leu	Gly	Gln	Glu	Pro	Ile	Glu	Thr	Leu	Ile	Pro	Ile	Ile	180	185	190	
Glu	Ser	Gly	Ala	Gln	Phe	Leu	Val	Leu	Gly	Lys	Asp	Glu	Phe	Ser	Thr	195	200	205	
Ala	Gln	Val	Ala	Thr	Leu	Leu	Asn	Glu	Leu	Gly	Leu	Gly	Glu	Thr	Pro	210	215	220	
Leu	Thr	Val	Leu	Ser	Asp	Leu	Gly	Ser	Thr	Asp	Glu	Glu	Ile	Thr	Gln	225	230	235	240
Gly	Thr	Ala	Ser	His	Pro	Pro	Ala	Ala	Val	Ser	Val	Leu	Asn	Val	Ile	245	250	255	
Ala	Val	Gly	Ala	Arg	Thr	Ala	Met	Pro	Lys	Pro	His	Phe	Glu	Gly	Asp	260	265	270	
Val	Ser	Asn	Glu	Asp	Leu	Arg	Ala	Leu	Thr	Val	Ala	Ala	Leu	Glu	Pro	275	280	285	
Thr	Gln	Gly	Gln	Met	Leu	Trp	Thr	Phe	Gly	Asp	Ile	Gly	Ala	Ala	Leu				

290	295	300
Ala Cys Asp Trp Leu Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser 305 310 315 320		
Phe Ala Ser Met Val Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly 325 330 335		
Val Ser Thr Leu Ser Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys 340 345 350		
Asp Ile Arg Tyr Val Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile 355 360 365		
Phe Met Asn Lys Gly Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp 370 375 380		
Met Met Leu Arg Pro Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu 385 390 395 400		
Asp Asn Ile Ala Lys Leu His Thr Leu Gln Glu Gln His Gly Gly Ile 405 410 415		
Ile Lys His Ile Arg Ile Asp Asp Thr Asp Val His Gln Trp Arg Val 420 425 430		
Thr Lys Pro Val Thr Pro Glu Ala Val Asn 435 440		

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 <212> DNA  
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 <223> FRXA01162

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 Met Tyr Ile Val Gly  
 1 5  
 att tgt cta caa tta gtg gtt atg agc caa ccg atg tca gca ccc gac 163  
 Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro Met Ser Ala Pro Asp  
 10 15 20  
 tcc gct cca gga aca gag cgc ggt cat gaa cgc acc cat ttt gcg gta 211  
 Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg Thr His Phe Ala Val  
 25 30 35  
 gtc ggt gac tcc cag gat cca gca cag gca aca gct cct aga gcg cca 259  
 Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr Ala Pro Arg Ala Pro  
 40 45 50  
 gca gaa tca att act ttg att ggt att ggt acc gat ggg ttt gag ggg 307  
 Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr Asp Gly Phe Glu Gly



55	60	65	
ctc gga ctc aag gca cag caa gca tta caa cgt gcc tct gtg gtg att Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg Ala Ser Val Val Ile 70 75 80 85			355
gga tca tgg cgc cag ctc aat ctc gta cct gat gcc att aag gca gag Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp Ala Ile Lys Ala Glu 90 95 100			403
cgt cgc cca tgg ccg ggt aat acc aag cat cct gat tta gat gcc ttg Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro Asp Leu Asp Ala Leu 105 110 115			451
ttt aaa gag ttc ctc ggt cgg cat gtt gct gtt ctg gcc tct ggc gat Phe Lys Glu Phe Leu Gly Arg His Val Ala Val Leu Ala Ser Gly Asp 120 125 130			499
cca ctg ttt tac ggc gtg ggc acc gca atg gtc cat gtg ctg ggg atg Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val His Val Leu Gly Met 135 140 145			547
gat aga ctc acg gtt att ccg gga cca tca tcc gcg tcg ctt gct tgc Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser Ala Ser Leu Ala Cys 150 155 160 165			595
gcc cgc ttg ggt tgg aca gtc aac cgc aca cgg gtg gtg tac cta gga Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg Val Val Tyr Leu Gly 170 175 180			643
caa gaa ccc att gag aca ctc atc ccg att att gaa tca ggc gct caa Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile Glu Ser Gly Ala Gln 185 190 195			691
ttc ctc gtc ttg ggt aaa gat gaa ttc agt aca gct caa gtt gcc acg Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr Ala Gln Val Ala Thr 200 205 210			739
ttg ttg aat gaa ctc gga ctg ggg gag act cca ctg act gtg ctc agc Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro Leu Thr Val Leu Ser 215 220 225			787
gat ttg ggc agt act gat gag gag atc acc caa ggc aca gct tca cat Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln Gly Thr Ala Ser His 230 235 240 245			835
cca cca gct gca gtg tct gtt ctc aac gtg att gct gtg gga gct cgc Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile Ala Val Gly Ala Arg 250 255 260			883
acc gca atg ccg aaa ccc cac ttt gaa ggc gac gta tca aac gaa gac Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp 265 270 275			931
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met 280 285 290			979
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta 1027 Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu			

295	300	305
cgc gca gcc ggc aac aag gcg cac gcc att agt ttt gcc tcc atg gtt 1075		
Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val 310 315 320 325		
gag caa agc caa agg aat gct cgc aaa cta ggt gta tcc acc ctc agt 1123		
Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser 330 335 340		
gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta 1171		
Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val 345 350 355		
caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc 1219		
Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly 360 365 370		
cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct 1267		
Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro 375 380 385		
gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag 1315		
Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys 390 395 400 405		
ctt cac aca ctc caa gaa caa cac ggc gga 1345		
Leu His Thr Leu Gln Glu Gln His Gly Gly 410 415		

&lt;210&gt; 816

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 816

Met Tyr Ile Val Gly Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro
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Met Ser Ala Pro Asp Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg
20 25 30

Thr His Phe Ala Val Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr
35 40 45

Ala Pro Arg Ala Pro Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr
50 55 60

Asp Gly Phe Glu Gly Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg
65 70 75 80

Ala Ser Val Val Ile Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp
85 90 95

Ala Ile Lys Ala Glu Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro  
 100 105 110  
 Asp Leu Asp Ala Leu Phe Lys Glu Phe Leu Gly Arg His Val Ala Val  
 115 120 125  
 Leu Ala Ser Gly Asp Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val  
 130 135 140  
 His Val Leu Gly Met Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser  
 145 150 155 160  
 Ala Ser Leu Ala Cys Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg  
 165 170 175  
 Val Val Tyr Leu Gly Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile  
 180 185 190  
 Glu Ser Gly Ala Gln Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr  
 195 200 205  
 Ala Gln Val Ala Thr Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro  
 210 215 220  
 Leu Thr Val Leu Ser Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln  
 225 230 235 240  
 Gly Thr Ala Ser His Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile  
 245 250 255  
 Ala Val Gly Ala Arg Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp  
 260 265 270  
 Val Ser Asn Glu Asp Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro  
 275 280 285  
 Thr Gln Gly Gln Met Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu  
 290 295 300  
 Ala Cys Asp Trp Leu Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser  
 305 310 315 320  
 Phe Ala Ser Met Val Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly  
 325 330 335  
 Val Ser Thr Leu Ser Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys  
 340 345 350  
 Asp Ile Arg Tyr Val Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile  
 355 360 365  
 Phe Met Asn Lys Gly Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp  
 370 375 380  
 Met Met Leu Arg Pro Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu  
 385 390 395 400  
 Asp Asn Ile Ala Lys Leu His Thr Leu Gln Glu Gln His Gly Gly  
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<211> 873
<212> DNA
<213> Corynebacterium glutamicum
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<223> RXA01692
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**<400> 817**

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gttcggggttc tggcaattgt tgggactagg attaatgccc atg acg att tcc caa	115
Met Thr Ile Ser Gln	
1 5	
gaa aac cag cca ata atc cag cca gtc tcc tta att ggt gga ggt cct	163
Glu Asn Gln Pro Ile Ile Gln Pro Val Ser Leu Ile Gly Gly Gly Pro	
10 15 20	
ggg gca tgg gac tta att acg gtg cgt ggg atg aat cgc ctt cag gag	211
Gly Ala Trp Asp Leu Ile Thr Val Arg Gly Met Asn Arg Leu Gln Glu	
25 30 35	
gct gat gtc att ttg gct gat cac ttg ggg ccc act gat gag ttg gaa	259
Ala Asp Val Ile Leu Ala Asp His Leu Gly Pro Thr Asp Glu Leu Glu	
40 45 50	
aaa ttg tgc gac atc agc tcg aag act gtt gtt gat gtg tcc aag ctt	307
Lys Leu Cys Asp Ile Ser Ser Lys Thr Val Val Asp Val Ser Lys Leu	
55 60 65	
ccg tat ggg cgg cag gtc act cag gag cgt act aat gag atg ctt gtt	355
Pro Tyr Gly Arg Gln Val Thr Gln Glu Arg Thr Asn Glu Met Leu Val	
70 75 80 85	
gaa tac gca cag cag gga cta aag gtg gtt cgc ctt aaa ggt ggt gac	403
Glu Tyr Ala Gln Gln Gly Leu Lys Val Val Arg Leu Lys Gly Gly Asp	
90 95 100	
cct tat gtc ttc ggt cgg ggt ttt gaa gag ttg gag ttt ttg ggc gag	451
Pro Tyr Val Phe Gly Arg Gly Phe Glu Glu Leu Glu Phe Leu Gly Glu	
105 110 115	
cat gga att gaa tgc gag gtc att ccg ggt gtg acc agt gcg gtg tcc	499
His Gly Ile Glu Cys Glu Val Ile Pro Gly Val Thr Ser Ala Val Ser	
120 125 130	
gtt cca gcg gcg gca ggt att cct att act aat ccg gga gtg gtg cat	547
Val Pro Ala Ala Ala Gly Ile Pro Ile Thr Asn Arg Gly Val Val His	
135 140 145	
tcc ttt acc gtg gtg tct gga cat ttg cct cca ggc cat ccg aag tca	595
Ser Phe Thr Val Val Ser Gly His Leu Pro Pro Gly His Pro Lys Ser	
150 155 160 165	
ctg gtt gat tgg gct gcg ttg gcc aaa tcg ggt ggc acc ttg tcc atc	643
Leu Val Asp Trp Ala Ala Leu Ala Lys Ser Gly Gly Thr Leu Ser Ile	
170 175 180	

atc atg ggt gtg aaa aat gcg ggt gcg att gcc cag gcg ctc atg gac 691  
 Ile Met Gly Val Lys Asn Ala Gly Ala Ile Ala Gln Ala Leu Met Asp  
                   185                                  190                                  195

ggc ggg ctt gat gca gat act cca gca gct gtt att cag gaa ggc act 739  
 Gly Gly Leu Asp Ala Asp Thr Pro Ala Ala Val Ile Gln Glu Gly Thr  
                   200                                  205                                  210

act gat gca caa cgc tca gtt cgg tgc acc ttg ggc aca ttg ggt gca 787  
 Thr Asp Ala Gln Arg Ser Val Arg Cys Thr Leu Gly Thr Leu Gly Ala  
                   215                                  220                                  225

gtc atg gtg gag gaa gag att aag cct cca gct gtg tat gtc att gga 835  
 Val Met Val Glu Glu Glu Ile Lys Pro Pro Ala Val Tyr Val Ile Gly  
                   230                                  235                                  240                                  245

caa gtt gct ggc ctc taagcagatc gcctaagaat ggg 873  
 Gln Val Ala Gly Leu  
                                   250

<210> 818

<211> 250

<212> PRT

<213> Corynebacterium glutamicum.

<400> 818

Met Thr Ile Ser Gln Glu Asn Gln Pro Ile Ile Gln Pro Val Ser Leu  
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Ile Gly Gly Gly Pro Gly Ala Trp Asp Leu Ile Thr Val Arg Gly Met  
                   20                                  25                                  30

Asn Arg Leu Gln Glu Ala Asp Val Ile Leu Ala Asp His Leu Gly Pro  
                   35                                  40                                  45

Thr Asp Glu Leu Glu Lys Leu Cys Asp Ile Ser Ser Lys Thr Val Val  
                   50                                  55                                  60

Asp Val Ser Lys Leu Pro Tyr Gly Arg Gln Val Thr Gln Glu Arg Thr  
   65                                  70                                  75                                  80

Asn Glu Met Leu Val Glu Tyr Ala Gln Gln Gly Leu Lys Val Val Arg  
                   85                                  90                                  95

Leu Lys Gly Gly Asp Pro Tyr Val Phe Gly Arg Gly Phe Glu Glu Leu  
                   100                                  105                                  110

Glu Phe Leu Gly Glu His Gly Ile Glu Cys Glu Val Ile Pro Gly Val  
                   115                                  120                                  125

Thr Ser Ala Val Ser Val Pro Ala Ala Ala Gly Ile Pro Ile Thr Asn  
                   130                                  135                                  140

Arg Gly Val Val His Ser Phe Thr Val Val Ser Gly His Leu Pro Pro  
   145                                  150                                  155                                  160

Gly His Pro Lys Ser Leu Val Asp Trp Ala Ala Leu Ala Lys Ser Gly  
                   165                                  170                                  175

Gly Thr Leu Ser Ile Ile Met Gly Val Lys Asn Ala Gly Ala Ile Ala  
 180 185 190

Gln Ala Leu Met Asp Gly Gly Leu Asp Ala Asp Thr Pro Ala Ala Val  
 195 200 205

Ile Gln Glu Gly Thr Thr Asp Ala Gln Arg Ser Val Arg Cys Thr Leu  
 210 215 220

Gly Thr Leu Gly Ala Val Met Val Glu Glu Glu Ile Lys Pro Pro Ala  
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Val Tyr Val Ile Gly Gln Val Ala Gly Leu  
 245 250

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(1894)  
 <223> RXN00371

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 Met Thr Ile Ala His  
 1 5

aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc 163  
 Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser  
 10 15 20

gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt 211  
 Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val  
 25 30 35

tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca 259  
 Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro  
 40 45 50

ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt 307  
 Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu  
 55 60 65

aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act 355  
 Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr  
 70 75 80 85

gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att 403  
 Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe Val Ala Thr Glu Ile  
 90 95 100

cct gtg ccg gaa gat aag ctt cag gct gcg gaa gat gag tac gag cgc 451  
 Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu Asp Glu Tyr Glu Arg  
 105 110 115

atc tgc att gaa gcg aag gag aac ggt gca cgc cgt aag cct cct cgt 499  
 Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg Arg Lys Pro Pro Arg  
 120 125 130

cca gca cca cca acc gct gca gag atc acg gaa gtt tct gag gcg act 547  
 Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu Val Ser Glu Ala Thr  
 135 140 145

cca gct cag att gtt gag ctt gtg cag gat gct ctt tct tat ggt gga 595  
 Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala Leu Ser Tyr Gly Gly  
 150 155 160 165

gat gtt att cgt ctt gtc acc ggc aac cca ttg agc agc gat gcc aca 643  
 Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu Ser Ser Asp Ala Thr  
 170 175 180

ctg gct gag atc tct gca gtt tcc gag gct ggc ctg gag ttc cag gtg 691  
 Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly Leu Glu Phe Gln Val  
 185 190 195

gtt cca ggt atg tct ttg cct gca acg gtt cct gca ttt gcg gga att 739  
 Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro Ala Phe Ala Gly Ile  
 200 205 210

gcg ttg ggt tct acc tac acc gaa act gat gtc aac ggt caa aac ttg 787  
 Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val Asn Gly Gln Asn Leu  
 215 220 225

gac tgg gat cag ttg gct agc gca cct cag cct ttg gtg ctg cag gcc 835  
 Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro Leu Val Leu Gln Ala  
 230 235 240 245

cgc gtg gat gac ctt tcc cgt att gca cag gaa cta aag gcc cgc aat 883  
 Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu Leu Lys Ala Arg Asn  
 250 255 260

atg tct ttg gaa act cct gtt tct gtc acc gct aac ggc acc acc cgt 931  
 Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala Asn Gly Thr Thr Arg  
 265 270 275

ttg cag cgc acc tat gac acc act tta ggt ctg ttg cac aag ctt gat 979  
 Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu Leu His Lys Leu Asp  
 280 285 290

gct gaa cta agc gga cct ttg gtt gtt acc ttg ggc aag ggt gtg gat  
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 Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu Gly Lys Gly Val Asp  
 295 300 305

gat cgc tcc aag tac tct tgg tgg gaa aac cgc gct ctg tac ggt tgg  
 1075  
 Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg Ala Leu Tyr Gly Trp  
 310 315 320 325

cgt gtg ctg gtg cct cgc gct cgg gag caa gcg gca tcc atg tcc gca  
 1123  
 Arg Val Leu Val Pro Arg Ala Arg Glu Gln Ala Ala Ser Met Ser Ala  
 330 335 340

cgt ctg agc agc cac ggc gct atc ccg cag gaa gtc cct acc att tct  
 1171

Arg Leu Ser Ser His Gly Ala Ile Pro Gln Glu Val Pro Thr Ile Ser  
 345 350 355  
 gtc gaa cca ccg cgc aac cca gcg caa atg gaa cgc gcc atc aag ggc  
 1219  
 Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala Ile Lys Gly  
 360 365 370  
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 Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser Val Asn Ala  
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 Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys Thr Ala Ala  
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 1459  
 Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu Tyr Phe Glu  
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 Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala Asp Ile Ala  
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 Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val Ala Phe Thr  
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 Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly Lys Pro His  
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 1747  
 Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala Ala Thr Ala



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cca	gaa	ctg	atc	gac	gct	ctt	gcg	gaa	cac	gtg	gcg	gat	ctg	cgc	gct
1843															
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Asn	Leu	Arg	Pro	Val	Ser	Ser	Phe	Glu	Gly	Gln	His	Glu	Gly	Gln	Thr
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Val	Arg	Ala	Ile	Thr	Asp	Glu	Gln	Val	Leu	Ser	Gly	Val	Arg	Ala	Phe
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Val	Ala	Thr	Glu	Ile	Pro	Val	Pro	Glu	Asp	Lys	Leu	Gln	Ala	Ala	Glu
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Asp	Glu	Tyr	Glu	Arg	Ile	Cys	Ile	Glu	Ala	Lys	Glu	Asn	Gly	Ala	Arg
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Arg	Lys	Pro	Pro	Arg	Pro	Ala	Pro	Pro	Thr	Ala	Ala	Glu	Ile	Thr	Glu
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Val	Ser	Glu	Ala	Thr	Pro	Ala	Gln	Ile	Val	Glu	Leu	Val	Gln	Asp	Ala
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Leu	Ser	Tyr	Gly	Gly	Asp	Val	Ile	Arg	Leu	Val	Thr	Gly	Asn	Pro	Leu
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Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly  
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 Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro  
 195 200 205  
 Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val  
 210 215 220  
 Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro  
 225 230 235 240  
 Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu  
 245 250 255  
 Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala  
 260 265 270  
 Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu  
 275 280 285  
 Leu His Lys Leu Asp Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu  
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 Gly Lys Gly Val Asp Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg  
 305 310 315 320  
 Ala Leu Tyr Gly Trp Arg Val Leu Val Pro Arg Ala Arg Glu Gln Ala  
 325 330 335  
 Ala Ser Met Ser Ala Arg Leu Ser Ser His Gly Ala Ile Pro Gln Glu  
 340 345 350  
 Val Pro Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu  
 355 360 365  
 Arg Ala Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu  
 370 375 380  
 Thr Ser Val Asn Ala Val Lys Ala Val Trp Glu Lys Ile Thr Glu Phe  
 385 390 395 400  
 Gly Leu Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly  
 405 410 415  
 Glu Lys Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu  
 420 425 430  
 Leu Pro Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe  
 435 440 445  
 Pro Glu Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro  
 450 455 460  
 Arg Ala Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu  
 465 470 475 480  
 Gly Trp Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala  
 485 490 495

Pro Pro Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp  
                   500                                  505                                  510

Ala Val Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile  
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Ala Gly Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met  
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Thr Ala Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro  
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Glu Ile Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val  
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aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc 163  
 Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser  
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gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt 211  
 Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val  
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tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca 259  
 Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro  
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ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt 307  
 Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu  
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aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act 355  
 Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr  
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gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att 403  
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90										95					100					
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Pro	Ala	Pro	Pro	Thr	Ala	Ala	Glu	Ile	Thr	Glu	Val	Ser	Glu	Ala	Thr					
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cca	gct	cag	att	gtt	gag	ctt	gtg	cag	gat	gct	ctt	tct	tat	ggg	gga	595				
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Asp	Val	Ile	Arg	Leu	Val	Thr	Gly	Asn	Pro	Leu	Ser	Ser	Asp	Ala	Thr					
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Leu	Ala	Glu	Ile	Ser	Ala	Val	Ser	Glu	Ala	Gly	Leu	Glu	Phe	Gln	Val					
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gac	tgg	gat	cag	ttg	gct	agc	gca	cct	cag	cct	ttg	gtg	ctg	cag	gcc	835				
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cgc	gtg	gat	gac	ctt	tcc	cgt	att	gca	cag	gaa	cta	aag	gcc	cgc	aat	883				
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Leu	Gln	Arg	Thr	Tyr	Asp	Thr	Thr	Leu	Gly	Leu	Leu	His	Lys	Leu	Asp					
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&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 822

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 Asn Leu Arg Pro Val Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr  
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 Glu Glu Leu Leu Pro Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly  
 50 55 60  
 Asn Pro Asp Leu Leu Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala  
 65 70 75 80  
 Val Arg Ala Ile Thr Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe  
 85 90 95  
 Val Ala Thr Glu Ile Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu  
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 Asp Glu Tyr Glu Arg Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg  
 115 120 125  
 Arg Lys Pro Pro Arg Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu  
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 Val Ser Glu Ala Thr Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala  
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 Leu Ser Tyr Gly Gly Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu  
 165 170 175  
 Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly  
 180 185 190  
 Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro  
 195 200 205  
 Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val  
 210 215 220  
 Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro  
 225 230 235 240  
 Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu  
 245 250 255  
 Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala  
 260 265 270  
 Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu  
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 Gly Lys Gly Val  
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 Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser  
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 Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu  
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 gat tca cgt tcc ttc gcg ggc gtc cgc atc gcc gca gtc ggt gaa aaa 192  
 Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys  
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 Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro  
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 Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu  
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 Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala  
 100 105 110  
 gat atc gca acc gac gtg ctt gtc gac ggc ctg acc cac ctt ggt tgg 384  
 Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp  
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 Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro  
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 Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val  
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 aaa cca cac cca cgc acc atc gtc gcg tgc atc gga ccc atg act gca 576  
 Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala  
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Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile  
 195 200 205

gcc gaa gta cca gaa ctg atc gac gct ctt gcg gaa cac gtg gcg gat 672  
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Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys  
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Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro  
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Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu  
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Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala  
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Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp  
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Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro  
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Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val  
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Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly  
 165 170 175

Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala  
 180 185 190

Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile  
 195 200 205

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Arg Lys Ala Ser

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<223> RXN00383

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Met Arg Phe Ala Ile  
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atc ggt gca ggc ctt gcg ggt ctg act gct gca tat gag atc cat aaa 163  
Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala Tyr Glu Ile His Lys  
10 15 20

gct gat ccc act gcc caa atc gat gtg ttg gaa gca ggc gaa cgc att 211  
Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu Ala Gly Glu Arg Ile  
25 30 35

ggc ggc aag ctt ttt acg gtg ccg ttt gct tcc gga cct acc gat att 259  
Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser Gly Pro Thr Asp Ile  
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gga gcg gag gcg ttt tta gct gcg cgt tcc gat gcg gtg gag ttt ttt 307  
Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp Ala Val Glu Phe Phe  
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Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser Pro Ser Ala Ala Lys  
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Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly Ala Gln Asp Thr Ala  
105 110 115

ttt gat tgg act cct ggc caa gac att tct gtt ggc gcc tta gtg cgc 499  
Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val Gly Ala Leu Val Arg  
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Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val Val Ser Ser Leu Leu



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Gly	Gly	Val	Tyr	Ser	Ser	Thr	Ala	Asp	Asp	Leu	Gly	Val	Arg	Ala	Ser	
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gtg	ccg	gca	ctt	gct	gca	gcc	ctt	gat	cag	ctg	gct	gag	gcc	ggc	gag	643
Val	Pro	Ala	Leu	Ala	Ala	Ala	Leu	Asp	Gln	Leu	Ala	Glu	Ala	Gly	Glu	
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Pro	Val	Thr	Leu	Ser	Ala	Ala	Val	Lys	Ala	Val	Glu	Ala	Gln	Arg	Glu	
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Ala	Ala	Lys	Thr	Thr	Ser	Glu	Thr	Arg	Pro	Val	Phe	Gln	Thr	Phe	Lys	
		200					205					210				
ggc	gga	tac	gcg	gag	ctg	tac	gaa	gcg	ttg	gca	gag	caa	tgc	ggc	gca	787
Gly	Gly	Tyr	Ala	Glu	Leu	Tyr	Glu	Ala	Leu	Ala	Glu	Gln	Cys	Gly	Ala	
	215					220					225					
gat	att	cac	ttg	gat	agt	ttc	gtt	tcc	gcc	atc	acc	aaa	gat	ggc	gaa	835
Asp	Ile	His	Leu	Asp	Ser	Phe	Val	Ser	Ala	Ile	Thr	Lys	Asp	Gly	Glu	
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ggt	ttt	gcc	atc	aag	ggc	ggc	ggc	gaa	ggc	acc	tac	gac	aag	gtg	att	883
Gly	Phe	Ala	Ile	Lys	Gly	Gly	Gly	Glu	Gly	Thr	Tyr	Asp	Lys	Val	Ile	
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Leu	Ala	Val	Pro	Ala	Pro	Thr	Ala	Ala	Val	Leu	Leu	Arg	Asp	Leu	Ala	
			265				270						275			
ccg	gcc	gca	gcg	cca	cat	ttg	cgc	gca	att	aag	ttg	gct	tct	tca	gca	979
Pro	Ala	Ala	Ala	Pro	His	Leu	Arg	Ala	Ile	Lys	Leu	Ala	Ser	Ser	Ala	
		280					285					290				
gtc	gtc	ggc	atg	cgt	ttc	gat	tcc	agc	gag	ggc	ctg	ccc	gac	aac	tcc	
1027																
Val	Val	Gly	Met	Arg	Phe	Asp	Ser	Ser	Glu	Gly	Leu	Pro	Asp	Asn	Ser	
	295					300					305					
ggc	gtc	ctg	gtc	gct	gtt	aat	gag	ccg	ggc	atc	acg	gcg	aag	gcc	ttc	
1075																
Gly	Val	Leu	Val	Ala	Val	Asn	Glu	Pro	Gly	Ile	Thr	Ala	Lys	Ala	Phe	
310					315					320					325	
acg	ttc	tcc	tca	aag	aag	tgg	cct	cac	ctg	gag	gct	cgc	ggg	ggc	gcg	
1123																
Thr	Phe	Ser	Ser	Lys	Lys	Trp	Pro	His	Leu	Glu	Ala	Arg	Gly	Gly	Ala	
				330					335					340		
ctc	gtg	cgc	gcg	tcg	ttc	ggc	agg	cta	ggc	gat	gag	gcg	tcg	gca	cgc	
1171																
Leu	Val	Arg	Ala	Ser	Phe	Gly	Arg	Leu	Gly	Asp	Glu	Ala	Ser	Ala	Arg	
			345					350					355			
atg	gac	gag	gat	ttg	ctt	gtc	gac	gcc	gcc	ctc	gac	gat	ctc	ctc	acc	
1219																
Met	Asp	Glu	Asp	Leu	Leu	Val	Asp	Ala	Ala	Leu	Asp	Asp	Leu	Leu	Thr	

360                                      365                                      370  
 ata acc ggg ttc gac ggc cgg gct gcc gga ctg ggt gaa att ttc gtg  
 1267  
 ile thr gly phe asp gly arg ala ala gly leu gly glu ile phe val  
 375                                      380                                      385  
 cag cgc tgg ttc ggt ggg ctc cca gcc tat gga gtt gat cac att gct  
 1315  
 gln arg trp phe gly gly leu pro ala tyr gly val asp his ile ala  
 390                                      395                                      400                                      405  
 acc gtt tcg gct gcg cgt gca gag atc gca gcc gtg cct ggc gtg gaa  
 1363  
 thr val ser ala ala arg ala glu ile ala ala val pro gly val glu  
 410                                      415                                      420  
 gca att ggc gcg tgg gct ggg gga gtg gga gtt ccc gca gtt atc gca  
 1411  
 ala ile gly ala trp ala gly gly val gly val pro ala val ile ala  
 425                                      430                                      435  
 gat gcc cag gca gca gta cac agg ttg ctg gga taagcaccca aaaacactat  
 1464  
 asp ala gln ala ala val his arg leu leu gly  
 440                                      445  
 tga  
 1467

<210> 826  
 <211> 448  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 826  
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 1                                      5                                      10                                      15  
 Tyr Glu Ile His Lys Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu  
 20                                      25                                      30  
 Ala Gly Glu Arg Ile Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser  
 35                                      40                                      45  
 Gly Pro Thr Asp Ile Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp  
 50                                      55                                      60  
 Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser  
 65                                      70                                      75                                      80  
 Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala  
 85                                      90                                      95  
 Phe Pro Ala Gly Gly Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly  
 100                                      105                                      110  
 Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val  
 115                                      120                                      125

Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val  
 130 135 140  
 Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp Asp Leu  
 145 150 155 160  
 Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp Gln Leu  
 165 170 175  
 Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val  
 180 185 190  
 Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val  
 195 200 205  
 Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala  
 210 215 220  
 Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile  
 225 230 235 240  
 Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr  
 245 250 255  
 Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu  
 260 265 270  
 Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala Ile Lys  
 275 280 285  
 Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly  
 290 295 300  
 Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro Gly Ile  
 305 310 315 320  
 Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu  
 325 330 335  
 Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp  
 340 345 350  
 Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu  
 355 360 365  
 Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu  
 370 375 380  
 Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly  
 385 390 395 400  
 Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala  
 405 410 415  
 Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val  
 420 425 430  
 Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly  
 435 440 445

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<222> (101)..(382)
<223> FRXA00376
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<210> 828
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<212> PRT
<213> Corynebacterium glutamicum
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Met Arg Phe Ala Ile Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala
 1             5             10             15

Tyr Glu Ile His Lys Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu
          20             25             30

Ala Gly Glu Arg Ile Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser
      35             40             45

Gly Pro Thr Asp Ile Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp

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50		55		60
Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser				
65		70		75 80
Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu				
	85		90	

<210> 829  
 <211> 1037  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1014)  
 <223> FRXA00383

<400> 829

gca ggc gcg caa gac acc gct ttt gat tgg act cct ggc caa gac att	48
Ala Gly Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile	
1 5 10 15	
tct gtt ggc gcc tta gtg cgc cgt cag tat ggc gat gag atc gtc gat	96
Ser Val Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp	
20 25 30	
act gtg gtg tct tcg ctg ctt ggt ggc gtt tat tcc tcc acc gct gat	144
Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp	
35 40 45	
gat ctg ggt gtg cgc gct tcc gtg ccg gca ctt gct gca gcc ctt gat	192
Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp	
50 55 60	
cag ctg gct gag gcc ggc gag ccg gtg act ctg tca gct gcg gtc aag	240
Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys	
65 70 75 80	
gcc gtg gaa gct cag cgg gaa gcc gca aaa aca act tca gaa acc cgc	288
Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg	
85 90 95	
ccc gtt ttc cag acc ttc aag ggc gga tac gcg gag ctg tac gaa gcg	336
Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala	
100 105 110	
ttg gca gag caa tgc ggt gca gat att cac ttg gat agt ttc gtt tcc	384
Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser	
115 120 125	
gcc atc acc aaa gat ggt gaa ggt ttt gcc atc aag ggc ggt ggc gaa	432
Ala Ile Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu	
130 135 140	
ggc acc tac gac aag gtg att ttg gcg gtt ccc gct cca acc gcc gct	480
Gly Thr Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala	
145 150 155 160	
gtg ctg ctc cgc gac ttg gca ccg gcc gca gcg cca cat ttg cgc gca	528

Val Leu Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala  
 165 170 175  
 att aag ttg gct tct tca gca gtc gtc ggc atg cgt ttc gat tcc agc 576  
 Ile Lys Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser  
 180 185 190  
 gag ggc ctg ccc gac aac tcc ggc gtc ctg gtc gct gtt aat gag ccg 624  
 Glu Gly Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro  
 195 200 205  
 ggc atc acg gcg aag gcc ttc acg ttc tcc tca aag aag tgg cct cac 672  
 Gly Ile Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His  
 210 215 220  
 ctg gag gct cgc ggg ggc gcg ctc gtg cgc gcg tcg ttc ggc agg cta 720  
 Leu Glu Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu  
 225 230 235 240  
 ggc gat gag gcg tcg gca cgc atg gac gag gat ttg ctt gtc gac gcc 768  
 Gly Asp Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala  
 245 250 255  
 gcc ctc gac gat ctc ctc acc ata acc ggg ttc gac ggc cgg gct gcc 816  
 Ala Leu Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala  
 260 265 270  
 gga ctg ggt gaa att ttc gtg cag cgc tgg ttc ggt ggg ctc cca gcc 864  
 Gly Leu Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala  
 275 280 285  
 tat gga gtt gat cac att gct acc gtt tcg gct gcg cgt gca gag atc 912  
 Tyr Gly Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile  
 290 295 300  
 gca gcc gtg cct ggc gtg gaa gca att ggc gcg tgg gct ggg gga gtg 960  
 Ala Ala Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val  
 305 310 315 320  
 gga gtt ccc gca gtt atc gca gat gcc cag gca gca gta cac agg ttg  
 1008  
 Gly Val Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu  
 325 330 335  
 ctg gga taagcaccca aaaacactat tga  
 1037  
 Leu Gly

&lt;210&gt; 830

&lt;211&gt; 338

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 830

Ala Gly Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile  
 1 5 10 15

Ser Val Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp  
 20 25 30

Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp  
 35 40 45  
 Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp  
 50 55 60  
 Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys  
 65 70 75 80  
 Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg  
 85 90 95  
 Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala  
 100 105 110  
 Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser  
 115 120 125  
 Ala Ile Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu  
 130 135 140  
 Gly Thr Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala  
 145 150 155 160  
 Val Leu Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala  
 165 170 175  
 Ile Lys Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser  
 180 185 190  
 Glu Gly Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro  
 195 200 205  
 Gly Ile Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His  
 210 215 220  
 Leu Glu Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu  
 225 230 235 240  
 Gly Asp Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala  
 245 250 255  
 Ala Leu Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala  
 260 265 270  
 Gly Leu Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala  
 275 280 285  
 Tyr Gly Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile  
 290 295 300  
 Ala Ala Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val  
 305 310 315 320  
 Gly Val Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu  
 325 330 335  
 Leu Gly

<400> 831															
acgccatcgc agcctgccct cctggccgca tcgaagtcct cgccaactac accgcattcc 60															
gagacctcaa aaaggctctg gagaaaggga ccgaacaata atg acc acc ctc aac 115															
Met Thr Thr Leu Asn 5															
atc ggc ctc atc ctc ccc gac gtc ctc gga act tac ggc gac gac ggc 163															
Ile Gly Leu Ile Leu Pro Asp Val Leu Gly Thr Tyr Gly Asp Asp Gly 20															
aac gca cta gtc ctg cgc caa cgc gca cgc atg cgt ggc att aat gct 211															
Asn Ala Leu Val Leu Arg Gln Arg Ala Arg Met Arg Gly Ile Asn Ala 35															
gaa atc cag cgc gtc acc ctc gac gac gcc gtc cct tcc acc ctt gat 259															
Glu Ile Gln Arg Val Thr Leu Asp Asp Ala Val Pro Ser Thr Leu Asp 50															
ctc tac tgc ctc ggc ggc ggc gag gac acc gca cag atc ctt gcc acc 307															
Leu Tyr Cys Leu Gly Gly Gly Glu Asp Thr Ala Gln Ile Leu Ala Thr 65															
gaa cac ctc acc aaa gac ggc ggc ctc caa acc gca gcc gcc gca ggc 355															
Glu His Leu Thr Lys Asp Gly Gly Leu Gln Thr Ala Ala Ala Ala Gly 85															
cgc ccc atc ttc gca gtc tgc gca ggt ctc cag gta ctc ggc gac tcc 403															
Arg Pro Ile Phe Ala Val Cys Ala Gly Leu Gln Val Leu Gly Asp Ser 100															
ttc cgc gcc gcc ggc cgt gtc atc gac ggc ctt ggg ctt atc gac gcc 451															
Phe Arg Ala Ala Gly Arg Val Ile Asp Gly Leu Gly Leu Ile Asp Ala 115															
acc acc gtc tct tta caa aaa cgc gcc atc gga gaa gtc gaa acg aca 499															
Thr Thr Val Ser Leu Gln Lys Arg Ala Ile Gly Glu Val Glu Thr Thr 130															
cca acc cgc gcc gga ttc acc gcc gag ctg acc gaa cga ctc acc ggc 547															
Pro Thr Arg Ala Gly Phe Thr Ala Glu Leu Thr Glu Arg Leu Thr Gly 145															
ttc gaa aac cac atg ggc gcc acc ctg ctc ggc ccc gac gcc gaa cca 595															
Phe Glu Asn His Met Gly Ala Thr Leu Leu Gly Pro Asp Ala Glu Pro 165															
ctc ggc cga gtc gtc cgc ggc gaa ggc aac acc gat gtc tgg gca gcc 643															
Leu Gly Arg Val Val Arg Gly Glu Gly Asn Thr Asp Val Trp Ala Ala 180															



tcc gaa aac acc gac gac caa cgc caa caa ttc gcc gaa ggc gcc gtc 691  
 Ser Glu Asn Thr Asp Asp Gln Arg Gln Gln Phe Ala Glu Gly Ala Val  
                   185                                  190                                  195

caa ggc agc atc atc gcc acc tac atg cac ggc ccc gca ctc gcc cga 739  
 Gln Gly Ser Ile Ile Ala Thr Tyr Met His Gly Pro Ala Leu Ala Arg  
                   200                                  205                                  210

aac ccc caa ctc gcc gac ctc atg ctc gca aaa gca atg ggt gtc gcg 787  
 Asn Pro Gln Leu Ala Asp Leu Met Leu Ala Lys Ala Met Gly Val Ala  
                   215                                  220                                  225

ctg aaa gac ctg gag cct ttg gac atc gac gtc atc gac cgc ctc cgc 835  
 Leu Lys Asp Leu Glu Pro Leu Asp Ile Asp Val Ile Asp Arg Leu Arg  
                   230                                  235                                  240                                  245

gcc gaa cgc ctg gcg tagcccccttc taaaccgggt cta 873  
 Ala Glu Arg Leu Ala  
                                   250

&lt;210&gt; 832

&lt;211&gt; 250

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 832

Met Thr Thr Leu Asn Ile Gly Leu Ile Leu Pro Asp Val Leu Gly Thr  
   1                  5                                  10                                  15

Tyr Gly Asp Asp Gly Asn Ala Leu Val Leu Arg Gln Arg Ala Arg Met  
                   20                                  25                                  30

Arg Gly Ile Asn Ala Glu Ile Gln Arg Val Thr Leu Asp Asp Ala Val  
                   35                                  40                                  45

Pro Ser Thr Leu Asp Leu Tyr Cys Leu Gly Gly Gly Glu Asp Thr Ala  
                   50                                  55                                  60

Gln Ile Leu Ala Thr Glu His Leu Thr Lys Asp Gly Gly Leu Gln Thr  
   65                                  70                                  75                                  80

Ala Ala Ala Ala Gly Arg Pro Ile Phe Ala Val Cys Ala Gly Leu Gln  
                   85                                  90                                  95

Val Leu Gly Asp Ser Phe Arg Ala Ala Gly Arg Val Ile Asp Gly Leu  
                   100                                  105                                  110

Gly Leu Ile Asp Ala Thr Thr Val Ser Leu Gln Lys Arg Ala Ile Gly  
                   115                                  120                                  125

Glu Val Glu Thr Thr Pro Thr Arg Ala Gly Phe Thr Ala Glu Leu Thr  
                   130                                  135                                  140

Glu Arg Leu Thr Gly Phe Glu Asn His Met Gly Ala Thr Leu Leu Gly  
   145                                  150                                  155                                  160

Pro Asp Ala Glu Pro Leu Gly Arg Val Val Arg Gly Glu Gly Asn Thr  
                   165                                  170                                  175

Asp Val Trp Ala Ala Ser Glu Asn Thr Asp Asp Gln Arg Gln Gln Phe  
 180 185 190  
 Ala Glu Gly Ala Val Gln Gly Ser Ile Ile Ala Thr Tyr Met His Gly  
 195 200 205  
 Pro Ala Leu Ala Arg Asn Pro Gln Leu Ala Asp Leu Met Leu Ala Lys  
 210 215 220  
 Ala Met Gly Val Ala Leu Lys Asp Leu Glu Pro Leu Asp Ile Asp Val  
 225 230 235 240  
 Ile Asp Arg Leu Arg Ala Glu Arg Leu Ala  
 245 250

<210> 833  
 <211> 1044  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1021)  
 <223> RXA02134

<400> 833  
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 ccgaagcgcc cgagcaaaac acggagtaac tttctaagcg atg tcc ggc aaa gca 115  
 Met Ser Gly Lys Ala  
 1 5  
 ggc ttt acc ccc gaa gat ccc gaa gac tca gac aac cgc cac ggg aac 163  
 Gly Phe Thr Pro Glu Asp Pro Glu Asp Ser Asp Asn Arg His Gly Asn  
 10 15 20  
 ccc ctt ttc gaa ggt atc ttt acc gca ctt aat tgg atg acc gtt ctc 211  
 Pro Leu Phe Glu Gly Ile Phe Thr Ala Leu Asn Trp Met Thr Val Leu  
 25 30 35  
 ccc gtc ccc ggc gca tca gtt ttt gat cgc acc acg ggc gcc cgg gta 259  
 Pro Val Pro Gly Ala Ser Val Phe Asp Arg Thr Thr Gly Ala Arg Val  
 40 45 50  
 atg gcc tct ttg ccc ttt gtt ggc ttc gtt ttc gga atg ttc acc gcg 307  
 Met Ala Ser Leu Pro Phe Val Gly Phe Val Phe Gly Met Phe Thr Ala  
 55 60 65  
 atc atc atg tgg gct atc ggc ccc att tca ggg gtg atc cac gtc gat 355  
 Ile Ile Met Trp Ala Ile Gly Pro Ile Ser Gly Val Ile His Val Asp  
 70 75 80 85  
 gga ctt tta gtt gcc gtt ctg atc gtc gcg ttc tgg gaa ctt ctt aat 403  
 Gly Leu Leu Val Ala Val Leu Ile Val Ala Phe Trp Glu Leu Leu Asn  
 90 95 100  
 cgg ttt atg cac ctc gac ggc ctc gca gat gtc tcc gat gct ttg ggt 451  
 Arg Phe Met His Leu Asp Gly Leu Ala Asp Val Ser Asp Ala Leu Gly  
 105 110 115

tcc tac gca gcc cca cca cgc gca cga gaa atc ctt gcc gat ccc cgc 499  
 Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile Leu Ala Asp Pro Arg  
 120 125 130

acc gga ctt ttc ggc ctc gcc acc gcc atg ctt tcc gtt ctc ctg cag 547  
 Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu Ser Val Leu Leu Gln  
 135 140 145

gtc gct gca gtc gca tcg ctt gtc gat tca acc gtg tgg tgg atg atc 595  
 Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr Val Trp Trp Met Ile  
 150 155 160 165

tgc ttc atc ccc gtt ctc ggc cgc atc gct gga caa gta acc gca ctg 643  
 Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly Gln Val Thr Ala Leu  
 170 175 180

aaa aac cac aac gcc ttc tcc ccc acc ggc ttt ggc gca cta gtc atc 691  
 Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe Gly Ala Leu Val Ile  
 185 190 195

gga acg gtg aaa ttt tgg tgg atc gcg ctg tgg ctc ttg gtt act gct 739  
 Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp Leu Leu Val Thr Ala  
 200 205 210

gcg ttg gct ttt tgg tgc gca gaa tta att tct cca ctt tca ccg ctg 787  
 Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser Pro Leu Ser Pro Leu  
 215 220 225

acc agt gtt aac act ccc ttt gtc gct gga cct ttc ccc gct gca atc 835  
 Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro Phe Pro Ala Ala Ile  
 230 235 240 245

aac ccc gcc tgg ctt gga ggc tgg gtt gcg ata acc gca gtc gtg gca 883  
 Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile Thr Ala Val Val Ala  
 250 255 260

tgt gtt ttc gca gca ctt ttc agc cgc cgc tta tca cga agt ttc ggt 931  
 Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu Ser Arg Ser Phe Gly  
 265 270 275

gga ctc aac gga gac tgc atc ggc gca tgc att cat ctc ggg gcg tcg 979  
 Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile His Leu Gly Ala Ser  
 280 285 290

att tct gca gtg atg ttt gct gtt gtc gcc aat gca atg gtg  
 1021  
 Ile Ser Ala Val Met Phe Ala Val Val Ala Asn Ala Met Val  
 295 300 305

taaagcgggtg gcgtcttttg gga  
 1044

&lt;210&gt; 834

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 834

Met Ser Gly Lys Ala Gly Phe Thr Pro Glu Asp Pro Glu Asp Ser Asp  
 1 5 10 15

Asn Arg His Gly Asn Pro Leu Phe Glu Gly Ile Phe Thr Ala Leu Asn  
 20 25 30  
 Trp Met Thr Val Leu Pro Val Pro Gly Ala Ser Val Phe Asp Arg Thr  
 35 40 45  
 Thr Gly Ala Arg Val Met Ala Ser Leu Pro Phe Val Gly Phe Val Phe  
 50 55 60  
 Gly Met Phe Thr Ala Ile Ile Met Trp Ala Ile Gly Pro Ile Ser Gly  
 65 70 75 80  
 Val Ile His Val Asp Gly Leu Leu Val Ala Val Leu Ile Val Ala Phe  
 85 90 95  
 Trp Glu Leu Leu Asn Arg Phe Met His Leu Asp Gly Leu Ala Asp Val  
 100 105 110  
 Ser Asp Ala Leu Gly Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile  
 115 120 125  
 Leu Ala Asp Pro Arg Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu  
 130 135 140  
 Ser Val Leu Leu Gln Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr  
 145 150 155 160  
 Val Trp Trp Met Ile Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly  
 165 170 175  
 Gln Val Thr Ala Leu Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe  
 180 185 190  
 Gly Ala Leu Val Ile Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp  
 195 200 205  
 Leu Leu Val Thr Ala Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser  
 210 215 220  
 Pro Leu Ser Pro Leu Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro  
 225 230 235 240  
 Phe Pro Ala Ala Ile Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile  
 245 250 255  
 Thr Ala Val Val Ala Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu  
 260 265 270  
 Ser Arg Ser Phe Gly Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile  
 275 280 285  
 His Leu Gly Ala Ser Ile Ser Ala Val Met Phe Ala Val Val Ala Asn  
 290 295 300  
 Ala Met Val  
 305

&lt;210&gt; 835

&lt;211&gt; 1197

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1174)

&lt;223&gt; RXA02135

&lt;400&gt; 835

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aaaacgtttt	aagaaaaag	tcgggttgaa	ggagttgtta	atg	ggt	cca	gca	gag	115
				Met	Val	Pro	Ala	Glu	
				1				5	

ctt	ttt	gcg	cgt	gtg	gaa	ttt	ccg	gat	cat	aaa	atc	ctg	gct	cag	acg	163
Leu	Phe	Ala	Arg	Val	Glu	Phe	Pro	Asp	His	Lys	Ile	Leu	Ala	Gln	Thr	
				10					15					20		

aag	gat	ttc	cat	gac	tcc	ctc	acc	aag	cca	ccc	gga	tct	ttg	ggc	aag	211
Lys	Asp	Phe	His	Asp	Ser	Leu	Thr	Lys	Pro	Pro	Gly	Ser	Leu	Gly	Lys	
			25					30					35			

ttg	gag	cag	atc	ggc	tgt	ttc	att	tcc	gca	tgc	cag	ggc	cag	att	ccg	259
Leu	Glu	Gln	Ile	Gly	Cys	Phe	Ile	Ser	Ala	Cys	Gln	Gly	Gln	Ile	Pro	
		40					45					50				

cca	cgt	cca	ctc	aac	aac	tca	aag	atc	ggt	ggt	ttc	gct	ggc	gat	cac	307
Pro	Arg	Pro	Leu	Asn	Asn	Ser	Lys	Ile	Val	Val	Phe	Ala	Gly	Asp	His	
		55				60					65					

ggc	ggt	gca	act	aaa	ggc	gtg	tcc	gcg	tac	cca	tcc	tca	gta	agc	ttg	355
Gly	Val	Ala	Thr	Lys	Gly	Val	Ser	Ala	Tyr	Pro	Ser	Ser	Val	Ser	Leu	
70					75					80					85	

cag	atg	gct	gaa	aac	att	aca	aac	ggt	ggc	gcc	gcc	atc	aac	gtg	att	403
Gln	Met	Ala	Glu	Asn	Ile	Thr	Asn	Gly	Gly	Ala	Ala	Ile	Asn	Val	Ile	
				90				95						100		

gca	cgc	acc	acc	ggc	acg	tcc	gtc	cga	ctt	att	gat	acc	tcc	ctc	gac	451
Ala	Arg	Thr	Thr	Gly	Thr	Ser	Val	Arg	Leu	Ile	Asp	Thr	Ser	Leu	Asp	
			105					110					115			

cac	gaa	gca	tgg	ggc	gac	gag	cgc	gta	tct	agg	tcc	tgc	gga	tcc	atc	499
His	Glu	Ala	Trp	Gly	Asp	Glu	Arg	Val	Ser	Arg	Ser	Cys	Gly	Ser	Ile	
		120					125					130				

gat	ggt	gaa	gac	gcc	atg	acc	caa	gaa	cag	gtc	gaa	cgc	gca	ctg	aag	547
Asp	Val	Glu	Asp	Ala	Met	Thr	Gln	Glu	Gln	Val	Glu	Arg	Ala	Leu	Lys	
		135				140					145					

atc	ggt	aag	cgc	att	gcg	gat	caa	gaa	gtg	gac	gca	ggc	gcc	gac	att	595
Ile	Gly	Lys	Arg	Ile	Ala	Asp	Gln	Glu	Val	Asp	Ala	Gly	Ala	Asp	Ile	
150					155					160					165	

tta	atc	ccc	ggc	gat	tta	gga	att	ggc	aac	acc	acc	acc	gcc	gct	gcc	643
Leu	Ile	Pro	Gly	Asp	Leu	Gly	Ile	Gly	Asn	Thr	Thr	Thr	Ala	Ala	Ala	
				170				175						180		

ctc	ggt	gga	acg	ttc	acc	ctc	gca	gag	cct	ggt	ggt	gtc	gta	ggc	cgc	691
Leu	Val	Gly	Thr	Phe	Thr	Leu	Ala	Glu	Pro	Val	Val	Val	Val	Gly	Arg	

185					190					195					
ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc														739	
Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu Lys Val Ser Ala Ile															
	200					205					210				
cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc														787	
Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala															
	215					220					225				
atc gcc cgg aaa atc tct tcc cca gac ctt gca gcc atg gca gca ttc														835	
Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Ala Met Ala Ala Phe															
	230				235					240				245	
att gcc caa gca gca gtt cga cgc acc ccc gtg ctt ctc gac ggc gtt														883	
Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val															
			250					255					260		
gta gtc acc gcc gca gcc ctc cta gcc aac aaa ctg gcc cca ggt gcc														931	
Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala															
			265				270						275		
agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc														979	
Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser															
	280					285						290			
gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg															
1027															
Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met															
	295					300					305				
tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag															
1075															
Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys															
	310				315				320					325	
att gcc gtt gac ctg atg aac gac atg tcg aca ttt tct tcc gcc ggc															
1123															
Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly															
			330				335						340		
gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg															
1171															
Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala Pro Glu Gln Asn Thr															
			345				350					355			
gag taactttcta agcgatgtcc ggc															
1197															
Glu															

&lt;210&gt; 836

&lt;211&gt; 358

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 836

Met	Val	Pro	Ala	Glu	Leu	Phe	Ala	Arg	Val	Glu	Phe	Pro	Asp	His	Lys
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Ile Leu Ala Gln Thr Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro  
 20 25 30  
 Gly Ser Leu Gly Lys Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys  
 35 40 45  
 Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val  
 50 55 60  
 Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro  
 65 70 75 80  
 Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala  
 85 90 95  
 Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile  
 100 105 110  
 Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg  
 115 120 125  
 Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val  
 130 135 140  
 Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp  
 145 150 155 160  
 Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr  
 165 170 175  
 Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val  
 180 185 190  
 Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu  
 195 200 205  
 Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg  
 210 215 220  
 Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala  
 225 230 235 240  
 Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val  
 245 250 255  
 Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys  
 260 265 270  
 Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr  
 275 280 285  
 Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile  
 290 295 300  
 Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala  
 305 310 315 320  
 Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr  
 325 330 335  
 Phe Ser Ser Ala Gly Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala

340 345 350

Pro Glu Gln Asn Thr Glu  
355

<210> 837  
<211> 645  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
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<223> RXA02136

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Met Arg Thr Leu Val  
1 5  
ctt ggc ggg gcc agg tct ggt aag tct gct ttt gca gaa tca ctt gtt 163  
Leu Gly Gly Ala Arg Ser Gly Lys Ser Ala Phe Ala Glu Ser Leu Val  
10 15 20  
gga tct ggt ccc gtt ttg tat gtc gca acg gca agg cct tcg gga gat 211  
Gly Ser Gly Pro Val Leu Tyr Val Ala Thr Ala Arg Pro Ser Gly Asp  
25 30 35  
gat cct gaa ttc gcc gag cgc att gcg gtt cat gcg gag cgg cgc cca 259  
Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His Ala Glu Arg Arg Pro  
40 45 50  
acg tct tgg gtg ttg gac gag gag ggg gac gtc gat aag ctt ctt gcc 307  
Thr Ser Trp Val Leu Asp Glu Glu Gly Asp Val Asp Lys Leu Leu Ala  
55 60 65  
tcg cca ccg gcc atg ccg gtg ctc gtt gat gac ctg ggc acc tgg ctc 355  
Ser Pro Pro Ala Met Pro Val Leu Val Asp Asp Leu Gly Thr Trp Leu  
70 75 80 85  
acg cac gcc acc gat gcg tgc gac ggt tgg gag gcg agt tcg gcg cag 403  
Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu Ala Ser Ser Ala Gln  
90 95 100  
ctt gag gcc aag atg gat ttg ctt atc gac gcc atc ctc cac ttt cag 451  
Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala Ile Leu His Phe Gln  
105 110 115  
ggc gaa gat ctg gta att gtt tca cct gaa gtt ggt atg gga atc gtc 499  
Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val Gly Met Gly Ile Val  
120 125 130  
ccg gaa tat aaa tct ggg cgc ctt ttt cgt gat cgc atc ggc aca ctt 547  
Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp Arg Ile Gly Thr Leu  
135 140 145  
aat cag cgt gtc gca gcg att tgc gag agg gtt gtc ttc gtg gtt gct 595  
Asn Gln Arg Val Ala Ala Ile Cys Glu Arg Val Val Phe Val Val Ala



150 155 160 165  
 ggt ctg cca cta gag ttg aaa acg ttt taagaaaaca gtcggtttga 642  
 Gly Leu Pro Leu Glu Leu Lys Thr Phe  
 170

agg 645

<210> 838  
 <211> 174  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 838  
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 Ala Glu Ser Leu Val Gly Ser Gly Pro Val Leu Tyr Val Ala Thr Ala  
 20 25 30  
 Arg Pro Ser Gly Asp Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His  
 35 40 45  
 Ala Glu Arg Arg Pro Thr Ser Trp Val Leu Asp Glu Glu Gly Asp Val  
 50 55 60  
 Asp Lys Leu Leu Ala Ser Pro Pro Ala Met Pro Val Leu Val Asp Asp  
 65 70 75 80  
 Leu Gly Thr Trp Leu Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu  
 85 90 95  
 Ala Ser Ser Ala Gln Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala  
 100 105 110  
 Ile Leu His Phe Gln Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val  
 115 120 125  
 Gly Met Gly Ile Val Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp  
 130 135 140  
 Arg Ile Gly Thr Leu Asn Gln Arg Val Ala Ala Ile Cys Glu Arg Val  
 145 150 155 160  
 Val Phe Val Val Ala Gly Leu Pro Leu Glu Leu Lys Thr Phe  
 165 170

<210> 839  
 <211> 575  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(552)  
 <223> RXN03114

<400> 839  
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cgc	cgc	gag	ttg	acg	gtg	ggg	ttg	gat	gct	ggg	gac	ggg	ccg	att	tta	96	
Arg	Arg	Glu	Leu	Thr	Val	Gly	Leu	Asp	Ala	Gly	Asp	Gly	Pro	Ile	Leu		
			20					25					30				
agg	cag	agc	ttt	gat	gtt	ggg	ttt	ttg	ctt	gtc	gac	gcc	tcc	ttc	cac	144	
Arg	Gln	Ser	Phe	Asp	Val	Gly	Phe	Leu	Leu	Val	Asp	Ala	Ser	Phe	His		
		35					40					45					
att	cat	atc	aat	ggc	gtg	tct	act	ggg	cag	tcg	gtt	gcg	ccg	gat	gat	192	
Ile	His	Ile	Asn	Gly	Val	Ser	Thr	Gly	Gln	Ser	Val	Ala	Pro	Asp	Asp		
	50					55				60							
gta	gtt	gag	gtg	gtg	cgt	ggg	ttg	gct	gat	gct	tcg	gag	ttg	tcc	gtg	240	
Val	Val	Glu	Val	Val	Arg	Gly	Leu	Ala	Asp	Ala	Ser	Glu	Leu	Ser	Val		
65					70			75						80			
gaa	agt	gtt	gct	gag	ttg	tgt	act	ccc	gtg	gca	ccg	gtt	tca	tta	tct	288	
Glu	Ser	Val	Ala	Glu	Leu	Cys	Thr	Pro	Val	Ala	Pro	Val	Ser	Leu	Ser		
				85				90						95			
gag	gca	cag	ggg	aat	cct	gcg	cct	att	ggg	tgg	ttg	gag	cat	gat	ggc	336	
Glu	Ala	Gln	Gly	Asn	Pro	Ala	Pro	Ile	Gly	Trp	Leu	Glu	His	Asp	Gly		
			100					105					110				
gtg	gtg	tcg	ttg	ggg	gcg	ggg	att	cca	ggg	ggg	cgg	gtg	gag	gct	cgt	384	
Val	Val	Ser	Leu	Gly	Ala	Gly	Ile	Pro	Gly	Gly	Arg	Val	Glu	Ala	Arg		
		115					120					125					
tta	gcg	cgt	ttt	att	gcg	gtg	att	gag	gcg	gag	acc	act	att	acc	cca	432	
Leu	Ala	Arg	Phe	Ile	Ala	Val	Ile	Glu	Ala	Glu	Thr	Thr	Ile	Thr	Pro		
	130					135					140						
tgg	aat	tcg	ttg	atc	att	cat	gat	ttg	tat	gag	ggg	gtt	gca	gaa	cag	480	
Trp	Asn	Ser	Leu	Ile	Ile	His	Asp	Leu	Tyr	Glu	Gly	Val	Ala	Glu	Gln		
145				150				155						160			
gtg	gtg	aag	gtt	ctg	gct	ccc	atg	ggg	ttg	gtt	ttt	gat	gct	aat	tca	528	
Val	Val	Lys	Val	Leu	Ala	Pro	Met	Gly	Leu	Val	Phe	Asp	Ala	Asn	Ser		
			165					170						175			
ccg	ctt	ctg	gag	tca	ccg	gct	ttg	taactcgcca	ttggtgcacg	tct						575	
Pro	Leu	Leu	Glu	Ser	Pro	Ala	Leu										
			180														

&lt;210&gt; 840

&lt;211&gt; 184

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 840

Thr	Pro	Gly	His	Phe	Val	Ala	Leu	Ala	Arg	Glu	Ile	Ala	Gly	Ala	Val		
1				5					10					15			
Arg	Arg	Glu	Leu	Thr	Val	Gly	Leu	Asp	Ala	Gly	Asp	Gly	Pro	Ile	Leu		
			20					25					30				
Arg	Gln	Ser	Phe	Asp	Val	Gly	Phe	Leu	Leu	Val	Asp	Ala	Ser	Phe	His		

35 40 45  
 Ile His Ile Asn Gly Val Ser Thr Gly Gln Ser Val Ala Pro Asp Asp  
 50 55 60  
 Val Val Glu Val Val Arg Gly Leu Ala Asp Ala Ser Glu Leu Ser Val  
 65 70 75 80  
 Glu Ser Val Ala Glu Leu Cys Thr Pro Val Ala Pro Val Ser Leu Ser  
 85 90 95  
 Glu Ala Gln Gly Asn Pro Ala Pro Ile Gly Trp Leu Glu His Asp Gly  
 100 105 110  
 Val Val Ser Leu Gly Ala Gly Ile Pro Gly Gly Arg Val Glu Ala Arg  
 115 120 125  
 Leu Ala Arg Phe Ile Ala Val Ile Glu Ala Glu Thr Thr Ile Thr Pro  
 130 135 140  
 Trp Asn Ser Leu Ile Ile His Asp Leu Tyr Glu Gly Val Ala Glu Gln  
 145 150 155 160  
 Val Val Lys Val Leu Ala Pro Met Gly Leu Val Phe Asp Ala Asn Ser  
 165 170 175  
 Pro Leu Leu Glu Ser Pro Ala Leu  
 180

<210> 841  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1177)  
 <223> RXN01810

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 Met Asn Asn Ala Phe  
 1 5  
 cga cgc acc ctt aca tcc gta gtc ctc gcc gct agc ttg gcc tta acg 163  
 Arg Arg Thr Leu Thr Ser Val Val Leu Ala Ala Ser Leu Ala Leu Thr  
 10 15 20  
 gcc tgc gca agc tgg gat tca cct acg gca tct tcc aat ggt gat ctg 211  
 Ala Cys Ala Ser Trp Asp Ser Pro Thr Ala Ser Ser Asn Gly Asp Leu  
 25 30 35  
 att gag gag atc cag gca agc tcc acc tca aca gat ccg cgc acc ttc 259  
 Ile Glu Glu Ile Gln Ala Ser Ser Thr Ser Thr Asp Pro Arg Thr Phe  
 40 45 50  
 aca ggc ttg agc atc gtg gaa gat atc ggc gat gtg gtt ccc gta acc 307  
 Thr Gly Leu Ser Ile Val Glu Asp Ile Gly Asp Val Val Pro Val Thr

55	60	65	
gac aac gcc tca cca gct ctg cca gtt tct ttg acc gac gct gat ggc Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu Thr Asp Ala Asp Gly 70 75 80 85			355
aac gac gtg gtg gtg gag aac gtg tcc cgc atc ctc cca ctg gat ctc Asn Asp Val Val Val Glu Asn Val Ser Arg Ile Leu Pro Leu Asp Leu 90 95 100			403
tac gga acc tat tcc aaa acc atc gct ggc ctg gga ctc gtg gac aat Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu Gly Leu Val Asp Asn 105 110 115			451
att gtg ggt cgt act gtt agt tcc acc gag cct gca ttg gcg gac att Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro Ala Leu Ala Asp Ile 120 125 130			499
gag gtg gtc acc act ggc gga cac acc ctc aat gct gaa gcg atc ctt Glu Val Val Thr Thr Gly Gly His Thr Leu Asn Ala Glu Ala Ile Leu 135 140 145			547
aat tta cat ccg act ttg gtg atc atc gac cac tcg atc ggc cca cgc Asn Leu His Pro Thr Leu Val Ile Ile Asp His Ser Ile Gly Pro Arg 150 155 160 165			595
gaa gtc atc gat cag atc cgc gca gct ggt gtc gcc acg gtg atc atg Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val Ala Thr Val Ile Met 170 175 180			643
tcg ccg cag cgt tcc att gcc tca att ggc gac gac atc cgc gac atc Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp Asp Ile Arg Asp Ile 185 190 195			691
gcc tcc gtc gtt gga ctt cct gaa gaa ggg gag aag ctc gcg gaa cgt Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu Lys Leu Ala Glu Arg 200 205 210			739
tcc gtt gct gaa gtc gaa gag gcc agc acg gtt gtc gat gaa ctc acc Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val Val Asp Glu Leu Thr 215 220 225			787
cca gaa gat ccc ctc aaa atg gta ttc ctc tat gcc cgc gga act ggt Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr Ala Arg Gly Thr Gly 230 235 240 245			835
gga gtg ttc ttc att ttg ggc gat gcc tat ggt gga cgc gat ctc att Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly Gly Arg Asp Leu Ile 250 255 260			883
gaa ggc ctg ggc ggc gtc gac atg gct gct gaa aag ggc atc atg gat Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu Lys Gly Ile Met Asp 265 270 275			931
ctg gca cca gcc aac gcg gaa gca ctt gcc gaa cta aat cca gac gtc Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu Leu Asn Pro Asp Val 280 285 290			979
ttc gtg atg atg tcg gaa gga cta gtc tcg aca gga ggt atc gac ggt 1027 Phe Val Met Met Ser Glu Gly Leu Val Ser Thr Gly Gly Ile Asp Gly			

295                      300                      305  
 ctt atg gaa cgc ccc ggc att gct cag aca acc gcc gga caa aac caa  
 1075  
 Leu Met Glu Arg Pro Gly Ile Ala Gln Thr Thr Ala Gly Gln Asn Gln  
 310                      315                      320                      325  
 cga gta ctg gcg ctt ccc gat ggt caa tca ttg gcc ttt ggt gcc caa  
 1123  
 Arg Val Leu Ala Leu Pro Asp Gly Gln Ser Leu Ala Phe Gly Ala Gln  
 330                      335                      340  
 act ggc gag ttg ttg ctc cgc gca tcc cgc gaa ctg tat gtg cag ggc  
 1171  
 Thr Gly Glu Leu Leu Leu Arg Ala Ser Arg Glu Leu Tyr Val Gln Gly  
 345                      350                      355  
 ggc gag tagatgggtg tgaaggaggt tga  
 1200  
 Gly Glu

<210> 842  
 <211> 359  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 842  
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 20                      25                      30  
 Ser Asn Gly Asp Leu Ile Glu Glu Ile Gln Ala Ser Ser Thr Ser Thr  
 35                      40                      45  
 Asp Pro Arg Thr Phe Thr Gly Leu Ser Ile Val Glu Asp Ile Gly Asp  
 50                      55                      60  
 Val Val Pro Val Thr Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu  
 65                      70                      75                      80  
 Thr Asp Ala Asp Gly Asn Asp Val Val Val Glu Asn Val Ser Arg Ile  
 85                      90                      95  
 Leu Pro Leu Asp Leu Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu  
 100                      105                      110  
 Gly Leu Val Asp Asn Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro  
 115                      120                      125  
 Ala Leu Ala Asp Ile Glu Val Val Thr Thr Gly Gly His Thr Leu Asn  
 130                      135                      140  
 Ala Glu Ala Ile Leu Asn Leu His Pro Thr Leu Val Ile Ile Asp His  
 145                      150                      155                      160  
 Ser Ile Gly Pro Arg Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val  
 165                      170                      175

Ala Thr Val Ile Met Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp  
 180 185 190

Asp Ile Arg Asp Ile Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu  
 195 200 205

Lys Leu Ala Glu Arg Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val  
 210 215 220

Val Asp Glu Leu Thr Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr  
 225 230 235 240

Ala Arg Gly Thr Gly Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly  
 245 250 255

Gly Arg Asp Leu Ile Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu  
 260 265 270

Lys Gly Ile Met Asp Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu  
 275 280 285

Leu Asn Pro Asp Val Phe Val Met Met Ser Glu Gly Leu Val Ser Thr  
 290 295 300

Gly Gly Ile Asp Gly Leu Met Glu Arg Pro Gly Ile Ala Gln Thr Thr  
 305 310 315 320

Ala Gly Gln Asn Gln Arg Val Leu Ala Leu Pro Asp Gly Gln Ser Leu  
 325 330 335

Ala Phe Gly Ala Gln Thr Gly Glu Leu Leu Leu Arg Ala Ser Arg Glu  
 340 345 350

Leu Tyr Val Gln Gly Gly Glu  
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&lt;210&gt; 843

&lt;211&gt; 963

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (933)

&lt;223&gt; RXS03205

&lt;400&gt; 843

gat tcc ggc att ccc acg cag ttg gtg gag ggc agc tgg ttt gaa ccg 48  
 Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro  
 1 5 10 15

gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg 96  
 Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val  
 20 25 30

gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat 144  
 Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp  
 35 40 45

cta	gac	ggc	gcg	acc	gcg	ttg	gtg	gtc	aaa	gaa	gcc	tgc	gcg	cat	ctc	192
Leu	Asp	Gly	Ala	Thr	Ala	Leu	Val	Val	Lys	Glu	Ala	Cys	Ala	His	Leu	
	50					55					60					
aac	cct	ggc	ggc	acc	gct	cac	ctg	ctc	ggc	gca	tgg	gtg	cat	tcc	gcg	240
Asn	Pro	Gly	Gly	Thr	Ala	His	Leu	Leu	Gly	Ala	Trp	Val	His	Ser	Ala	
	65				70					75					80	
gat	caa	tcg	tgg	cag	cag	cg	gtt	gca	gaa	tgg	ttg	ccg	gat	aac	ggc	288
Asp	Gln	Ser	Trp	Gln	Gln	Arg	Val	Ala	Glu	Trp	Leu	Pro	Asp	Asn	Gly	
				85					90					95		
tat	gtt	gct	tgg	gtt	att	gag	cg	gac	gcc	gtg	agc	ccc	gcg	cag	tat	336
Tyr	Val	Ala	Trp	Val	Ile	Glu	Arg	Asp	Ala	Val	Ser	Pro	Ala	Gln	Tyr	
			100					105					110			
gtg	ggc	acg	tgg	ctt	agt	gat	gag	tcc	ctc	gat	ctg	cgt	agc	ccc	gag	384
Val	Gly	Thr	Trp	Leu	Ser	Asp	Glu	Ser	Leu	Asp	Leu	Arg	Ser	Pro	Glu	
		115					120					125				
gca	gca	gca	cg	acc	acc	gcg	tgg	ctt	aac	cac	ttt	gaa	aaa	gcc	aag	432
Ala	Ala	Ala	Arg	Thr	Thr	Ala	Trp	Leu	Asn	His	Phe	Glu	Lys	Ala	Lys	
		130				135					140					
gtt	caa	ggc	gtt	ggc	ttt	ggc	ttc	atc	gcc	atc	caa	cgt	ctg	gag	gaa	480
Val	Gln	Gly	Val	Gly	Phe	Gly	Phe	Ile	Ala	Ile	Gln	Arg	Leu	Glu	Glu	
	145				150					155					160	
gac	gag	gcg	gat	gag	aaa	tcc	gat	atc	ttg	gct	gaa	tcc	atg	acc	cag	528
Asp	Glu	Ala	Asp	Glu	Lys	Ser	Asp	Ile	Leu	Ala	Glu	Ser	Met	Thr	Gln	
				165					170					175		
tac	ttc	gag	gat	cct	ctc	ggc	cct	gaa	att	gag	gag	tac	ttc	acc	cg	576
Tyr	Phe	Glu	Asp	Pro	Leu	Gly	Pro	Glu	Ile	Glu	Glu	Tyr	Phe	Thr	Arg	
			180					185					190			
acc	gca	tgg	ctt	cgt	gaa	caa	act	cg	gat	tcc	att	ctg	agc	tcc	cg	624
Thr	Ala	Trp	Leu	Arg	Glu	Gln	Thr	Arg	Asp	Ser	Ile	Leu	Ser	Ser	Arg	
		195					200					205				
ttc	aaa	gtt	cg	cct	ggc	gtg	gcc	cgg	gaa	caa	atc	agc	ctg	gcc	gat	672
Phe	Lys	Val	Arg	Pro	Gly	Val	Ala	Arg	Glu	Gln	Ile	Ser	Leu	Ala	Asp	
	210					215					220					
gcg	gaa	gaa	ggc	atg	ggc	ttt	agt	cct	gtc	acg	ttg	agg	ctc	acc	cg	720
Ala	Glu	Glu	Gly	Met	Gly	Phe	Ser	Pro	Val	Thr	Leu	Arg	Leu	Thr	Arg	
	225				230					235					240	
acc	gat	ggc	cct	cgt	tgg	tcc	cat	gat	gtt	gat	gag	cat	gtg	gct	tcc	768
Thr	Asp	Gly	Pro	Arg	Trp	Ser	His	Asp	Val	Asp	Glu	His	Val	Ala	Ser	
				245					250					255		
atc	gtc	gca	gga	ctt	aac	cca	cat	gga	ctc	ccc	ttt	gaa	gaa	atc	ctg	816
Ile	Val	Ala	Gly	Leu	Asn	Pro	His	Gly	Leu	Pro	Phe	Glu	Glu	Ile	Leu	
			260					265					270			
gaa	atg	tac	gcg	atg	gct	caa	ggc	atc	gag	gga	gaa	tcc	ctg	cac	aac	864
Glu	Met	Tyr	Ala	Met	Ala	Gln	Gly	Il	Glu	Gly	Glu	Ser	Leu	His	Asn	
		275					280					285				
ggc	gcc	att	gcg	gcg	ttg	gtg	gat	ctc	atc	cg	cac	gga	ttg	gtg	ttg	912

Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu  
 290 295 300

ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aagccgtttt 963  
 Pro Ala Asp Leu Leu Asp Ser  
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<210> 844

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 844

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro  
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Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val  
 20 25 30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp  
 35 40 45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu  
 50 55 60

Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala  
 65 70 75 80

Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly  
 85 90 95

Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr  
 100 105 110

Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu  
 115 120 125

Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys  
 130 135 140

Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu  
 145 150 155 160

Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln  
 165 170 175

Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg  
 180 185 190

Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg  
 195 200 205

Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp  
 210 215 220

Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg  
 225 230 235 240

Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser  
 245 250 255



Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu  
 260 265 270

Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn  
 275 280 285

Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu  
 290 295 300

Pro Ala Asp Leu Leu Asp Ser  
 305 310

<210> 845  
 <211> 956  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(933)  
 <223> FRXA00306

<400> 845  
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 1 5 10 15

gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg 96  
 Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val  
 20 25 30

gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat 144  
 Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp  
 35 40 45

cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc 192  
 Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu  
 50 55 60

aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg 240  
 Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala  
 65 70 75 80

gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt 288  
 Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly  
 85 90 95

tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat 336  
 Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr  
 100 105 110

gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag 384  
 Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu  
 115 120 125

gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag 432  
 Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys  
 130 135 140

gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa 480  
 Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu  
 145 150 155 160  
 gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag 528  
 Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln  
 165 170 175  
 tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc 576  
 Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg  
 180 185 190  
 acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc 624  
 Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg  
 195 200 205  
 ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat 672  
 Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp  
 210 215 220  
 gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc 720  
 Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg  
 225 230 235 240  
 acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc 768  
 Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser  
 245 250 255  
 atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg 816  
 Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu  
 260 265 270  
 gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac 864  
 Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn  
 275 280 285  
 ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg 912  
 Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu  
 290 295 300  
 ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aag 956  
 Pro Ala Asp Leu Leu Asp Ser  
 305 310

&lt;210&gt; 846

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 846

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro  
 1 5 10 15

Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val  
 20 25 30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp  
 35 40 45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu

50					55					60					
Asn	Pro	Gly	Gly	Thr	Ala	His	Leu	Leu	Gly	Ala	Trp	Val	His	Ser	Ala
65					70					75					80
Asp	Gln	Ser	Trp	Gln	Gln	Arg	Val	Ala	Glu	Trp	Leu	Pro	Asp	Asn	Gly
				85					90					95	
Tyr	Val	Ala	Trp	Val	Ile	Glu	Arg	Asp	Ala	Val	Ser	Pro	Ala	Gln	Tyr
			100					105					110		
Val	Gly	Thr	Trp	Leu	Ser	Asp	Glu	Ser	Leu	Asp	Leu	Arg	Ser	Pro	Glu
			115				120					125			
Ala	Ala	Ala	Arg	Thr	Thr	Ala	Trp	Leu	Asn	His	Phe	Glu	Lys	Ala	Lys
			130			135					140				
Val	Gln	Gly	Val	Gly	Phe	Gly	Phe	Ile	Ala	Ile	Gln	Arg	Leu	Glu	Glu
145					150					155					160
Asp	Glu	Ala	Asp	Glu	Lys	Ser	Asp	Ile	Leu	Ala	Glu	Ser	Met	Thr	Gln
				165					170					175	
Tyr	Phe	Glu	Asp	Pro	Leu	Gly	Pro	Glu	Ile	Glu	Glu	Tyr	Phe	Thr	Arg
			180					185					190		
Thr	Ala	Trp	Leu	Arg	Glu	Gln	Thr	Arg	Asp	Ser	Ile	Leu	Ser	Ser	Arg
			195				200					205			
Phe	Lys	Val	Arg	Pro	Gly	Val	Ala	Arg	Glu	Gln	Ile	Ser	Leu	Ala	Asp
			210			215					220				
Ala	Glu	Glu	Gly	Met	Gly	Phe	Ser	Pro	Val	Thr	Leu	Arg	Leu	Thr	Arg
225					230					235					240
Thr	Asp	Gly	Pro	Arg	Trp	Ser	His	Asp	Val	Asp	Glu	His	Val	Ala	Ser
				245					250					255	
Ile	Val	Ala	Gly	Leu	Asn	Pro	His	Gly	Leu	Pro	Phe	Glu	Glu	Ile	Leu
			260					265					270		
Glu	Met	Tyr	Ala	Met	Ala	Gln	Gly	Ile	Glu	Gly	Glu	Ser	Leu	His	Asn
		275					280					285			
Gly	Ala	Ile	Ala	Ala	Leu	Val	Asp	Leu	Ile	Arg	His	Gly	Leu	Val	Leu
			290			295					300				
Pro	Ala	Asp	Leu	Leu	Asp	Ser									
305					310										

&lt;210&gt; 847

&lt;211&gt; 819

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(796)

&lt;223&gt; RXC01715

**<400> 847**

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ccactgacac tggcaaagat ccacgaaagg aagttaccct gtg agc gag ctc gat 115  
Val Ser Glu Leu Asp  
1 5

att aaa cag ctc aac aaa ctg cag cgc tac tct cag tgg gcg gtg ttc 163  
Ile Lys Gln Leu Asn Lys Leu Gln Arg Tyr Ser Gln Trp Ala Val Phe  
10 15 20

cgt gct att cct gga gcg ctc gat gat gat cgc aca gaa gtc act gac 211  
Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg Thr Glu Val Thr Asp  
25 30 35

caa gca gcc aag ttc ttt gcc gac ctt gaa gca gaa ggc aaa gtc act 259  
Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala Glu Gly Lys Val Thr  
40 45 50

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gtc cgt ggc att tac aac gcc tcc ggc ctg cgc gca gac gct gac tac 307
Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg Ala Asp Ala Asp Tyr
      55                      60                      65
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atg atc tgg tgg cac gca gaa gaa ttc gaa gac att cag aag gcc ttc 355  
Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp Ile Gln Lys Ala Phe  
70 75 80 85

gct gat ttc cgc cgc acc acc att ttg ggt cag gtt tct gag gtc ttc 403  
Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln Val Ser Glu Val Phe  
90 95 100

tgg atc gga aac gct ctc cac cgt cca tct gag ttc aac aag gct cac 451  
Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu Phe Asn Lys Ala His  
105 110 115

ttg	cct	tca	ttc	atc	atg	ggt	gaa	gaa	gca	aag	gac	tgg	atc	act	gtt	499
Leu	Pro	Ser	Phe	Ile	Met	Gly	Glu	Glu	Ala	Lys	Asp	Trp	Ile	Thr	Val	
		120					125					130				

tac	ccg	ttc	gtg	cgc	agc	tac	gac	tgg	tac	atc	atg	gag	ccc	ttg	aag	547
Tyr	Pro	Phe	Val	Arg	Ser	Tyr	Asp	Trp	Tyr	Ile	Met	Glu	Pro	Leu	Lys	
135						140					145					

cgt tcc cgc att ctc cgc gag cac gga caa gct gct gtg gaa ttc cca 595  
Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala Ala Val Glu Phe Pro  
150 155 160 165

gat gtt cgt gcc aac act gtg ccg gct ttc gca ctg ggt gac tac gaa 643  
Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala Leu Gly Asp Tyr Glu  
170 175 180

tgg gtg ctg gct ttc gag gct gat gag ttg cac cgc att gtc gat ttg 691  
 Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His Arg Ile Val Asp Leu  
 185 190 195

atg cac aag atg cgt tac acc gag gct cgc ctc cac gtc cgt gag gag 739  
Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu His Val Arg Glu Glu  
200 205 210

ctg cca ttt att tct gga cag cgc gtc gac att gca gat ctg att aag 787  
Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile Ala Asp Leu Ile Lys

215 220 225 819  
 gtt ctt cct taaaagctgc ttttctaaac gat  
 Val Leu Pro  
 230

<210> 848  
 <211> 232  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 848  
 Val Ser Glu Leu Asp Ile Lys Gln Leu Asn Lys Leu Gln Arg Tyr Ser  
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 Gln Trp Ala Val Phe Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg  
 20 25 30  
 Thr Glu Val Thr Asp Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala  
 35 40 45  
 Glu Gly Lys Val Thr Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg  
 50 55 60  
 Ala Asp Ala Asp Tyr Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp  
 65 70 75 80  
 Ile Gln Lys Ala Phe Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln  
 85 90 95  
 Val Ser Glu Val Phe Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu  
 100 105 110  
 Phe Asn Lys Ala His Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys  
 115 120 125  
 Asp Trp Ile Thr Val Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile  
 130 135 140  
 Met Glu Pro Leu Lys Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala  
 145 150 155 160  
 Ala Val Glu Phe Pro Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala  
 165 170 175  
 Leu Gly Asp Tyr Glu Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His  
 180 185 190  
 Arg Ile Val Asp Leu Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu  
 195 200 205  
 His Val Arg Glu Glu Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile  
 210 215 220  
 Ala Asp Leu Ile Lys Val Leu Pro  
 225 230

<210> 849  
 <211> 1587

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1564)

&lt;223&gt; RXN00420

&lt;400&gt; 849

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				Met	Asn	Ser	Ser	His	
				1				5	

ggc	acg	tcc	agc	tcc	ggc	gct	tcg	gcc	ggt	gcc	cac	gga	gcc	ctt	ccc	163
Gly	Thr	Ser	Ser	Ser	Gly	Ala	Ser	Ala	Gly	Ala	His	Gly	Ala	Leu	Pro	
				10					15					20		

cta	gaa	gct	cag	aaa	ctg	aac	ggt	tgg	ggc	cgc	aca	gcc	ccc	acc	acc	211
Leu	Glu	Ala	Gln	Lys	Leu	Asn	Gly	Trp	Gly	Arg	Thr	Ala	Pro	Thr	Thr	
			25					30					35			

gct	gag	gta	ctt	acc	acc	cca	gac	cta	gac	atc	att	gtg	gat	gca	gtc	259
Ala	Glu	Val	Leu	Thr	Thr	Pro	Asp	Leu	Asp	Ile	Ile	Val	Asp	Ala	Val	
		40					45					50				

cgc	caa	gtc	gct	gaa	caa	aac	gac	tcc	aag	ccg	gac	tac	ctc	aag	cgc	307
Arg	Gln	Val	Ala	Glu	Gln	Asn	Asp	Ser	Lys	Pro	Asp	Tyr	Leu	Lys	Arg	
	55					60					65					

ggc	gtg	att	gcc	cgt	ggc	atg	ggt	cgt	tcc	tat	ggt	gac	cca	gcc	caa	355
Gly	Val	Ile	Ala	Arg	Gly	Met	Gly	Arg	Ser	Tyr	Gly	Asp	Pro	Ala	Gln	
70					75					80					85	

aac	gcc	ggt	ggc	ctt	gtc	att	gac	atg	cag	cca	ctg	aac	aaa	atc	cac	403
Asn	Ala	Gly	Gly	Leu	Val	Ile	Asp	Met	Gln	Pro	Leu	Asn	Lys	Ile	His	
				90					95					100		

tcg	att	gat	cct	gat	tct	gcg	atc	gtc	gat	gta	gat	ggc	ggc	gtc	acc	451
Ser	Ile	Asp	Pro	Asp	Ser	Ala	Ile	Val	Asp	Val	Asp	Gly	Gly	Val	Thr	
			105					110					115			

ctc	gat	cag	ctc	atg	aag	gct	gcc	ctg	cca	tat	ggc	ctc	tgg	gtt	cct	499
Leu	Asp	Gln	Leu	Met	Lys	Ala	Ala	Leu	Pro	Tyr	Gly	Leu	Trp	Val	Pro	
		120					125					130				

gtc	ctt	ccc	ggc	acc	cgc	caa	gtc	acc	atc	ggt	ggc	gca	atc	gga	cca	547
Val	Leu	Pro	Gly	Thr	Arg	Gln	Val	Thr	Ile	Gly	Gly	Ala	Ile	Gly	Pro	
	135					140					145					

gac	atc	cac	ggt	aag	aac	cac	cac	tct	gca	ggt	tcc	ttc	ggc	gac	cac	595
Asp	Ile	His	Gly	Lys	Asn	His	His	Ser	Ala	Gly	Ser	Phe	Gly	Asp	His	
150					155					160				165		

gtg	gtc	tcc	atg	gaa	ctc	ctc	gtt	gca	gac	gga	cgc	atc	ctg	cac	ctc	643
Val	Val	Ser	Met	Glu	Leu	Leu	Val	Ala	Asp	Gly	Arg	Ile	Leu	His	Leu	
				170					175					180		

gag	cca	gaa	ggc	acc	gcc	gaa	gac	cca	cag	ggc	gac	ctg	ttc	tgg	gca	691
Glu	Pro	Glu	Gly	Thr	Ala	Glu	Asp	Pro	Gln	Gly	Asp	Leu	Phe	Trp	Ala	

185							190					195					
acc gtt ggt ggc atg ggc ctg	acc ggc atc atc gtc cgt gca cgc atc	739															
Thr Val Gly Gly Met Gly Leu	Thr Gly Ile Ile Val Arg Ala Arg Ile																
200	205	210															
cgc atg acc aag acg gaa acc gcc tac ttc att gcg gac acc gac cgc	787																
Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile Ala Asp Thr Asp Arg																	
215	220	225															
acc aac aac ttg gaa gaa acc gtt gcg ttc cac tcc gac gga tca gag	835																
Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His Ser Asp Gly Ser Glu																	
230	235	240	245														
cac aac tac acc tat tct tct gcg tgg ttc gat gtc atc agc cct gag	883																
His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp Val Ile Ser Pro Glu																	
250	255	260															
cca aag ctt ggc cgc tcc acc atc tcc cgt ggt tcc ctg gca aca ctt	931																
Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly Ser Leu Ala Thr Leu																	
265	270	275															
gct cag ctg gaa gaa ttg gca cca aag ctg gcc aag gat cca ctg aag	979																
Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala Lys Asp Pro Leu Lys																	
280	285	290															
ttt aat gct cca cag ctg atg aag gtt cca gat atc ttc cca tcc tgg																	
1027																	
Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp Ile Phe Pro Ser Trp																	
295	300	305															
act ttg aac aag ctg acc ctt tcc gca gtc ggt gtg gct tac tac gcc																	
1075																	
Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly Val Ala Tyr Tyr Ala																	
310	315	320	325														
atg ggt gca cca gcg aaa aac cag gtg aaa aac ctc acc cag ttc tac																	
1123																	
Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe Tyr																	
330	335	340															
caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc aag																	
1171																	
Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser Lys																	
345	350	355															
ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag cct																	
1219																	
Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu Pro																	
360	365	370															
ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc gca																	
1267																	
Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser Ala																	
375	380	385															
ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg tcc																	
1315																	
Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu Ser																	
390	395	400	405														

tac cca atg cca ggc tgg aac gtc tgc gtt gac ttc cct atc cgc cca  
1363  
Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg Pro  
410 415 420

ggc ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa ttc  
1411  
Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu Phe  
425 430 435

ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag aac  
1459  
Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu Asn  
440 445 450

ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga aat  
1507  
Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg Asn  
455 460 465

gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga ctt  
1555  
Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg Leu  
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gag ctt tct taagaaaggg cttgaactaa aca  
1587  
Glu Leu Ser

<210> 850

<211> 488

<212> PRT

<213> Corynebacterium glutamicum

<400> 850

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His Gly Ala Leu Pro Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg  
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Thr Ala Pro Thr Thr Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile  
35 40 45

Ile Val Asp Ala Val Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro  
50 55 60

Asp Tyr Leu Lys Arg Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr  
65 70 75 80

Gly Asp Pro Ala Gln Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro  
85 90 95

Leu Asn Lys Ile His Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val  
100 105 110

Asp Gly Gly Val Thr Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr  
115 120 125



Gly Leu Trp Val Pro Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly  
 130 135 140  
 Gly Ala Ile Gly Pro Asp Ile His Gly Lys Asn His His Ser Ala Gly  
 145 150 155 160  
 Ser Phe Gly Asp His Val Val Ser Met Glu Leu Leu Val Ala Asp Gly  
 165 170 175  
 Arg Ile Leu His Leu Glu Pro Glu Gly Thr Ala Glu Asp Pro Gln Gly  
 180 185 190  
 Asp Leu Phe Trp Ala Thr Val Gly Gly Met Gly Leu Thr Gly Ile Ile  
 195 200 205  
 Val Arg Ala Arg Ile Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile  
 210 215 220  
 Ala Asp Thr Asp Arg Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His  
 225 230 235 240  
 Ser Asp Gly Ser Glu His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp  
 245 250 255  
 Val Ile Ser Pro Glu Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly  
 260 265 270  
 Ser Leu Ala Thr Leu Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala  
 275 280 285  
 Lys Asp Pro Leu Lys Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp  
 290 295 300  
 Ile Phe Pro Ser Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly  
 305 310 315 320  
 Val Ala Tyr Tyr Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn  
 325 330 335  
 Leu Thr Gln Phe Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg  
 340 345 350  
 Gly Tyr Gly Ser Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr  
 355 360 365  
 Glu Ala Val Glu Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser  
 370 375 380  
 Gly His Tyr Ser Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn  
 385 390 395 400  
 Arg Ala Pro Leu Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp  
 405 410 415  
 Phe Pro Ile Arg Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys  
 420 425 430  
 Arg Val Met Glu Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg  
 435 440 445  
 Thr Ser Ala Glu Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp

450                      455                      460  
 Leu Lys Thr Arg Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp  
 465                      470                      475                      480  
 Met Ser Arg Arg Leu Glu Leu Ser  
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 gcc atg ggt gca cca gcg aaa aac cag gtg aaa aac ctc acc cag ttc 96  
 Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe  
 20                      25                      30  
 tac caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc 144  
 Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser  
 35                      40                      45  
 aag ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag 192  
 Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu  
 50                      55                      60  
 cct ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc 240  
 Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser  
 65                      70                      75                      80  
 gca ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg 288  
 Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu  
 85                      90                      95  
 tcc tac cca atg cca ggc tgg aac gtc tgc gtt gac ttc cct atc cgc 336  
 Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg  
 100                      105                      110  
 cca ggt ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa 384  
 Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu  
 115                      120                      125  
 ttc ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag 432  
 Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu  
 130                      135                      140  
 aac ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga 480  
 Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg  
 145                      150                      155                      160  
 aat gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga 528

Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg  
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ctt gag ctt tct taagaaaggg cttgaactaa aca 563  
 Leu Glu Leu Ser  
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<210> 852  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 852  
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 Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe  
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 Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser  
 35 40 45  
 Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu  
 50 55 60  
 Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser  
 65 70 75 80  
 Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu  
 85 90 95  
 Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg  
 100 105 110  
 Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu  
 115 120 125  
 Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu  
 130 135 140  
 Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg  
 145 150 155 160  
 Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg  
 165 170 175  
 Leu Glu Leu Ser  
 180

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 <213> Corynebacterium glutamicum

<220>  
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 <223> FRXA00426

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ggc acg tcc agc tcc ggc gct tcg gcc ggt gcc cac gga gcc ctt ccc 163  
Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala His Gly Ala Leu Pro  
10 15 20

cta gaa gct cag aaa ctg aac ggt tgg ggc cgc aca gcc ccc acc acc 211  
Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg Thr Ala Pro Thr Thr  
25 30 35

gct gag gta ctt acc acc cca gac cta gac atc att gtg gat gca gtc 259  
Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile Ile Val Asp Ala Val  
40 45 50

cgc caa gtc gct gaa caa aac gac tcc aag ccg gac tac ctc aag cgc 307  
 Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro Asp Tyr Leu Lys Arg  
 55 60 65

ggc gtg att gcc cgt ggc atg ggt cgt tcc tat ggt gac cca gcc caa 355  
Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr Gly Asp Pro Ala Gln  
70 75 80 85

aac gcc ggt ggc ctt gtc att gac atg cag cca ctg aac aaa atc cac 403  
Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro Leu Asn Lys Ile His  
90 95 100

tcg att gat cct gat tct gcg atc gtc gat gta gat ggc ggc gtc acc 451  
Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val Asp Gly Gly Val Thr  
105 110 115

ctc gat cag ctc atg aag gct gcc ctg cca tat ggc ctc tgg gtt cct 499  
Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr Gly Leu Trp Val Pro  
120 125 130

gtc ctt ccc ggc acc cgc caa gtc acc atc ggt ggc gca atc gga cca 547  
Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly Gly Ala Ile Gly Pro  
135 140 145

gac atc cac ggt aag aac cac cac tct gca ggt tcc ttc ggc gac cac 595  
Asp Ile His Gly Lys Asn His His Ser Ala Gly Ser Phe Gly Asp His  
150 155 160 165

gtg gtc tcc atg gaa ctc ctc gtt gca 622  
Val Val Ser Met Glu Leu Leu Val Ala  
170

<213> *Corynebacterium glutamicum*

Met Asn Ser Ser His Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala  
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taccgatccc	cttccttgaa	gtttcgctaa	cctggcgtac	atg	act	ctt	tcc	ctt								115
				Met	Thr	Leu	Ser	Leu								
				1				5								
cct cca att ggt ttc ggc acc gtt cat ctt gat ggc gca cct ggc gtt																163
Pro Pro Ile Gly Phe Gly Thr Val His Leu Asp Gly Ala Pro Gly Val																
				10				15						20		
gaa gcc atc gct act gcc att gat gct ggt tac cgc ctc atc gac acc																211
Glu Ala Ile Ala Thr Ala Ile Asp Ala Gly Tyr Arg Leu Ile Asp Thr																
				25				30						35		
gcg tac aac tat gaa aat gaa ggt acc gtg ggc aag gct gtc cgc gag																259
Ala Tyr Asn Tyr Glu Asn Glu Gly Thr Val Gly Lys Ala Val Arg Glu																
				40				45					50			
tcg ggt gtc ccc cgc gag gaa ttg att gtt acc agt aag ctc cct ggc																307

Ser	Gly	Val	Pro	Arg	Glu	Glu	Leu	Ile	Val	Thr	Ser	Lys	Leu	Pro	Gly		
55						60					65						
cgc	ttc	cat	gct	cgc	gat	cta	gga	cgc	gtc	cgc	att	gag	gaa	agt	cta	355	
Arg	Phe	His	Ala	Arg	Asp	Leu	Gly	Arg	Val	Arg	Ile	Glu	Glu	Ser	Leu	85	
70					75				80								
tac	cgc	ctc	aac	tta	gat	tac	atc	gat	ctc	ctc	ttg	att	cac	tgg	cct	403	
Tyr	Arg	Leu	Asn	Leu	Asp	Tyr	Ile	Asp	Leu	Leu	Leu	Ile	His	Trp	Pro	100	
				90					95								
aat	ccc	agc	aag	gat	ctc	tac	gtc	gag	gcg	tgg	gaa	acg	ctg	att	gaa	451	
Asn	Pro	Ser	Lys	Asp	Leu	Tyr	Val	Glu	Ala	Trp	Glu	Thr	Leu	Ile	Glu	115	
			105					110									
gtc	cgc	gat	gct	ggc	ctg	gtc	aag	cac	atc	gga	gtg	tct	aac	ttc	ctt	499	
Val	Arg	Asp	Ala	Gly	Leu	Val	Lys	His	Ile	Gly	Val	Ser	Asn	Phe	Leu		
		120					125					130					
cca	aat	cac	att	gat	cgc	ctg	cgc	cgc	gaa	acc	ggt	gaa	ctg	ccg	gcc	547	
Pro	Asn	His	Ile	Asp	Arg	Leu	Arg	Arg	Glu	Thr	Gly	Glu	Leu	Pro	Ala		
	135					140					145						
gtt	aac	cag	atc	gag	ttg	cac	ccc	tat	ttc	ccg	cag	gtg	gag	cag	gta	595	
Val	Asn	Gln	Ile	Glu	Leu	His	Pro	Tyr	Phe	Pro	Gln	Val	Glu	Gln	Val		
150					155					160					165		
gat	ttc	cac	gat	gag	ctg	ggc	atc	att	acc	gag	gcc	tgg	agc	ccg	ctc	643	
Asp	Phe	His	Asp	Glu	Leu	Gly	Ile	Ile	Thr	Glu	Ala	Trp	Ser	Pro	Leu		
				170					175					180			
agc	aac	ggt	cgc	gga	ctc	gtc	gaa	gag	cca	ttg	ctc	aag	gaa	atc	ggc	691	
Ser	Asn	Gly	Arg	Gly	Leu	Val	Glu	Glu	Pro	Leu	Leu	Lys	Glu	Ile	Gly		
			185					190					195				
gag	cgc	tac	ggg	gtc	ggc	agc	ggc	gaa	atc	gcc	ctc	gct	tgg	cat	cac	739	
Glu	Arg	Tyr	Gly	Val	Gly	Ser	Gly	Glu	Ile	Ala	Leu	Ala	Trp	His	His		
		200					205					210					
gcc	agg	gga	atc	gtt	ccg	att	cca	cgc	tcc	acc	aac	ccg	gcc	agg	cag	787	
Ala	Arg	Gly	Ile	Val	Pro	Ile	Pro	Arg	Ser	Thr	Asn	Pro	Ala	Arg	Gln		
	215					220					225						
cgc	agc	aac	ttg	gag	gcg	gta	aag	att	tcg	ctt	atc	gac	gaa	gac	gtc	835	
Arg	Ser	Asn	Leu	Glu	Ala	Val	Lys	Ile	Ser	Leu	Ile	Asp	Glu	Asp	Val		
230					235					240					245		
cag	gcg	att	acc	gct	ttg	gcg	cgc	aaa	aac	ggc	cgg	atc	aaa	gat	caa	883	
Gln	Ala	Ile	Thr	Ala	Leu	Ala	Arg	Lys	Asn	Gly	Arg	Ile	Lys	Asp	Gln		
				250					255					260			
gat	cca	gcc	gtc	tat	gaa	gaa	ttc	tagatagttta	catcaagggtt	ccg						930	
Asp	Pro	Ala	Val	Tyr	Glu	Glu	Phe										
			265														

&lt;210&gt; 856

&lt;211&gt; 269

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 856

Met Thr Leu Ser Leu Pro Pro Ile Gly Phe Gly Thr Val His Leu Asp  
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 Gly Ala Pro Gly Val Glu Ala Ile Ala Thr Ala Ile Asp Ala Gly Tyr  
 20 25 30  
 Arg Leu Ile Asp Thr Ala Tyr Asn Tyr Glu Asn Glu Gly Thr Val Gly  
 35 40 45  
 Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu Ile Val Thr  
 50 55 60  
 Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly Arg Val Arg  
 65 70 75 80  
 Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile Asp Leu Leu  
 85 90 95  
 Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val Glu Ala Trp  
 100 105 110  
 Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys His Ile Gly  
 115 120 125  
 Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg Arg Glu Thr  
 130 135 140  
 Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro Tyr Phe Pro  
 145 150 155 160  
 Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile Ile Thr Glu  
 165 170 175  
 Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu Glu Pro Leu  
 180 185 190  
 Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly Glu Ile Ala  
 195 200 205  
 Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro Arg Ser Thr  
 210 215 220  
 Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys Ile Ser Leu  
 225 230 235 240  
 Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg Lys Asn Gly  
 245 250 255  
 Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe  
 260 265

&lt;210&gt; 857

&lt;211&gt; 695

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (672)

&lt;223&gt; FRXA00708

&lt;400&gt; 857

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Thr	Val	Gly	Lys	Ala	Val	Arg	Glu	Ser	Gly	Val	Pro	Arg	Glu	Glu	Leu	
1				5					10					15		
att	gtt	acc	agt	aag	ctc	cct	ggc	cgc	ttc	cat	gct	cgc	gat	cta	gga	96
Ile	Val	Thr	Ser	Lys	Leu	Pro	Gly	Arg	Phe	His	Ala	Arg	Asp	Leu	Gly	
			20					25					30			
cgc	gtc	cgc	att	gag	gaa	agt	cta	tac	cgc	ctc	aac	tta	gat	tac	atc	144
Arg	Val	Arg	Ile	Glu	Glu	Ser	Leu	Tyr	Arg	Leu	Asn	Leu	Asp	Tyr	Ile	
		35					40					45				
gat	ctc	ctc	ttg	att	cac	tgg	cct	aat	ccc	agc	aag	gat	ctc	tac	gtc	192
Asp	Leu	Leu	Leu	Ile	His	Trp	Pro	Asn	Pro	Ser	Lys	Asp	Leu	Tyr	Val	
	50					55					60					
gag	gcg	tgg	gaa	acg	ctg	att	gaa	gtc	cgc	gat	gct	ggc	ctg	gtc	aag	240
Glu	Ala	Trp	Glu	Thr	Leu	Ile	Glu	Val	Arg	Asp	Ala	Gly	Leu	Val	Lys	
65					70				75						80	
cac	atc	gga	gtg	tct	aac	ttc	ctt	cca	aat	cac	att	gat	cgc	ctg	cgc	288
His	Ile	Gly	Val	Ser	Asn	Phe	Leu	Pro	Asn	His	Ile	Asp	Arg	Leu	Arg	
				85					90					95		
cgc	gaa	acc	ggg	gaa	ctg	ccg	gcc	gtt	aac	cag	atc	gag	ttg	cac	ccc	336
Arg	Glu	Thr	Gly	Glu	Leu	Pro	Ala	Val	Asn	Gln	Ile	Glu	Leu	His	Pro	
			100					105					110			
tat	ttc	ccg	cag	gtg	gag	cag	gta	gat	ttc	cac	gat	gag	ctg	ggc	atc	384
Tyr	Phe	Pro	Gln	Val	Glu	Gln	Val	Asp	Phe	His	Asp	Glu	Leu	Gly	Ile	
		115					120					125				
att	acc	gag	gcc	tgg	agc	ccg	ctc	agc	aac	ggg	cgc	gga	ctc	gtc	gaa	432
Ile	Thr	Glu	Ala	Trp	Ser	Pro	Leu	Ser	Asn	Gly	Arg	Gly	Leu	Val	Glu	
	130					135					140					
gag	cca	ttg	ctc	aag	gaa	atc	ggc	gag	cgc	tac	ggg	gtc	ggc	agc	ggc	480
Glu	Pro	Leu	Leu	Lys	Glu	Ile	Gly	Glu	Arg	Tyr	Gly	Val	Gly	Ser	Gly	
145				150					155						160	
gaa	atc	gcc	ctc	gct	tgg	cat	cac	gcc	agg	gga	atc	gtt	ccg	att	cca	528
Glu	Ile	Ala	Leu	Ala	Trp	His	His	Ala	Arg	Gly	Ile	Val	Pro	Ile	Pro	
				165					170					175		
cgc	tcc	acc	aac	ccg	gcc	agg	cag	cgc	agc	aac	ttg	gag	gcg	gta	aag	576
Arg	Ser	Thr	Asn	Pro	Ala	Arg	Gln	Arg	Ser	Asn	Leu	Glu	Ala	Val	Lys	
			180					185					190			
att	tcg	ctt	atc	gac	gaa	gac	gtc	cag	gcg	att	acc	gct	ttg	gcg	cgc	624
Ile	Ser	Leu	Ile	Asp	Glu	Asp	Val	Gln	Ala	Ile	Thr	Ala	Leu	Ala	Arg	
		195					200					205				
aaa	aac	ggc	cgg	atc	aaa	gat	caa	gat	cca	gcc	gtc	tat	gaa	gaa	ttc	672
Lys	Asn	Gly	Arg	Ile	Lys	Asp	Gln	Asp	Pro	Ala	Val	Tyr	Glu	Glu	Phe	
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tagatagttta	catcaagggtt	ccg														695



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 <211> 224  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 858  
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 Arg Val Arg Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile  
 35 40 45  
 Asp Leu Leu Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val  
 50 55 60  
 Glu Ala Trp Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys  
 65 70 75 80  
 His Ile Gly Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg  
 85 90 95  
 Arg Glu Thr Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro  
 100 105 110  
 Tyr Phe Pro Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile  
 115 120 125  
 Ile Thr Glu Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu  
 130 135 140  
 Glu Pro Leu Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly  
 145 150 155 160  
 Glu Ile Ala Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro  
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 Arg Ser Thr Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys  
 180 185 190  
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&lt;223&gt; RXA02373

&lt;400&gt; 859

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Gln Ser Leu Met Asp Gln Lys Asn Lys Leu Ser Lys Ser Glu Gly Ile
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Gly Val Phe Lys Val Asp Pro Asp Glu Ala Glu Arg Val Val Thr Glu
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gaa gag ctg ttt att act acc aag ttg tgg aac gat cgc cac ctg gat 451
Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn Asp Arg His Leu Asp
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Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys Leu Gly Leu Asp Tyr
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Val Asp Leu Tyr Leu Val His Trp Pro Ala Pro Lys Asn Asp Asn Tyr
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atc ggt gtg tgc aac ttc ctg cca gag cac cta gaa aag ctg ctg gca 643
Ile Gly Val Cys Asn Phe Leu Pro Glu His Leu Glu Lys Leu Leu Ala
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gag gca acc act gtg cct gcc att aac cag att gag ctg cac cca gct 691
Glu Ala Thr Thr Val Pro Ala Ile Asn Gln Ile Glu Leu His Pro Ala
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Leu Gln Gln Arg Asp Ala Val Glu Ala Ser Leu Ala Ala Gly Ile Thr
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 Glu Glu Pro Ile Ala Ala Ala Ala Lys Asn His Gly Lys Thr Pro Ala  
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cag gtt gtt atc cgt tgg cac ctg cag aac ggt ttc gtt gtg ttc ccc 883  
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 Lys Thr Val Thr Lys Ser Arg Met Val Glu Asn Ile Asp Val Phe Asp  
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<400> 860

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Lys Ser Glu Gly Ile Pro Leu Val Thr Leu Asn Asp Gly Lys Thr Ile  
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Pro Gln Leu Gly Phe Gly Val Phe Lys Val Asp Pro Asp Glu Ala Glu  
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Arg Val Val Thr Glu Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr  
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Ala Ala Ile Tyr Gly Asn Glu Glu Gly Val Gly Arg Ala Ile Ala Lys  
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Ser Gly Ile Pro Arg Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn  
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Asp Arg His Leu Asp Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys  
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Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Val His Trp Pro Ala Pro  
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 Phe Asp Leu Gly Ala Glu Glu Pro Ile Ala Ala Ala Ala Lys Asn His  
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 Gly Lys Thr Pro Ala Gln Val Val Ile Arg Trp His Leu Gln Asn Gly  
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 Phe Val Val Phe Pro Lys Thr Val Thr Lys Ser Arg Met Val Glu Asn  
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Asn  
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 Met Ile Thr Ala Thr  
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 gca ctg cat ggg tgt tca ctg att gat ggc gag tgg gtc gct gga aaa 163  
 Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu Trp Val Ala Gly Lys  
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 Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr Asn Ala Ser Leu Asn  
 25 30 35  
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Ser	Ala	Lys	Arg	Ala	Phe	Glu	Ser	Tyr	Arg	Leu	Thr	Thr	Pro	Glu	Val		
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Arg	Ala	Asp	Phe	Leu	Asp	Ser	Ile	Ala	Asp	Asn	Ile	Asp	Ala	Leu	Ser		
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Ala	Glu	Thr	Val	Arg	Ser	Gly	Gln	Phe	His	Arg	Val	Arg	Ile	Glu	Arg		
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Gly	Pro	Arg	Ile	Asp	Leu	Arg	Gln	Arg	Gln	Val	Pro	Leu	Gly	Pro	Val		
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gcg	gta	ttc	ggg	gca	agc	aac	ttc	ccc	gtc	gct	ttc	tct	act	gct	ggg	595	
Ala	Val	Phe	Gly	Ala	Ser	Asn	Phe	Pro	Val	Ala	Phe	Ser	Thr	Ala	Gly		
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Gly	Asp	Thr	Ala	Ser	Ala	Leu	Ala	Ala	Gly	Cys	Pro	Val	Val	Phe	Lys		
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gcg	cat	aat	gcg	cac	cct	gga	aca	gct	gag	ctc	gtc	ggg	caa	gcg	gtg	691	
Ala	His	Asn	Ala	His	Pro	Gly	Thr	Ala	Glu	Leu	Val	Gly	Gln	Ala	Val		
			185					190					195				
cgg	gga	gcc	gtc	gaa	aag	cat	gag	ttt	gat	gct	ggg	gtg	ttt	aac	ctt	739	
Arg	Gly	Ala	Val	Glu	Lys	His	Glu	Phe	Asp	Ala	Gly	Val	Phe	Asn	Leu		
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Leu	Ser	Gln	Thr	Ala	Phe	Ser	Arg	Pro	Val	Pro	Val	Pro	Val	Phe	Ala		
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Glu	Met	Ser	Ala	Thr	Asn	Pro	Val	Phe	Val	Phe	Pro	Gly	Ala	Leu	Ala		
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gat	ttg	gat	gca	tcg	agt	tcc	ttg	gct	gag	gcg	ttt	acc	gct	tcc	gtc	979	
Asp	Leu	Asp	Ala	Ser	Ser	Ser	Leu	Ala	Glu	Ala	Phe	Thr	Ala	Ser	Val		

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ccg cgc ggt gtt gtt ggt gat gct ttt gtg gcg ctc gta gca gcc aaa 1075		
Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala Leu Val Ala Ala Lys 310 315 320 325		
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Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr Gln Gly Ile Ala Gln 330 335 340		
gca tgg cag cgc gga gtc gac aac ctt gca gca cag cca agt gta aaa 1171		
Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala Gln Pro Ser Val Lys 345 350 355		
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Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu Asn Ala Pro Gly Pro 360 365 370		
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Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu Asn Asn Val Val Leu 375 380 385		
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Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val Val Arg Tyr Asp Ser 390 395 400 405		
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gcc acg atc cac gca tcc cag gat gat ttc cag gaa gtc tcg aaa ctt 1411		
Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln Glu Val Ser Lys Leu 425 430 435		
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Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val Leu Tyr Gly Gly Trp 440 445 450		
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Pro Thr Gly Val Glu Val Gly His Thr Val Ile His Gly Gly Pro Tyr 455 460 465		
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Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val Gly Thr Leu Ala Ile 470 475 480 485		

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Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr Phe Pro Ala Glu Leu  
490 495 500

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1651

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Ile Asp Arg  
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<212> PRT

<213> Corynebacterium glutamicum

<400> 862

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35 40 45

Arg Ala Ala Thr Thr Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu  
50 55 60

Thr Thr Pro Glu Val Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn  
65 70 75 80

Ile Asp Ala Leu Ser Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr  
85 90 95

Gly Leu Gly Thr Thr Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn  
100 105 110

Gln Leu Arg Leu Phe Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg  
115 120 125

Val Arg Ile Glu Arg Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val  
130 135 140

Pro Leu Gly Pro Val Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala  
145 150 155 160

Phe Ser Thr Ala Gly Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys  
165 170 175

Pro Val Val Phe Lys Ala His Asn Ala His Pro Gly Thr Ala Glu Leu  
180 185 190

Val Gly Gln Ala Val Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala  
195 200 205

Gly Val Phe Asn Leu Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu  
 210 215 220  
 Leu Ala Ala Asp Pro Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg  
 225 230 235 240  
 Gln Gly Gly Leu Ala Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro  
 245 250 255  
 Val Pro Val Phe Ala Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe  
 260 265 270  
 Pro Gly Ala Leu Ala Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala  
 275 280 285  
 Phe Thr Ala Ser Val Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro  
 290 295 300  
 Gly Leu Val Phe Ile Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala  
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 Leu Val Ala Ala Lys Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr  
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 Gln Gly Ile Ala Gln Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala  
 340 345 350  
 Gln Pro Ser Val Lys Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu  
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 Asn Ala Pro Gly Pro Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu  
 370 375 380  
 Asn Asn Val Val Leu Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val  
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 Val Arg Tyr Asp Ser Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu  
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 Glu Gly Gln Leu Thr Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln  
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 Glu Val Ser Lys Leu Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val  
 435 440 445  
 Leu Tyr Gly Gly Trp Pro Thr Gly Val Glu Val Gly His Thr Val Ile  
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 His Gly Gly Pro Tyr Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val  
 465 470 475 480  
 Gly Thr Leu Ala Ile Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr  
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 40 45  
 atc aaa gca gct ggc gct gct tcc gtt gct gtt gtt gat ttc gat gcg 307  
 Ile Lys Ala Ala Gly Ala Ala Ser Val Ala Val Val Asp Phe Asp Ala 65  
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 Leu Asp Thr Glu Ser His Pro Ala Ala Ile Asp Ala Ala Phe Glu Asn 85  
 70 75 80  
 ggc gac gtt gac gta gca atc gtg gct ttc ggc atc ctc ggc gac aac 403  
 Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly Ile Leu Gly Asp Asn 100  
 90 95  
 gaa gca cag tgg cgc gac caa gca cta gca gtg gaa gca acc acc gtg 451  
 Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val Glu Ala Thr Thr Val 115  
 105 110  
 aac tac acc gcc ggc ggt tcc gta ggt gta ctg ctg ggc cag aaa ttt 499  
 Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu Leu Gly Gln Lys Phe 130  
 120 125  
 gag cag cag ggc cac ggc acc atc gtg gca ttg tcc tct gtg gca ggc 547  
 Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu Ser Ser Val Ala Gly 145  
 135 140  
 cag cga gtc cgc cgc tcc aac ttt gtc tac ggc tcc gcc aag gca ggt 595  
 Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly Ser Ala Lys Ala Gly 165  
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 Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala Leu Arg Gly Ser Gly 180  
 170 175

gcc aac gta ttg gtg gtt cgc cca ggc cag gta cgc acc aag atg tcc 691  
 Ala Asn Val Leu Val Val Arg Pro Gly Gln Val Arg Thr Lys Met Ser  
                   185                                  190                                  195

gca gat ggt ggc gaa gcc cca ctg acc gtc aac cgc gaa gac gtg gca 739  
 Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn Arg Glu Asp Val Ala  
                   200                                  205                                  210

gat gct gtt tat gat gca gtg gtg aac aag aag gac atc atc ttt gtc 787  
 Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys Asp Ile Ile Phe Val  
                   215                                  220                                  225

cac cca ctg ttc cag tac gtc tct ttt gcg ttc caa ttc att ccg cga 835  
 His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe Gln Phe Ile Pro Arg  
                   230                                  235                                  240                                  245

gca atc ttc cgc aag ctg ccg ttc taacggaagt tacggaagtt acg 882  
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<213> Corynebacterium glutamicum

<400> 864

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                   20                                  25                                  30

Pro Ser His Val Thr Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp  
                   35                                  40                                  45

Ala Ala Val Ala Glu Ile Lys Ala Ala Gly Ala Ala Ser Val Ala Val  
                   50                                  55                                  60

Val Asp Phe Asp Ala Leu Asp Thr Glu Ser His Pro Ala Ala Ile Asp  
   65                                  70                                  75                                  80

Ala Ala Phe Glu Asn Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly  
                   85                                  90                                  95

Ile Leu Gly Asp Asn Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val  
                   100                                  105                                  110

Glu Ala Thr Thr Val Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu  
                   115                                  120                                  125

Leu Gly Gln Lys Phe Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu  
                   130                                  135                                  140

Ser Ser Val Ala Gly Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly  
   145                                  150                                  155                                  160

Ser Ala Lys Ala Gly Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala  
                   165                                  170                                  175

Leu Arg Gly Ser Gly Ala Asn Val Leu Val Val Arg Pro Gly Gln Val  
 180 185 190  
 Arg Thr Lys Met Ser Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn  
 195 200 205  
 Arg Glu Asp Val Ala Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys  
 210 215 220  
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 Gln Phe Ile Pro Arg Ala Ile Phe Arg Lys Leu Pro Phe  
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 Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp  
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 cag ggc ttt aga act cag ttt tta acc cgc atg gct gac gat atc ggc 144  
 Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly  
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 Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly  
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 Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly  
 65 70 75 80  
 tgg gaa gct ttc cag cca tgg gca att gtg tcc atg gca gtt gct gct 288  
 Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala  
 85 90 95  
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 Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val  
 100 105 110  
 gca aca ggc att gcg ttg gtg aca acc tgc att atc ttg gcg atg aat 384  
 Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn  
 115 120 125  
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 Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met

130	135	140	
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ggc ggc att att tac ttg ggt gtt tcg gct act ttc tat act ttg ttc Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe 165 170 175			528
acc ggt gct atc gcg ctt tct gcg gtc gcg gtg tgc atc gtg gtg gcg Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala 180 185 190			576
gct att gtg cag cgc tcc atc aaa cca ctg ctg tgg ctt gca gtg ctg Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu 195 200 205			624
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ctg gcc tcc atc aac gga gcg gag cgc tct ggc gat tcc gca aca cac Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His 225 230 235 240			720
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aat cta att gtg gtc ctc gtg ctg ctt ggc ggc ctc tac tac gcg caa 1104 Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln 355 360 365			

gat ctg ccg cag aag aac gca cga gct atc gat ctg gcc tat acc gat  
1152

Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp  
370 375 380

act gat ggc tac ggc gag cgc gcg gat ctg tat ccg gcc gga gct gca  
1200

Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala  
385 390 395 400

cgt tat tac aag gac atc aac gat cat ctg ctt gat caa gga ttc gag  
1248

Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu  
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cct tcc gaa act gtc gtg ctg aca gac gaa ctc gat ttc atg tcc tac  
1296

Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr  
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1344

Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro  
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ctt ggt gag ttc gga aac agg aac gca ttc atc gaa gat ctc gcg atc  
1392

Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile  
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cga agc tgg gat gag ttg gct gat cct caa caa ttc agc gac gcc ttg  
1440

Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu  
465 470 475 480

aac acc tct cca tgg acg atc cct gag gtg ttc atc ttc cgt ggc tcc  
1488

Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser  
485 490 495

atc gat gat cct gac gcc ggt tgg aaa tac gac gtg gct gaa gat ctg  
1536

Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu  
500 505 510

tac ccg aac aat cca aac gtg cgc ttc cgc ggc gtg tac ttt aac ccg  
1584

Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro  
515 520 525

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1632

Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val  
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1673

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 <213> Corynebacterium glutamicum

<400> 866

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Trp	Glu	Ala	Phe	Gln	Pro	Trp	Ala	Ile	Val	Ser	Met	Ala	Val	Ala	Ala
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Ser	Val	Leu	Val	Pro	Val	Trp	Gln	Arg	Ile	Thr	Gly	Ser	Leu	Pro	Val
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		115					120					125			
Ser	Glu	Glu	Pro	Tyr	Ala	Ala	Ile	Val	Ala	Met	Gly	Ile	Pro	Ala	Met
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Gly	Gly	Ile	Ile	Tyr	Leu	Gly	Val	Ser	Ala	Thr	Phe	Tyr	Thr	Leu	Phe
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Thr	Gly	Ala	Ile	Ala	Leu	Ser	Ala	Val	Ala	Val	Cys	Ile	Val	Val	Ala
			180					185					190		
Ala	Ile	Val	Gln	Arg	Ser	Ile	Lys	Pro	Leu	Leu	Trp	Leu	Ala	Val	Leu
		195					200					205			
Gly	Gly	Gly	Ser	Ile	Val	Ile	Ala	Leu	Ile	Ser	Trp	Gly	Pro	Tyr	Leu
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Leu	Ala	Ser	Ile	Asn	Gly	Ala	Glu	Arg	Ser	Gly	Asp	Ser	Ala	Thr	His
225					230					235					240
Tyr	Leu	Pro	Leu	Glu	Gly	Thr	Gln	Phe	Pro	Val	Pro	Phe	Leu	Ala	Ser
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Ser	Val	Val	Gly	Leu	Leu	Cys	Leu	Val	Gly	Leu	Ile	Tyr	Leu	Val	Val
			260				265						270		
Arg	Phe	His	Asn	Asn	Glu	Val	Arg	Ala	Met	Trp	Val	Gly	Ile	Ala	Val
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Phe	Tyr	Ala	Trp	Met	Gly	Met	Ser	Met	Ala	Ile	Thr	Leu	Leu	Gly	Asn

290	295	300
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Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr 325 330 335		
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr 340 345 350		
Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln 355 360 365		
Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp 370 375 380		
Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala 385 390 395 400		
Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu 405 410 415		
Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr 420 425 430		
Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro 435 440 445		
Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile 450 455 460		
Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu 465 470 475 480		
Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser 485 490 495		
Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu 500 505 510		
Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro 515 520 525		
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Val Val Thr His Asn Glu 545 550		

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 <212> DNA  
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<220>  
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accttatgac ctccagtagtg tgggtgggcgt gaaacagcga atg gtc ggt tca agt 115  
 Met Val Gly Ser Ser  
 1 5

ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg 163  
 Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser  
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ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat 211  
 Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn  
 25 30 35

tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc 259  
 Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val  
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gcg gaa gaa atg ctc ggc acg atg ttg gat gcg gaa gtc tct cgt tcg 307  
 Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser  
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gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc 355  
 Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu  
 70 75 80 85

ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat 403  
 Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp  
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gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg 451  
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 Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu  
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gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga 547  
 Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly  
 135 140 145

tat tcc ggt tgg cag tta gcg gtc acc cac gct gca tcc aat cat gca 595  
 Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala  
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gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg 643  
 Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu  
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ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta 691  
 Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu  
 185 190 195

ggt gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act 739  
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 200 205 210

gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca 787  
 Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr



215	220	225	
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Gly Arg Asp Ala Glu Val	Gln Ser Tyr Leu Asp	Asn Arg Gly Arg Ile	
230	235	240 245	
att gtc gat gct ctt gat	act gca gcc aaa gga	tta ggc att agc ccc	883
Ile Val Asp Ala Leu Asp	Thr Ala Ala Lys Gly	Leu Gly Ile Ser Pro	
	250	255 260	
gct gtc aca gcc acc acc	tgg gtg cgt gat cgt	ccc gga gtg aca gct	931
Ala Val Thr Ala Thr Thr	Trp Val Arg Asp Arg	Pro Gly Val Thr Ala	
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gtc atc gtg ggc gct cgc	aca cat gaa cag ctg	tca cat ctt ctc aag	979
Val Ile Val Gly Ala Arg	Thr His Glu Gln Leu	Ser His Leu Leu Lys	
	280	285 290	
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Ala Glu Ser Val Thr Leu	Pro Thr Pro Ile Thr	Gln Ala Leu Asp Asp	
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Val Ser Leu			
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Lys Ala Phe Ile Asn Ser	Gly Gly Thr Leu Ile	Asp Val Ser Pro Asn	
	35	40 45	
Tyr Thr Thr Gly Val Ala	Glu Glu Met Leu Gly	Thr Met Leu Asp Ala	
	50	55 60	
Glu Val Ser Arg Ser Ala	Val Val Ile Ser Ser	Ser Ala Gly Val Asn	
	65	70 75 80	
Pro Ala Leu Pro Leu Gly	Arg Arg Val Asp Cys	Ser Arg Arg Asn Leu	
	85	90 95	
Ile Ala Gln Leu Asp Val	Thr Leu Arg Ala Leu	Asn Thr Asp Tyr Leu	
	100	105 110	
Asp Leu Trp Ser Val Gly	Tyr Trp Asp Glu Gly	Thr Pro Pro His Glu	
	115	120 125	
Val Ala Asp Thr Leu Asp	Tyr Ala Val Arg Thr	Gly Arg Val Arg Tyr	
	130	135 140	

Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala  
145 150 155 160

Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln  
165 170 175

Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro  
180 185 190

Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly  
195 200 205

Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser  
210 215 220

Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp  
225 230 235 240

Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly  
245 250 255

Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg  
260 265 270

Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu  
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Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr  
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Gln Ala Leu Asp Asp Val Ser Leu  
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<211> 621

<212> DNA

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<220>

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<223> RXS03074

<400> 869

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Met Thr Gln Ser Ala  
1 5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163  
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
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gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211  
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
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ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259

Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
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 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307  
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
                     55                                    60                                    65  
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355  
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala  
                     70                                    75                                    80                                    85  
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403  
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
                                     90                                    95                                    100  
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
                                     105                                    110                                    115  
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499  
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
                     120                                    125                                    130  
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547  
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
                     135                                    140                                    145  
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
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 Gln

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                     20                                    25                                    30  
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
                     35                                    40                                    45  
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
                     50                                    55                                    60  
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
                     65                                    70                                    75                                    80  
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
                     85                                    90                                    95  
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100	105	110
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Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe		
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Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr		
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Glu Ala Pro Ile Lys Gln		
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 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
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 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
 25 30 35  
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 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
 40 45 50  
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 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
 55 60 65  
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355  
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 70 75 80 85  
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403  
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
 90 95 100  
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
 105 110 115  
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Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
 120 125 130

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 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
 135 140 145

gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
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 Gln

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Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
 35 40 45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
 50 55 60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
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Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
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Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr  
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe  
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Glu Ala Pro Ile Lys Gln  
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gaatcgtatc cgtacctgga gacgatctag actggttgctgc atg tcc agc acg cca 115
                                         Met Ser Ser Thr Pro
                                         1                               5

gct caa gat ctt gcc cgc gcc gtt att gat tcc ctc gca cca cac gtc 163
Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser Leu Ala Pro His Val
                        10                               15                               20

act gac gtg gtg tta tgc cca gga tcc agg aac tca ccg ttg tcg ctt 211
Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn Ser Pro Leu Ser Leu
                        25                               30                               35

gag ttg ctg gcg cgg cag gat ctg cgt gtc cat gtg cgt atc gac gag 259
Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His Val Arg Ile Asp Glu
                        40                               45                               50

cgc agc gcc tca ttt ttg gcg ctg tcc cta gcg cgt acc cag gcc cgg 307
Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala Arg Thr Gln Ala Arg
                        55                               60                               65

ccg gtg gct gtg gtg atg acc tcc ggc acg gct gta gct aac tgc ctg 355
Pro Val Ala Val Val Met Thr Ser Gly Thr Ala Val Ala Asn Cys Leu
                        70                               75                               80                               85

cct gct gtt gct gaa gct gcg cat gcc cat atc ccg ttg att gtg ctc 403
Pro Ala Val Ala Glu Ala Ala His Ala His Ile Pro Leu Ile Val Leu
                        90                               95                               100

tct gct gac cgt cct gca cat ttg gtg gga acg ggg gcg agc caa acg 451
Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr Gly Ala Ser Gln Thr
                        105                               110                               115

att aac cag acc ggt att ttt ggt gat ctt gca ccg acg gtc ggt atc 499
Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala Pro Thr Val Gly Ile
                        120                               125                               130

act gag ctg gat cag gta gcg cag att gct gaa agc ctt gct cag ggg 547
Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu Ser Leu Ala Gln Gly
                        135                               140                               145

gct tcc cag att ccg cgt cat ttc aat ctt gca ctt gat gtt cct ttg 595
Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala Leu Asp Val Pro Leu
                        150                               155                               160                               165

gtt gct cct gaa ctg cca gag ctt cat ggt gag gca gtt gga gca tca 643
Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu Ala Val Gly Ala Ser
                        170                               175                               180

tgg acg cat cgc tgg atc aac cac ggt gag gtg acc gtg gac ctg ggg 691
Trp Thr His Arg Trp Ile Asn His Gly Glu Val Thr Val Asp Leu Gly
                        185                               190                               195

gag cac acc ctc gtg att gcc ggt gat gaa gca tgg gaa gtg gaa ggg 739

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Glu His Thr L u Val Ile Ala Gly Asp Glu Ala Trp Glu Val Glu Gly  
 200 205 210

ctg gaa gat gtg ccc acc atc gct gaa cct act gca cca aag cct tat 787  
 Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr Ala Pro Lys Pro Tyr  
 215 220 225

aat ccg gtg cac cca ctg gct gct gaa atc ttg ctg aag gag cag gtc 835  
 Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu Leu Lys Glu Gln Val  
 230 235 240 245

tcc gcg gaa ggc tat gtg gta aac acc agg cct gat cat gtg atc gtg 883  
 Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro Asp His Val Ile Val  
 250 255 260

gtg gga cac ccc acg ctg cac cgc gga gtg ttg aag ttg atg tca gat 931  
 Val Gly His Pro Thr Leu His Arg Gly Val Leu Lys Leu Met Ser Asp  
 265 270 275

cct ggc att aaa tta act gtg ctt tca cgc acc gat atc atc act gat 979  
 Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr Asp Ile Ile Thr Asp  
 280 285 290

ccc ggc cgc cat gcc gat cag gtg ggc agc aca gtg aaa gtc acc ggc  
 1027  
 Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr Val Lys Val Thr Gly  
 295 300 305

acc cag gaa aag cag tgg cta aag atc tgt tcg gca gca tca gaa ctt  
 1075  
 Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser Ala Ala Ser Glu Leu  
 310 315 320 325

gcg gcc gat ggt gtg cgt gac gtc ctg gac aac caa gaa ttc ggt ttc  
 1123  
 Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn Gln Glu Phe Gly Phe  
 330 335 340

acc ggc ctc cat gtt gcc gca gcc gtg gcg gat acc tta ggc acc ggc  
 1171  
 Thr Gly Leu His Val Ala Ala Ala Val Ala Asp Thr Leu Gly Thr Gly  
 345 350 355

gat act ctc ttt gct gca gca tcc aac tca atc cgt gac ctc tcc ctg  
 1219  
 Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu  
 360 365 370

gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc  
 1267  
 Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val  
 375 380 385

gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct  
 1315  
 Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala  
 390 395 400 405

gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc  
 1363  
 Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala

410 415 420  
 ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc  
 1411  
 Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile  
 425 430 435  
 ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac  
 1459  
 Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn  
 440 445 450  
 gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt  
 1507  
 Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly  
 455 460 465  
 ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc  
 1555  
 Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser  
 470 475 480 485  
 atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac  
 1603  
 Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp  
 490 495 500  
 aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc  
 1651  
 Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser  
 505 510 515  
 gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca  
 1699  
 Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala  
 520 525 530  
 caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt  
 1749  
 Gln Gln Gln Ala Leu Met Asp Thr Val His  
 535 540  
 gcg  
 1752

&lt;210&gt; 874

&lt;211&gt; 543

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 874

Met Ser Ser Thr Pro Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser  
 1 5 10 15  
 Leu Ala Pro His Val Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn  
 20 25 30  
 Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His  
 35 40 45



Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala  
 50 55 60  
 Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala  
 65 70 75 80  
 Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile  
 85 90 95  
 Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr  
 100 105 110  
 Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala  
 115 120 125  
 Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu  
 130 135 140  
 Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala  
 145 150 155 160  
 Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu  
 165 170 175  
 Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val  
 180 185 190  
 Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala  
 195 200 205  
 Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr  
 210 215 220  
 Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu  
 225 230 235 240  
 Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro  
 245 250 255  
 Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu  
 260 265 270  
 Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr  
 275 280 285  
 Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr  
 290 295 300  
 Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser  
 305 310 315 320  
 Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn  
 325 330 335  
 Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp  
 340 345 350  
 Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile  
 355 360 365  
 Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe

370	375	380	
Ser Pro Arg Gly Val	Ala Gly Ile Asp Gly	Ser Val Ala Gln Ala Ile	
385	390	395	400
Gly Thr Ser Leu Ala Val	Gln Ser Arg His Pro Asp Glu Ile Arg Ala		
	405	410	415
Pro Arg Thr Val Ala Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile			
	420	425	430
Gly Gly Leu Leu Ile Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr			
	435	440	445
Ile Val Val Ser Asn Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu			
	450	455	460
Thr Gly Ala Asp Gly Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr			
	465	470	475
Pro His Asp Ala Ser Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu			
	485	490	495
His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp			
	500	505	510
Thr Thr Glu Val Ser Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg			
	515	520	525
Asp Thr Arg Arg Ala Gln Gln Gln Ala Leu Met Asp Thr Val His			
	530	535	540

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 <211> 1080  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1057)  
 <223> RXA02319

<400> 875  
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 Met Ser Asn Tyr Ser  
 1 5  
 acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163  
 Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe  
 10 15 20  
 gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211  
 Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg  
 25 30 35  
 gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259  
 Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn  
 40 45 50

gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac	307
Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His	
55 60 65	
gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc	355
Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly	
70 75 80 85	
ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa	403
Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln	
90 95 100	
cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc	451
Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg	
105 110 115	
gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa	499
Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys	
120 125 130	
gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc	547
Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg	
135 140 145	
acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc	595
Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly	
150 155 160 165	
ggt ggg cac tcc ctc cat gtc gtt tgc gac ctc acc atc gct tcc cgc	643
Gly Gly His Ser Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg	
170 175 180	
caa gaa gca cgc ttc aag caa acc gac gct gac gtg gga tcc ttc gac	691
Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp	
185 190 195	
gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac	739
Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn	
200 205 210	
gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg	787
Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met	
215 220 225	
caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa	835
Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu	
230 235 240 245	
aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc	883
Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr	
250 255 260	
ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc	931
Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu	
265 270 275	
atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg	979
Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met	
280 285 290	

acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa  
 1027  
 Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu  
 295 300 305

ccc aac tgg aat gaa ttc cct tac tac tac tagtgagttc atgggggtcct  
 1077  
 Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr  
 310 315

aaa  
 1080

<210> 876  
 <211> 319  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 876  
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Thr Val Pro Gly Phe Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His  
 20 25 30

Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg  
 35 40 45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr  
 50 55 60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu  
 65 70 75 80

Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys  
 85 90 95

Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala  
 100 105 110

Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp  
 115 120 125

Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val  
 130 135 140

Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn  
 145 150 155 160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu  
 165 170 175

Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp  
 180 185 190

Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met  
 195 200 205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr  
 210 215 220

Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp  
 225 230 235 240  
 His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn  
 245 250 255  
 Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu  
 260 265 270  
 Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr  
 275 280 285  
 Arg Leu Ala Tyr Met Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe  
 290 295 300  
 Leu Glu Lys Arg Glu Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr  
 305 310 315

<210> 877  
 <211> 1017  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(994)  
 <223> RXS00393

<400> 877  
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 Met Ser His Thr Glu  
 1 5  
 ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163  
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg  
 10 15 20  
 ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211  
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly  
 25 30 35  
 gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259  
 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala  
 40 45 50  
 ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307  
 Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp  
 55 60 65  
 tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355  
 Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu  
 70 75 80 85  
 cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403  
 Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala  
 90 95 100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451  
 Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser  
 105 110 115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499  
 Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu  
 120 125 130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547  
 Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly  
 135 140 145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595  
 Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met  
 150 155 160 165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643  
 Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala  
 170 175 180

gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691  
 Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn  
 185 190 195

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739  
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu  
 200 205 210

gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787  
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu  
 215 220 225

att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835  
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp  
 230 235 240 245

cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883  
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala  
 250 255 260

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc 931  
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile  
 265 270 275

ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg 979  
 Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu  
 280 285 290

gca tta gcg ttt agc taaaacgctt ttcgacgctc ccc  
 1017  
 Ala Leu Ala Phe Ser  
 295

&lt;210&gt; 878

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 878

Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp

1	5	10	15
Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val	20	25	30
Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp	35	40	45
Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val	50	55	60
Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp	65	70	75
Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys	85	90	95
Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala	100	105	110
Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly	115	120	125
Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro	130	135	140
Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly	145	150	155
Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser	165	170	175
Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly	180	185	190
Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr	195	200	205
Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys	210	215	220
Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu	225	230	235
Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu	245	250	255
Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp	260	265	270
Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala	275	280	285
Val Leu Thr Gly Leu Ala Leu Ala Phe Ser	290	295	

&lt;210&gt; 879

&lt;211&gt; 1005

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(982)

&lt;223&gt; FRXA00393

&lt;400&gt; 879

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tctattcatt tcacaatagc gtttcacact ccccatagc ctgccgaacg tatttcaagc 60

aattgcgcga tcgagtatgt gatggggaaa gatagagggtt atg tct cac acg gaa 115
                                         Met Ser His Thr Glu
                                         1                               5

ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
                        10                               15                               20

ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
                        25                               30                               35

gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
                        40                               45                               50

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp
                        55                               60                               65

tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu
70                               75                               80                               85

cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala
                        90                               95                               100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser
                        105                               110                               115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu
                        120                               125                               130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly
                        135                               140                               145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
150                               155                               160                               165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
                        170                               175                               180

gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn
                        185                               190                               195

```



aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739  
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu  
200 205 210

gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787  
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu  
215 220 225

att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835  
Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp  
230 235 240 245

```

cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca      883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
                250                      255                      260

```

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg 931  
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser  
 265 270 275

gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979  
Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro Cys Ser Arg Ala Trp  
280 285 290

```
cat tagcgtttag ctaaaacgct ttt
1005
His
```

```
<210> 880
<211> 294
<212> PRT
<213> Corynebacterium glutamicum
```

```

<400> 880
Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp
  1          5          10          15

Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val
          20          25          30

Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp
          35          40          45

Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
          50          55          60

Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp
  65          70          75          80

Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
          85          90          95

Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
          100          105          110

Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
          115          120          125

Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro

```

130	135	140
Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly 145 150 155 160		
Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser 165 170 175		
Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly 180 185 190		
Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr 195 200 205		
Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys 210 215 220		
Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu 225 230 235 240		
Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu 245 250 255		
Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp 260 265 270		
Leu Ile Pro Ser Ser Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro 275 280 285		
Cys Ser Arg Ala Trp His 290		

<210> 881  
 <211> 843  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(820)  
 <223> RXA00391

<400> 881  
 atcttgtaga tcccaccgca attctgggag atctcgagga cgcaatctct ggaagaaaac 60  
 tttcctcccc atccctgtac aagataaaac ccgtgcacag ttg ctg cgc gat tct 115  
 Leu Leu Arg Asp Ser  
 1 5  
 caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc 163  
 Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala  
 10 15 20  
 act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg 211  
 Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu  
 25 30 35  
 aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa 259  
 Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly Gly Glu  
 40 45 50

ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag 307  
 Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln  
 55 60 65

gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat 355  
 Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp  
 70 75 80 85

ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa 403  
 Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Ala Glu  
 90 95 100

ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451  
 Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln  
 105 110 115

tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499  
 Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu  
 120 125 130

ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547  
 Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg  
 135 140 145

att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595  
 Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser  
 150 155 160 165

tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643  
 Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly  
 170 175 180

gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691  
 Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met  
 185 190 195

att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739  
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn  
 200 205 210

gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787  
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile  
 215 220 225

ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840  
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His  
 230 235 240

tgc 843

&lt;210&gt; 882

&lt;211&gt; 240

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 882

Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile  
 1 5 10 15

Ala Leu Val Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala  
 20 25 30

Gln Leu Thr Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln  
 35 40 45

Phe Leu Gly Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His  
 50 55 60

Ile Ala Gly Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu  
 65 70 75 80

Pro Leu Ala Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala  
 85 90 95

Gly Ala Ala Ala Glu Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser  
 100 105 110

Leu Thr Pro Met Gln Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile  
 115 120 125

Glu Ala Leu Lys Leu Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu  
 130 135 140

Ser Lys Gln Ala Arg Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val  
 145 150 155 160

Thr Thr Tyr Gly Ser Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly  
 165 170 175

Lys Pro Ile Pro Gly Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu  
 180 185 190

Leu Gly Gly Pro Met Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His  
 195 200 205

Pro Asp Phe Ala Asn Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu  
 210 215 220

Leu His Asp Gly Ile Leu Thr Val Thr Gly Arg Val Asp Thr Arg His  
 225 230 235 240

&lt;210&gt; 883

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(361)

&lt;223&gt; RXS02908

&lt;400&gt; 883

gccaacgagg gttggtttac cacctctgat tcaggtgaac tccacgacgg gattctcacc 60

gtgactggtc gcgtggatac ccgtcattga ttccgggtgga ttg aag ttg cac cca 115  
 Leu Lys Leu His Pro

																1											5
gag	gta	ctg	gaa	cgt	gcc	atc	gca	gat	att	aaa	ggg	gtc	acc	gcg	gcg	163											
Glu	Val	Leu	Glu	Arg	Ala	Ile	Ala	Asp	Ile	Lys	Gly	Val	Thr	Ala	Ala												
				10					15					20													
tgt	gtt	gtg	ggg	att	ccc	gat	ccc	cga	tta	ggc	caa	gca	att	gtg	gcc	211											
Cys	Val	Val	Gly	Ile	Pro	Asp	Pro	Arg	Leu	Gly	Gln	Ala	Ile	Val	Ala												
				25					30					35													
gcg	tac	tcc	gga	tcg	atc	agt	ccg	tct	gaa	gtt	att	gaa	ggc	ctc	gac	259											
Ala	Tyr	Ser	Gly	Ser	Ile	Ser	Pro	Ser	Glu	Val	Ile	Glu	Gly	Leu	Asp												
				40					45					50													
gat	cta	cct	cgt	tgg	cag	ctt	ccc	aaa	cgg	ctg	aag	cat	ctg	gaa	tct	307											
Asp	Leu	Pro	Arg	Trp	Gln	Leu	Pro	Lys	Arg	Leu	Lys	His	Leu	Glu	Ser												
				55					60					65													
ttg	ccc	agc	att	ggg	cct	gga	aaa	gct	gat	cga	cgt	gct	atc	gcg	aag	355											
Leu	Pro	Ser	Ile	Gly	Pro	Gly	Lys	Ala	Asp	Arg	Arg	Ala	Ile	Ala	Lys												
				70					75					80													
ctg	ttt	tagtcttcat				tcttgctggc				tgc						384											
Leu	Phe																										

```
<210> 884
<211> 87
<212> PRT
<213> Corynebacterium glutamicum
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<400> 884
Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys
  1                      5              10                15
Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly
          20                  25                 30
Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val
        35             40               45
Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu
   50                   55                 60
Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg
  65           70             75                80
Arg Ala Ile Ala Lys Leu Phe
            85
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<210> 885
<211> 705
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(682)
<223> RXA00997
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&lt;400&gt; 885

cccattctgtg gcagatcgaa tgcacccacc gcggagaagt cgtcgcacga accacactgc 60

gcaccatggg gctgaacaag tagccctata ctcgggcacc atg act aca tgg aaa 115  
 Met Thr Thr Trp Lys  
 1 5

gag ctc aca gat aac aac cca gcg cac tca gaa aac tac gcg cag cgc 163  
 Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu Asn Tyr Ala Gln Arg  
 10 15 20

tgg cga aac ctc gcc gca gca ggc aat gat att tac ggc gaa gcc cgc 211  
 Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile Tyr Gly Glu Ala Arg  
 25 30 35

ctc att gat gcc atg gca ccc agg gga gcg aaa atc ttg gat gct ggc 259  
 Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys Ile Leu Asp Ala Gly  
 40 45 50

tgc ggc cag gga cgc atc ggt ggc tac ctg tcc aag caa ggc cac gat 307  
 Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser Lys Gln Gly His Asp  
 55 60 65

gtt cta ggc aca gac ctt gat ccc atc ctg att gat tac gcc aag cag 355  
 Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile Asp Tyr Ala Lys Gln  
 70 75 80 85

gac ttt cca gaa gct cgc tgg gtg gtg gga gat ctc tct gtt gat cag 403  
 Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp Leu Ser Val Asp Gln  
 90 95 100

atc tca gag act gat ttt gat ctc att gtc tcc gcc ggc aac gtc atg 451  
 Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser Ala Gly Asn Val Met  
 105 110 115

ggc ttt ctc gct gag gat ggt cgc gaa cct gca cta gcc aac att cac 499  
 Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala Leu Ala Asn Ile His  
 120 125 130

cgc gca ctg ggc gcc gat ggc cgc gct gtc atc ggt ttc ggc gca gga 547  
 Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile Gly Phe Gly Ala Gly  
 135 140 145

cgt gga tgg gtc ttt gga gac ttc ctc gaa gtc gca gaa cgc gtg ggc 595  
 Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val Ala Glu Arg Val Gly  
 150 155 160 165

ctc gag ttg gaa aat gct ttt gag tct tgg gat ctt aag cct ttt gtc 643  
 Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp Leu Lys Pro Phe Val  
 170 175 180

caa ggc tct gag ttc tta gtg gcg gta ttt acc aag aag taacacctct 692  
 Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr Lys Lys  
 185 190

atcttgcacc tga 705

&lt;210&gt; 886

&lt;211&gt; 194

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 886

Met Thr Thr Trp Lys Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu  
 1 5 10 15

Asn Tyr Ala Gln Arg Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile  
 20 25 30

Tyr Gly Glu Ala Arg Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys  
 35 40 45

Ile Leu Asp Ala Gly Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser  
 50 55 60

Lys Gln Gly His Asp Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile  
 65 70 75 80

Asp Tyr Ala Lys Gln Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp  
 85 90 95

Leu Ser Val Asp Gln Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser  
 100 105 110

Ala Gly Asn Val Met Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala  
 115 120 125

Leu Ala Asn Ile His Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile  
 130 135 140

Gly Phe Gly Ala Gly Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val  
 145 150 155 160

Ala Glu Arg Val Gly Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp  
 165 170 175

Leu Lys Pro Phe Val Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr  
 180 185 190

Lys Lys

&lt;210&gt; 887

&lt;211&gt; 861

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(838)

&lt;223&gt; RXA02189

&lt;400&gt; 887

aatggcaaaa atgggcacat acgatactga tgggaccaat gggaaaacct caagccacca 60

attgagccag ttctctcaag caaaccgata ctggtgggat gtg gac gcg gcc gac 115  
 Val Asp Ala Ala Asp  
 1 5

tat cac gaa cgc cac cct tct tat tta ggc acg gat tcc gct cac ggc	163
Tyr His Glu Arg His Pro Ser Tyr Leu Gly Thr Asp Ser Ala His Gly	
10 15 20	
gag ttc tac tgg tgc ccc gag atg ctg cat gaa aaa gat gta cgt ctt	211
Glu Phe Tyr Trp Cys Pro Glu Met Leu His Glu Lys Asp Val Arg Leu	
25 30 35	
ctt ggc act ccc gca gca ctc tcc ggc aag aaa att tta gag atc ggt	259
Leu Gly Thr Pro Ala Ala Leu Ser Gly Lys Lys Ile Leu Glu Ile Gly	
40 45 50	
tgc ggc tgc gca ccg tgt gct cgg tgg ctg gcc aat gat gtt ccg aat	307
Cys Gly Ser Ala Pro Cys Ala Arg Trp Leu Ala Asn Asp Val Pro Asn	
55 60 65	
gcc ttt gtc acc gct ttc gac att tct tca caa atg ctc aaa tac gca	355
Ala Phe Val Thr Ala Phe Asp Ile Ser Ser Gln Met Leu Lys Tyr Ala	
70 75 80 85	
ggt cac gac cat aac gta cac ctc gta cag gcc gat gca atg tca ctc	403
Gly His Asp His Asn Val His Leu Val Gln Ala Asp Ala Met Ser Leu	
90 95 100	
ccc tac gcc gac agt tcc ttt gac gtg gtc ttt tcc gtt ttc ggc gcc	451
Pro Tyr Ala Asp Ser Ser Phe Asp Val Val Phe Ser Val Phe Gly Ala	
105 110 115	
atc ccc ttt gtg gag gat tcc gcc gca ctc atg aag gaa atc gcg cgc	499
Ile Pro Phe Val Glu Asp Ser Ala Ala Leu Met Lys Glu Ile Ala Arg	
120 125 130	
gtc ctc aaa ccc ggc gga cgc ctc att ttc tcc atc acc cac ccg atg	547
Val Leu Lys Pro Gly Gly Arg Leu Ile Phe Ser Ile Thr His Pro Met	
135 140 145	
cgc tgg att ttc ctc gac gat ccc ggc ccc gca ggc ctc acc gcg atc	595
Arg Trp Ile Phe Leu Asp Asp Pro Gly Pro Ala Gly Leu Thr Ala Ile	
150 155 160 165	
acc agc tac ttc gac cag cgc ggc tac gtc gaa gaa gac gag gaa acc	643
Thr Ser Tyr Phe Asp Gln Arg Gly Tyr Val Glu Glu Asp Glu Glu Thr	
170 175 180	
ggt gct tta agc tat gcg gaa cag cac cgc acc atg ggc gcg cgg atc	691
Gly Ala Leu Ser Tyr Ala Glu Gln His Arg Thr Met Gly Ala Arg Ile	
185 190 195	
aat gag ctt atc gac gcc tcc ctc cac tta gat cac ctc atc gaa cca	739
Asn Glu Leu Ile Asp Ala Ser Leu His Leu Asp His Leu Ile Glu Pro	
200 205 210	
gaa tgg cca gat gag ttg gaa gaa aac tgg ggc caa tgg tca cca ctt	787
Glu Trp Pro Asp Glu Leu Glu Glu Asn Trp Gly Gln Trp Ser Pro Leu	
215 220 225	
cga gga aag ctc ttc ccc ggg aca gca atc ttc ctc gcc acg tac cgc	835
Arg Gly Lys Leu Phe Pro Gly Thr Ala Ile Phe Leu Ala Thr Tyr Arg	
230 235 240 245	
ccc taaaaaacca acggcgctca ttt	861



Pro

&lt;210&gt; 888

&lt;211&gt; 246

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 888

Val Asp Ala Ala Asp Tyr His Glu Arg His Pro Ser Tyr Leu Gly Thr  
 1 5 10 15  
 Asp Ser Ala His Gly Glu Phe Tyr Trp Cys Pro Glu Met Leu His Glu  
 20 25 30  
 Lys Asp Val Arg Leu Leu Gly Thr Pro Ala Ala Leu Ser Gly Lys Lys  
 35 40 45  
 Ile Leu Glu Ile Gly Cys Gly Ser Ala Pro Cys Ala Arg Trp Leu Ala  
 50 55 60  
 Asn Asp Val Pro Asn Ala Phe Val Thr Ala Phe Asp Ile Ser Ser Gln  
 65 70 75 80  
 Met Leu Lys Tyr Ala Gly His Asp His Asn Val His Leu Val Gln Ala  
 85 90 95  
 Asp Ala Met Ser Leu Pro Tyr Ala Asp Ser Ser Phe Asp Val Val Phe  
 100 105 110  
 Ser Val Phe Gly Ala Ile Pro Phe Val Glu Asp Ser Ala Ala Leu Met  
 115 120 125  
 Lys Glu Ile Ala Arg Val Leu Lys Pro Gly Gly Arg Leu Ile Phe Ser  
 130 135 140  
 Ile Thr His Pro Met Arg Trp Ile Phe Leu Asp Asp Pro Gly Pro Ala  
 145 150 155 160  
 Gly Leu Thr Ala Ile Thr Ser Tyr Phe Asp Gln Arg Gly Tyr Val Glu  
 165 170 175  
 Glu Asp Glu Glu Thr Gly Ala Leu Ser Tyr Ala Glu Gln His Arg Thr  
 180 185 190  
 Met Gly Ala Arg Ile Asn Glu Leu Ile Asp Ala Ser Leu His Leu Asp  
 195 200 205  
 His Leu Ile Glu Pro Glu Trp Pro Asp Glu Leu Glu Glu Asn Trp Gly  
 210 215 220  
 Gln Trp Ser Pro Leu Arg Gly Lys Leu Phe Pro Gly Thr Ala Ile Phe  
 225 230 235 240  
 Leu Ala Thr Tyr Arg Pro  
 245

&lt;210&gt; 889

&lt;211&gt; 813

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(790)

&lt;223&gt; RXA02311

&lt;400&gt; 889

cattttgggt atcggttggt tgtccatcgg tggagctaag ggcgctaagc atcgcagcca 60

aataacctcc cactaaagct cctggggttag actcgaacgc gtg gct aaa gca gat 115  
 Val Ala Lys Ala Asp  
 1 5

tta gac aag gac ccc ttc gac gta gcg tca atg ttc gat gac gtc gga 163  
 Leu Asp Lys Asp Pro Phe Asp Val Ala Ser Met Phe Asp Asp Val Gly  
 10 15 20

aag aac tac gat ctc acc aat acc gtg ctt tct ttt ggt cag gac cgt 211  
 Lys Asn Tyr Asp Leu Thr Asn Thr Val Leu Ser Phe Gly Gln Asp Arg  
 25 30 35

gtg tgg cga aag cgc act agg cag cgc ctg gac ctc aag cca ggg gag 259  
 Val Trp Arg Lys Arg Thr Arg Gln Arg Leu Asp Leu Lys Pro Gly Glu  
 40 45 50

aag gtg ctt gat cta gct gca gga aca gcc gtt tcc acc gtg gag ttg 307  
 Lys Val Leu Asp Leu Ala Ala Gly Thr Ala Val Ser Thr Val Glu Leu  
 55 60 65

gca aaa tcc ggc gcg ttt tgt gtg gcg tgt gat ttc tcc cag ggc atg 355  
 Ala Lys Ser Gly Ala Phe Cys Val Ala Cys Asp Phe Ser Gln Gly Met  
 70 75 80 85

ctc gcc gca ggt aaa gac cgc gat gtg tcc aag gtt gtg ggc gat ggc 403  
 Leu Ala Ala Gly Lys Asp Arg Asp Val Ser Lys Val Val Gly Asp Gly  
 90 95 100

atg cag ttg ccg ttt gca gac aac agc ttt gat gct gtg acc att tct 451  
 Met Gln Leu Pro Phe Ala Asp Asn Ser Phe Asp Ala Val Thr Ile Ser  
 105 110 115

tat ggt ctg cgc aat att cac gat ttc cgc gct ggc ctg aaa gaa atg 499  
 Tyr Gly Leu Arg Asn Ile His Asp Phe Arg Ala Gly Leu Lys Glu Met  
 120 125 130

gcc cgc gtg act aaa cct ggt gga cgc ctc acc gtg gcg gag ttc tcc 547  
 Ala Arg Val Thr Lys Pro Gly Gly Arg Leu Thr Val Ala Glu Phe Ser  
 135 140 145

acc ccc gtg atc cct gtg ttc ggc acc gtg tac aag gag tac ctc atg 595  
 Thr Pro Val Ile Pro Val Phe Gly Thr Val Tyr Lys Glu Tyr Leu Met  
 150 155 160 165

cgc ctg ctg ccc cag gcg gcg cgc gca gta tgc tcc aac ccg gag gcc 643  
 Arg Leu Leu Pro Gln Ala Ala Arg Ala Val Ser Ser Asn Pro Glu Ala  
 170 175 180

tac att tac ctg gct gat tcc atc cgc gca tgg cct agc cag gcg gaa 691  
 Tyr Ile Tyr Leu Ala Asp Ser Ile Arg Ala Trp Pro Ser Gln Ala Glu

185	190	195	
cta gca cgg gag atc aac cag aat ggt tgg tca gat tgc ggt tgg cag			739
Leu Ala Arg Glu Ile Asn Gln Asn Gly Trp Ser Asp Cys Gly Trp Gln			
200	205	210	
aac ctg acc ttc ggc atc gtc gcg ctg cac tcg gcg att aaa cca gag			787
Asn Leu Thr Phe Gly Ile Val Ala Leu His Ser Ala Ile Lys Pro Glu			
215	220	225	
aac tagtcgagtc ccacagaggg gag			813
Asn			
230			

&lt;210&gt; 890

&lt;211&gt; 230

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 890

Val	Ala	Lys	Ala	Asp	Leu	Asp	Lys	Asp	Pro	Phe	Asp	Val	Ala	Ser	Met
1				5					10					15	

Phe	Asp	Asp	Val	Gly	Lys	Asn	Tyr	Asp	Leu	Thr	Asn	Thr	Val	Leu	Ser
			20					25					30		

Phe	Gly	Gln	Asp	Arg	Val	Trp	Arg	Lys	Arg	Thr	Arg	Gln	Arg	Leu	Asp
		35					40					45			

Leu	Lys	Pro	Gly	Glu	Lys	Val	Leu	Asp	Leu	Ala	Ala	Gly	Thr	Ala	Val
	50					55					60				

Ser	Thr	Val	Glu	Leu	Ala	Lys	Ser	Gly	Ala	Phe	Cys	Val	Ala	Cys	Asp
65					70					75					80

Phe	Ser	Gln	Gly	Met	Leu	Ala	Ala	Gly	Lys	Asp	Arg	Asp	Val	Ser	Lys
				85					90					95	

Val	Val	Gly	Asp	Gly	Met	Gln	Leu	Pro	Phe	Ala	Asp	Asn	Ser	Phe	Asp
			100					105					110		

Ala	Val	Thr	Ile	Ser	Tyr	Gly	Leu	Arg	Asn	Ile	His	Asp	Phe	Arg	Ala
		115					120					125			

Gly	Leu	Lys	Glu	Met	Ala	Arg	Val	Thr	Lys	Pro	Gly	Gly	Arg	Leu	Thr
	130					135					140				

Val	Ala	Glu	Phe	Ser	Thr	Pro	Val	Ile	Pro	Val	Phe	Gly	Thr	Val	Tyr
145					150					155					160

Lys	Glu	Tyr	Leu	Met	Arg	Leu	Leu	Pro	Gln	Ala	Ala	Arg	Ala	Val	Ser
				165					170					175	

Ser	Asn	Pro	Glu	Ala	Tyr	Ile	Tyr	Leu	Ala	Asp	Ser	Ile	Arg	Ala	Trp
			180					185					190		

Pro	Ser	Gln	Ala	Glu	Leu	Ala	Arg	Glu	Ile	Asn	Gln	Asn	Gly	Trp	Ser
		195					200					205			

Asp	Cys	Gly	Trp	Gln	Asn	Leu	Thr	Phe	Gly	Ile	Val	Ala	Leu	His	Ser
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225	230		
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gatattgaaa tgacgtattc ctgattgggc tgaaaaaatct	115		
	Val Thr Ser Pro Glu	1	5
tta caa aac atc ctt aac aat tat tgg agc ggc agg gca gag gct tac	163		
Leu Gln Asn Ile Leu Asn Asn Tyr Trp Ser Gly Arg Ala Glu Ala Tyr	10	15	20
cac ctc aac caa acc caa agc gag cgt gca caa ttt gaa cgc ccc atc	211		
His Leu Asn Gln Thr Gln Ser Glu Arg Ala Gln Phe Glu Arg Pro Ile	25	30	35
tgg gaa aag gtg tgg tcg aag gct ttg cct atc gtg tcg gaa gaa gcg	259		
Trp Glu Lys Val Trp Ser Lys Ala Leu Pro Ile Val Ser Glu Glu Ala	40	45	50
gta aag gtt ctc gat ctt ggc tgt ggc gct ggt tat gtc acc cac ctt	307		
Val Lys Val Leu Asp Leu Gly Cys Gly Ala Gly Tyr Val Thr His Leu	55	60	65
cta agc gat tgc gga tac gaa aca atc ggc gtt gat ggt tct gag gaa	355		
Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val Asp Gly Ser Glu Glu	70	75	85
atg atc aat caa gct acg cag gag aat ggt ctt cgc agg tcg acg ggt	403		
Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu Arg Arg Ser Thr Gly	90	95	100
cgg gcg act gcc att ttt cag gtc ggg gat gcg cat gat ccc gag ttc	451		
Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala His Asp Pro Glu Phe	105	110	115
cgg gaa ggc tct ttt gat gcg ata acc agc cgg tat gtg ttg tgg act	499		
Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg Tyr Val Leu Trp Thr	120	125	130
ctg ctg gat ccc cag gca gcg att aat cgt tgg gtg tct ttg cta aaa	547		
Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp Val Ser Leu Leu Lys	135	140	145
cct ggt ggg gtt att gcg tgc gta gat gcg gct tgg tat ccg aag ggc	595		
Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala Trp Tyr Pro Lys Gly			

150	155	160	165	
att gat gct ggc acg gaa gta gat tca gtg gat ggt ccg agt gct ttc				643
Ile Asp Ala Gly Thr Glu Val Asp Ser Val Asp Gly Pro Ser Ala Phe	170	175	180	
gta gag acc tat acc ccg gaa ctt ttg agg aat ctt ccc atg tca acg				691
Val Glu Thr Tyr Thr Pro Glu Leu Leu Arg Asn Leu Pro Met Ser Thr	185	190	195	
acc tcc act ggc cac aat ttc gca gag ctt ttc cac aac gct ggc ctc				739
Thr Ser Thr Gly His Asn Phe Ala Glu Leu Phe His Asn Ala Gly Leu	200	205	210	
aaa gaa gtc aca ttg aca ccc att gag ggg ctg gct gaa ctt gac cag				787
Lys Glu Val Thr Leu Thr Pro Ile Glu Gly Leu Ala Glu Leu Asp Gln	215	220	225	
cga ttt ggc ctc tca cca ggg cat gag tcg act ccg cag ttc cta ttc				835
Arg Phe Gly Leu Ser Pro Gly His Glu Ser Thr Pro Gln Phe Leu Phe	230	235	240	245
agg gga att aaa tcc agt tagtgctggt ttaagcggtc gag				876
Arg Gly Ile Lys Ser Ser	250			

&lt;210&gt; 892

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 892

Val Thr Ser Pro Glu Leu Gln Asn Ile Leu Asn Asn Tyr Trp Ser Gly	1	5	10	15
Arg Ala Glu Ala Tyr His Leu Asn Gln Thr Gln Ser Glu Arg Ala Gln	20	25	30	
Phe Glu Arg Pro Ile Trp Glu Lys Val Trp Ser Lys Ala Leu Pro Ile	35	40	45	
Val Ser Glu Glu Ala Val Lys Val Leu Asp Leu Gly Cys Gly Ala Gly	50	55	60	
Tyr Val Thr His Leu Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val	65	70	75	80
Asp Gly Ser Glu Glu Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu	85	90	95	
Arg Arg Ser Thr Gly Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala	100	105	110	
His Asp Pro Glu Phe Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg	115	120	125	
Tyr Val Leu Trp Thr Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp	130	135	140	
Val Ser Leu Leu Lys Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala				

145					150					155					160
Trp	Tyr	Pro	Lys	Gly	Ile	Asp	Ala	Gly	Thr	Glu	Val	Asp	Ser	Val	Asp
				165					170					175	
Gly	Pro	Ser	Ala	Phe	Val	Glu	Thr	Tyr	Thr	Pro	Glu	Leu	Leu	Arg	Asn
			180					185					190		
Leu	Pro	Met	Ser	Thr	Thr	Ser	Thr	Gly	His	Asn	Phe	Ala	Glu	Leu	Phe
		195					200					205			
His	Asn	Ala	Gly	Leu	Lys	Glu	Val	Thr	Leu	Thr	Pro	Ile	Glu	Gly	Leu
	210					215					220				
Ala	Glu	Leu	Asp	Gln	Arg	Phe	Gly	Leu	Ser	Pro	Gly	His	Glu	Ser	Thr
225					230					235					240
Pro	Gln	Phe	Leu	Phe	Arg	Gly	Ile	Lys	Ser	Ser					
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<213> Corynebacterium glutamicum
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Met Thr Ser Arg Asp 5															
gat caa ccc caa gat ctg ctt tcg ctt gca gaa ctt gcc gcc acc aga 163															
Asp Gln Pro Gln Asp Leu Leu Ser Leu Ala Glu Leu Ala Ala Thr Arg 20															
gct tta acc aca gac gaa ctt gaa gca ctc aac aac gcc aat tat ggc 211															
Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn Asn Ala Asn Tyr Gly 35															
ctc gac cgc aat ctg ggg ctg cgc tac acc acc atc gag ccc ggc cgg 259															
Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr Ile Glu Pro Gly Arg 50															
gtg gtc agc gaa ctt cac gtg gca tcc aag cac ctg caa gtg gtg ggc 307															
Val Val Ser Glu Leu His Val Ala Ser Lys His Leu Gln Val Val Gly 65															
ttg gtc aac ggt ggt gtc tac gcc gcc atc gcc gaa tcc act gga tca 355															
Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala Glu Ser Thr Gly Ser 85															
gtc gcc agc atg att tcc gcc cct gga aaa atg gtc gtc ggc atc aac 403															
Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met Val Val Gly Ile Asn 100															

aac aac acc gac ttc att tct gct gtg agc tcc ggt gtc atc gtg gcc 451  
 Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser Gly Val Ile Val Ala  
                   105                                  110                                  115

gaa gca acg ccg att cag cta ggt ggc cgc acc cat ctg tgg cag atc 499  
 Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr His Leu Trp Gln Ile  
                   120                                  125                                  130

gaa tgc acc cac cgc gga gaa gtc gtc gca cga acc aca ctg cgc acc 547  
 Glu Cys Thr His Arg Gly Glu Val Val Ala Arg Thr Thr Leu Arg Thr  
                   135                                  140                                  145

atg gtg ctg aac aag tagccctata ctcgggcacc atg 585  
 Met Val Leu Asn Lys  
 150

<210> 894

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 894

Met Thr Ser Arg Asp Asp Gln Pro Gln Asp Leu Leu Ser Leu Ala Glu  
   1                                  5                                  10                                  15

Leu Ala Ala Thr Arg Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn  
                   20                                  25                                  30

Asn Ala Asn Tyr Gly Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr  
                   35                                  40                                  45

Ile Glu Pro Gly Arg Val Val Ser Glu Leu His Val Ala Ser Lys His  
                   50                                  55                                  60

Leu Gln Val Val Gly Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala  
   65                                  70                                  75                                  80

Glu Ser Thr Gly Ser Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met  
                   85                                  90                                  95

Val Val Gly Ile Asn Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser  
                   100                                  105                                  110

Gly Val Ile Val Ala Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr  
                   115                                  120                                  125

His Leu Trp Gln Ile Glu Cys Thr His Arg Gly Glu Val Val Ala Arg  
                   130                                  135                                  140

Thr Thr Leu Arg Thr Met Val Leu Asn Lys  
 145                                  150

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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cccaaaacgt ccacaaccag gaaggctaag caggatcctc atg act gct cac tgg 115  
 Met Thr Ala His Trp  
 1 5

aaa caa aac caa aag aac ctc atg ctg ttt tcg ggt cgt gcg cac cca 163  
 Lys Gln Asn Gln Lys Asn Leu Met Leu Phe Ser Gly Arg Ala His Pro  
 10 15 20

gaa ctg gca gaa gct gta gct aaa gag ctc gac gtc aac gtc acc cca 211  
 Glu Leu Ala Glu Ala Val Ala Lys Glu Leu Asp Val Asn Val Thr Pro  
 25 30 35

atg acg gca cgc gat ttc gcc aac ggt gaa atc tac gtc cgc ttc gag 259  
 Met Thr Ala Arg Asp Phe Ala Asn Gly Glu Ile Tyr Val Arg Phe Glu  
 40 45 50

gaa tca gtt cgt ggc tcc gac tgc ttc gtc ctg cag tcc cac acc cag 307  
 Glu Ser Val Arg Gly Ser Asp Cys Phe Val Leu Gln Ser His Thr Gln  
 55 60 65

cct ctc aac aag tgg ctc atg gaa cag ctg ctg atg atc gac gct ttg 355  
 Pro Leu Asn Lys Trp Leu Met Glu Gln Leu Leu Met Ile Asp Ala Leu  
 70 75 80 85

aag cgt ggt tcc gca aag cgc atc acc gcg atc ctg ccg ttc tac cca 403  
 Lys Arg Gly Ser Ala Lys Arg Ile Thr Ala Ile Leu Pro Phe Tyr Pro  
 90 95 100

tat gcc cgc cag gac aag aag cac cgc ggc cgc gag cca att tct gct 451  
 Tyr Ala Arg Gln Asp Lys Lys His Arg Gly Arg Glu Pro Ile Ser Ala  
 105 110 115

cgc ctc atc gcc gac ctc atg ctc acc gct ggc gcg gac cgt atc gtg 499  
 Arg Leu Ile Ala Asp Leu Met Leu Thr Ala Gly Ala Asp Arg Ile Val  
 120 125 130

tcc gtg gac ttg cac acc gat cag atc cag ggc ttc ttc gac ggc cca 547  
 Ser Val Asp Leu His Thr Asp Gln Ile Gln Gly Phe Phe Asp Gly Pro  
 135 140 145

gtc gat cac atg cac gcc atg ccg atc ctc acc gat cac atc aag gaa 595  
 Val Asp His Met His Ala Met Pro Ile Leu Thr Asp His Ile Lys Glu  
 150 155 160 165

aac tac aac ctg gac aac atc tgc gtg gtc tcc cct gac gca ggt cgc 643  
 Asn Tyr Asn Leu Asp Asn Ile Cys Val Val Ser Pro Asp Ala Gly Arg  
 170 175 180

gtg aag gtt gca gag aag tgg gct aac acc ttg ggc gat gcc cca atg 691  
 Val Lys Val Ala Glu Lys Trp Ala Asn Thr Leu Gly Asp Ala Pro Met  
 185 190 195

gcg ttc gtg cac aag acc cgc tcc acc gag gta gca aac cag gtt gtc 739  
 Ala Phe Val His Lys Thr Arg Ser Thr Glu Val Ala Asn Gln Val Val



200	205	210	
gcc aac cgc gtc gtc ggt gac gtc gac ggc aag gac tgc gtg ctt ctc			787
Ala Asn Arg Val Val Gly Asp Val Asp Gly Lys Asp Cys Val Leu Leu			
215	220	225	
gac gac atg atc gac act ggc ggc acc atc gcc ggc gct gtg ggc gtc			835
Asp Asp Met Ile Asp Thr Gly Gly Thr Ile Ala Gly Ala Val Gly Val			
230	235	240	245
ctg aag aag gct ggc gca aag tca gtc gtc atc gcc tgc acc cac ggt			883
Leu Lys Lys Ala Gly Ala Lys Ser Val Val Ile Ala Cys Thr His Gly			
	250	255	260
gtg ttc tct gac cca gcc cgc gag cgc ctg tct gca tgc ggt gct gaa			931
Val Phe Ser Asp Pro Ala Arg Glu Arg Leu Ser Ala Cys Gly Ala Glu			
	265	270	275
gaa gtc atc acc acc gac acc ctg cca cag tcc acc gag ggc tgg agc			979
Glu Val Ile Thr Thr Asp Thr Leu Pro Gln Ser Thr Glu Gly Trp Ser			
	280	285	290
aac ctg acc gtt ttg tcg atc gca ccg ctg ctg gct cgc acc atc aac			
1027			
Asn Leu Thr Val Leu Ser Ile Ala Pro Leu Leu Ala Arg Thr Ile Asn			
	295	300	305
gag atc ttc gaa aac ggt tcc gtc acc acc ctc ttc gag ggc gag gcc			
1075			
Glu Ile Phe Glu Asn Gly Ser Val Thr Thr Leu Phe Glu Gly Glu Ala			
310	315	320	325
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1098			

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 896  
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 Val Asn Val Thr Pro Met Thr Ala Arg Asp Phe Ala Asn Gly Glu Ile  
 35 40 45  
 Tyr Val Arg Phe Glu Glu Ser Val Arg Gly Ser Asp Cys Phe Val Leu  
 50 55 60  
 Gln Ser His Thr Gln Pro Leu Asn Lys Trp Leu Met Glu Gln Leu Leu  
 65 70 75 80  
 Met Ile Asp Ala Leu Lys Arg Gly Ser Ala Lys Arg Ile Thr Ala Ile  
 85 90 95  
 Leu Pro Phe Tyr Pro Tyr Ala Arg Gln Asp Lys Lys His Arg Gly Arg

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Glu	Pro	Ile	Ser	Ala	Arg	Leu	Ile	Ala	Asp	Leu	Met	Leu	Thr	Ala	Gly		
115						120						125					
Ala	Asp	Arg	Ile	Val	Ser	Val	Asp	Leu	His	Thr	Asp	Gln	Ile	Gln	Gly		
130						135						140					
Phe	Phe	Asp	Gly	Pro	Val	Asp	His	Met	His	Ala	Met	Pro	Ile	Leu	Thr		
145						150						155					
Asp	His	Ile	Lys	Glu	Asn	Tyr	Asn	Leu	Asp	Asn	Ile	Cys	Val	Val	Ser		
165						170						175					
Pro	Asp	Ala	Gly	Arg	Val	Lys	Val	Ala	Glu	Lys	Trp	Ala	Asn	Thr	Leu		
180						185						190					
Gly	Asp	Ala	Pro	Met	Ala	Phe	Val	His	Lys	Thr	Arg	Ser	Thr	Glu	Val		
195						200						205					
Ala	Asn	Gln	Val	Val	Ala	Asn	Arg	Val	Val	Gly	Asp	Val	Asp	Gly	Lys		
210						215						220					
Asp	Cys	Val	Leu	Leu	Asp	Asp	Met	Ile	Asp	Thr	Gly	Gly	Thr	Ile	Ala		
225						230						235					
Gly	Ala	Val	Gly	Val	Leu	Lys	Lys	Ala	Gly	Ala	Lys	Ser	Val	Val	Ile		
245						250						255					
Ala	Cys	Thr	His	Gly	Val	Phe	Ser	Asp	Pro	Ala	Arg	Glu	Arg	Leu	Ser		
260						265						270					
Ala	Cys	Gly	Ala	Glu	Glu	Val	Ile	Thr	Thr	Asp	Thr	Leu	Pro	Gln	Ser		
275						280						285					
Thr	Glu	Gly	Trp	Ser	Asn	Leu	Thr	Val	Leu	Ser	Ile	Ala	Pro	Leu	Leu		
290						295						300					
Ala	Arg	Thr	Ile	Asn	Glu	Ile	Phe	Glu	Asn	Gly	Ser	Val	Thr	Thr	Leu		
305						310						315					
Phe						Glu						Ala					
325																	

&lt;210&gt; 897

&lt;211&gt; 1470

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1447)

&lt;223&gt; RXN00558

&lt;400&gt; 897

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 Val Val Lys Lys Pro  
 1 5

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Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile Leu Val Phe Lys Asp	
10 15 20	
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Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro Ile Leu Glu Ser Leu	
25 30 35	
cgc gga aac atc gcc atc gga cac acc cga tac acc acc gcc ggc gga	259
Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr Thr Thr Ala Gly Gly	
40 45 50	
aac acc tgg gaa aat gcc cag cct atg ttc cgc atg gca cca gat ggc	307
Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg Met Ala Pro Asp Gly	
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acc gat atc gcc ctt gga cac aac ggc aac ctg att aat tac atc gag	355
Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu Ile Asn Tyr Ile Glu	
70 75 80 85	
ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc gat ccc gcc aag aag	403
Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val Asp Pro Ala Lys Lys	
90 95 100	
cca tca gat acc gat gtg ctc act gga ctg ctc gca agc ggc gtc cat	451
Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu Ala Ser Gly Val His	
105 110 115	
gac gga aat aat ctc ttt gat tcc gcc aag gaa ctc ctc ccc agc gtc	499
Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu Leu Leu Pro Ser Val	
120 125 130	
aag gga gcc tac tgc ctc acc ttc acc gac gga cac acc ctg tac gca	547
Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly His Thr Leu Tyr Ala	
135 140 145	
gcg cgt gat cca ttc ggc atc cgc cca ctg tcc atc ggc cgc ctc gag	595
Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser Ile Gly Arg Leu Glu	
150 155 160 165	
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Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala Leu Asp Ile Val Gly	
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185 190 195	
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Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu Thr Thr Arg Lys Gly	
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Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro Asp Ser Val Ile Lys	
215 220 225	
gga aga aac gtc aac gaa gcc cga ctt gaa atc ggc cgc aag ctc gct	835
Gly Arg Asn Val Asn Glu Ala Arg Leu Glu Ile Gly Arg Lys Leu Ala	
230 235 240 245	

gca gaa gca cca gca gtc ggc gat cta gtc atc cca acc cca gaa tca 883  
 Ala Glu Ala Pro Ala Val Gly Asp Leu Val Ile Pro Thr Pro Glu Ser  
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ggc acc cca gca gca gtt gga ttc gcc caa gca tct ggc atc cca ttc 931  
 Gly Thr Pro Ala Ala Val Gly Phe Ala Gln Ala Ser Gly Ile Pro Phe  
 265 270 275

ggc caa ggc atg gtc aaa aac gcc tac gtt ggc cga acc ttc atc cag 979  
 Gly Gln Gly Met Val Lys Asn Ala Tyr Val Gly Arg Thr Phe Ile Gln  
 280 285 290

cct tcc gac act ctc cgc caa ctg gga atc cgc ctc aag ctg aac cca  
 1027  
 Pro Ser Asp Thr Leu Arg Gln Leu Gly Ile Arg Leu Lys Leu Asn Pro  
 295 300 305

ttg cgc gag gtt atc gcc gga aag cgc ctt gtg gtt gtg gat gat tcc  
 1075  
 Leu Arg Glu Val Ile Ala Gly Lys Arg Leu Val Val Val Asp Asp Ser  
 310 315 320 325

atc gtc cgc ggt aac acc caa cgc gcc gtg atc cgc atg ttg cgc gaa  
 1123  
 Ile Val Arg Gly Asn Thr Gln Arg Ala Val Ile Arg Met Leu Arg Glu  
 330 335 340

gcc ggt gca gct gag gtt cac gta cgc atc gcc tca cca ccc gtg aaa  
 1171  
 Ala Gly Ala Ala Glu Val His Val Arg Ile Ala Ser Pro Pro Val Lys  
 345 350 355

tgg cca tgc ttc tac ggc atc gat ttt gcc acc cca ggc gaa ctc att  
 1219  
 Trp Pro Cys Phe Tyr Gly Ile Asp Phe Ala Thr Pro Gly Glu Leu Ile  
 360 365 370

gcc aac gct gtc acc agt gac aac gaa gca gaa atg gta gaa gca gtc  
 1267  
 Ala Asn Ala Val Thr Ser Asp Asn Glu Ala Glu Met Val Glu Ala Val  
 375 380 385

cgc tcc gca atc ggc gca gac acc ctc ggc tac gtc tcc atc gac tcc  
 1315  
 Arg Ser Ala Ile Gly Ala Asp Thr Leu Gly Tyr Val Ser Ile Asp Ser  
 390 395 400 405

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 1363  
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 410 415 420

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 1411  
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 425 430 435

gac cta gtc cgc aag atg caa gca acc gcc tca agt taagatcggt  
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 Asp Leu Val Arg Lys Met Gln Ala Thr Ala Ser Ser  
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1470

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<212> PRT
<213> Corynebacterium glutamicum
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Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr
      35      40      45
Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg
      50      55      60
Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu
 65      70      75      80
Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val
      85      90      95
Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu
      100      105      110
Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu
      115      120      125
Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly
 130      135      140
His Thr Leu Tyr Ala Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser
 145      150      155      160
Ile Gly Arg Leu Glu Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala
      165      170      175
Leu Asp Ile Val Gly Ala Ser His Val Arg Glu Val Glu Pro Gly Glu
      180      185      190
Leu Ile Ala Ile Asp Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu
      195      200      205
Thr Thr Arg Lys Gly Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro
 210      215      220
Asp Ser Val Ile Lys Gly Arg Asn Val Asn Glu Ala Arg Leu Glu Ile
 225      230      235      240
Gly Arg Lys Leu Ala Ala Glu Ala Pro Ala Val Gly Asp Leu Val Ile
      245      250      255
Pro Thr Pro Glu Ser Gly Thr Pro Ala Ala Val Gly Phe Ala Gln Ala
      260      265      270

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Ser Gly Ile Pro Phe Gly Gln Gly Met Val Lys Asn Ala Tyr Val Gly  
 275 280 285  
 Arg Thr Phe Ile Gln Pro Ser Asp Thr Leu Arg Gln Leu Gly Ile Arg  
 290 295 300  
 Leu Lys Leu Asn Pro Leu Arg Glu Val Ile Ala Gly Lys Arg Leu Val  
 305 310 315 320  
 Val Val Asp Asp Ser Ile Val Arg Gly Asn Thr Gln Arg Ala Val Ile  
 325 330 335  
 Arg Met Leu Arg Glu Ala Gly Ala Ala Glu Val His Val Arg Ile Ala  
 340 345 350  
 Ser Pro Pro Val Lys Trp Pro Cys Phe Tyr Gly Ile Asp Phe Ala Thr  
 355 360 365  
 Pro Gly Glu Leu Ile Ala Asn Ala Val Thr Ser Asp Asn Glu Ala Glu  
 370 375 380  
 Met Val Glu Ala Val Arg Ser Ala Ile Gly Ala Asp Thr Leu Gly Tyr  
 385 390 395 400  
 Val Ser Ile Asp Ser Met Val Ala Ala Thr Glu Gln Pro Ala Asn Glu  
 405 410 415  
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Ser

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<220>  
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 <223> FRXA00558

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 Val Val Lys Lys Pro Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile 15  
 1 5 10  
 ctg gtt ttc aaa gat ttg ggc cta gtc tcc caa gtt ttc gac caa cca 156  
 Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro 30  
 20 25 30  
 att ctg gaa tcc ctc cgc gga aac atc gcc atc gga cac acc cga tac 204  
 Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr

35	40	45	
acc acc gcc ggc gga aac acc tgg gaa aat gcc cag cct atg ttc cgc			252
Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg			
50	55	60	
atg gca cca gat ggc acc gat atc gcc ctt gga cac aac ggc aac ctg			300
Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu			
65	70	75	80
att aat tac atc gag ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc			348
Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val			
85	90	95	
gat ccc gcc aag aag cca tca gat acc gat gtg ctc act gga ctg ctc			396
Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu			
100	105	110	
gca agc ggc gtc cat gac gga aat aat ctc ttt gat tcc gcc aag gaa			444
Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu			
115	120	125	
ctc ctc ccc agc gtc aag gga gcc tac tgc ctc acc ttc acc gac gga			492
Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly			
130	135	140	
cac acc ctg taagcagcgc gtgatccatt cgg			524
His Thr Leu			
145			
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<212> PRT			
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Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro			
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Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr			
35	40	45	
Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg			
50	55	60	
Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu			
65	70	75	80
Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val			
85	90	95	
Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu			
100	105	110	
Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu			
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His Thr Leu  
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 <223> RXN00626

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 Met Arg Ile Leu Val  
 1 5

atc ggc tcg ggc gcc cgt gag cac gcc ctc ctc cgt gga ctg tca act 163  
 Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu Arg Gly Leu Ser Thr  
 10 15 20

gac cct gca acc act gaa ctc cac gtt gcc cca ggt aac gct ggt ctt 211  
 Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro Gly Asn Ala Gly Leu  
 25 30 35

gga tcg atc gca act gtc cac cct ggc atc aag gct gat gat cca gag 259  
 Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys Ala Asp Asp Pro Glu  
 40 45 50

gct gtc act gcg ttg gct aaa gaa ctg aac tct gat ctg gtt gtt atc 307  
 Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser Asp Leu Val Val Ile  
 55 60 65

ggc cca gag atc cct ttg gtt gcg ggt gtt gct gat gca ctt cgc gcg 355  
 Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala Asp Ala Leu Arg Ala  
 70 75 80 85

gcg ggt atc gct gtg ttt ggt cct aac aag gac gct gct cgt atc gag 403  
 Ala Gly Ile Ala Val Phe Gly Pro Asn Lys Asp Ala Ala Arg Ile Glu  
 90 95 100

ggc tcc aag gct ttc gct aag gat gtc atg gct gcg cag ggt gtt cgt 451  
 Gly Ser Lys Ala Phe Ala Lys Asp Val Met Ala Ala Gln Gly Val Arg  
 105 110 115

act gct cat gct gag act att act cct ggt gcg tct tct gaa gat att 499  
 Thr Ala His Ala Glu Thr Ile Thr Pro Gly Ala Ser Ser Glu Asp Ile  
 120 125 130

gat gct gcc ata gat cgt ttc ggc cca acg tgg gtt gtc aag gat gat 547  
 Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp Val Val Lys Asp Asp  
 135 140 145

ggc ttg tct gcg ggc aag ggt gtt gtg gtt acc ccc gat cgt gca gca 595



1239

cgt gtt ctt aac gtg atc ggt gtg ggt gag acc ctg gag gct gca cgc  
1267

Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu Glu Ala Ala Arg  
375 380 385

gat aac gcg tac acc acc atc aag gac att gaa ctt gag gga agc cac  
1315

Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu Glu Gly Ser His  
390 395 400 405

tac cgc agc gat atc gca ttg gct gca tta gag ggt cgt atc tcg atc  
1363

Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly Arg Ile Ser Ile  
410 415 420

taaaagcagt acgcagatag gct  
1386

<210> 902

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 902

Met Arg Ile Leu Val Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu  
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Arg Gly Leu Ser Thr Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro  
20 25 30

Gly Asn Ala Gly Leu Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys  
35 40 45

Ala Asp Asp Pro Glu Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser  
50 55 60

Asp Leu Val Val Ile Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala  
65 70 75 80

Asp Ala Leu Arg Ala Ala Gly Ile Ala Val Phe Gly Pro Asn Lys Asp  
85 90 95

Ala Ala Arg Ile Glu Gly Ser Lys Ala Phe Ala Lys Asp Val Met Ala  
100 105 110

Ala Gln Gly Val Arg Thr Ala His Ala Glu Thr Ile Thr Pro Gly Ala  
115 120 125

Ser Ser Glu Asp Ile Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp  
130 135 140

Val Val Lys Asp Asp Gly Leu Ser Ala Gly Lys Gly Val Val Val Thr  
145 150 155 160

Pro Asp Arg Ala Ala Ala Arg Ala His Val Asp Ala Val Leu Glu Gly  
165 170 175

Gly Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser  
180 185 190

Leu Phe Cys Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala  
 195 200 205  
 Gln Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly  
 210 215 220  
 Gly Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val  
 225 230 235 240  
 Gln Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val  
 245 250 255  
 Ala Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp  
 260 265 270  
 Gly Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp  
 275 280 285  
 Pro Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val  
 290 295 300  
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 305 310 315 320  
 Glu Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn  
 325 330 335  
 Tyr Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala  
 340 345 350  
 Asp Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu  
 355 360 365  
 Val Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr  
 370 375 380  
 Leu Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu  
 385 390 395 400  
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 405 410 415  
 Gly Arg Ile Ser Ile  
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<210> 903  
 <211> 364  
 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(364)  
 <223> FRXA00629

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 Met Arg Ile Leu Val

									1								5	
atc ggc tcg ggc gcc cgt gag cac gcc ctc ctc cgt gga ctg tca act																		163
Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu Arg Gly Leu Ser Thr																		
	10									15							20	
gac cct gca acc act gaa ctc cac gtt gcc cca ggt aac gct ggt ctt																		211
Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro Gly Asn Ala Gly Leu																		
	25									30							35	
gga tcg atc gca act gtc cac cct ggc atc aag gct gat gat cca gag																		259
Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys Ala Asp Asp Pro Glu																		
	40									45							50	
gct gtc act gcg ttg gct aaa gaa ctg aac tct gat ctg gtt gtt atc																		307
Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser Asp Leu Val Val Ile																		
	55									60							65	
ggc cca gag atc cct ttg gtt gcg ggt gtt gct gat gca ctt cgc gcg																		355
Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala Asp Ala Leu Arg Ala																		
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gcg ggt atc																		364
Ala Gly Ile																		

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<210> 904
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<212> PRT
<213> Corynebacterium glutamicum
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Gly Asn Ala Gly Leu Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys
      35                               40                      45

Ala Asp Asp Pro Glu Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser
      50                               55                      60

Asp Leu Val Val Ile Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala
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Asp Ala Leu Arg Ala Ala Gly Ile
      85

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<212> DNA
<213> Corynebacterium glutamicum
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Asp Arg Ala Ala Ala Arg Ala His Val Asp Ala Val Leu Glu Gly Gly	
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aat cca gtt ttg ctg gag tcc ttc ctt gat ggc cct gag gtt tcc ctg	96
Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser Leu	
20 25 30	
ttc ttc ctg gtt gat ggc gag acg gta gtt cct ctg ctg cca gcg cag	144
Phe Phe Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln	
35 40 45	
gat cac aag cgt gcg tac gac aac gat gag ggc cca aac act ggt ggc	192
Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly	
50 55 60	
atg ggt gct tat gcg ccg ctt cct tgg ctg cct gaa gat ggc gtc cag	240
Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln	
65 70 75 80	
cgc att gtc gat gag gtc tgc gtt cct gtt gct cgt gag atg gtg gca	288
Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala	
85 90 95	
cgt ggt tgc gcg tac tcc ggt ctg ctt tac gca ggt atc gca tgg ggt	336
Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly	
100 105 110	
gca gaa ggc cct gca gta gtg gag ttc aac tgc cgc ttc ggc gat cca	384
Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro	
115 120 125	
gaa acc cag gct gta ctg gca cta ctg aag act cct cta gca gta ctg	432
Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu	
130 135 140	
ctc aac gca gtt gct act gga acc ttg gca gag cag cca gca ctg gag	480
Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu	
145 150 155 160	
tgg gag gat gct tac gcc ctg act gtg gtg ttg gct tct tac aac tac	528
Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr	
165 170 175	
cca gag gca cct cgt act ggt gat gtc atc cgc aac gct gat gca gat	576
Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp	
180 185 190	
aac gtt ctt cac gct ggt acc gca ctc aat gct gaa ggc gag ctg gtc	624
Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu Val	
195 200 205	
tct gcg ggc ggt cgt gtt ctt aac gtg atc ggt gtg ggt gag acc ctg	672
Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu	
210 215 220	
gag gct gca cgc gat aac gcg tac acc acc atc aag gac att gaa ctt	720
Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu	
225 230 235 240	

gag gga agc cac tac cgc agc gat atc gca ttg gct gca tta gag ggt 768  
 Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly  
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 Arg Ile Ser Ile  
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<210> 906

<211> 260

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 906

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                   20                                  25                                  30

Phe Phe Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln  
                   35                                  40                                  45

Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly  
           50                                  55                                  60

Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln  
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Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala  
                   85                                  90                                  95

Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly  
                   100                                  105                                  110

Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro  
           115                                  120                                  125

Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu  
           130                                  135                                  140

Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu  
   145                                  150                                  155                                  160

Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr  
                   165                                  170                                  175

Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp  
                   180                                  185                                  190

Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu Val  
                   195                                  200                                  205

Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu  
           210                                  215                                  220

Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu  
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Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly  
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Arg Ile Ser Ile  
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 Val Asn Ser Asp Ser  
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acg acc acc att gtc gtg cta gct tcc gga aca ggc acc ctc ctt cag 163  
 Thr Thr Thr Ile Val Val Leu Ala Ser Gly Thr Gly Thr Leu Leu Gln  
 10 15 20

tca ctc att gaa gcg caa ggt acc tat tcg atc gtg ggc gtt gtc tct 211  
 Ser Leu Ile Glu Ala Gln Gly Thr Tyr Ser Ile Val Gly Val Val Ser  
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gac gtc gaa tgc cct gca ctt tcc aga gcc gca gat gca ggt att gat 259  
 Asp Val Glu Cys Pro Ala Leu Ser Arg Ala Ala Asp Ala Gly Ile Asp  
 40 45 50

act gca gtt gtt ccg ctt gga aaa gat cgt gca cag tgg aac cac gag 307  
 Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala Gln Trp Asn His Glu  
 55 60 65

ctt gca gac gca gtt gca gta agc gac cca gat ttg gtg gtc tct gcg 355  
 Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp Leu Val Val Ser Ala  
 70 75 80 85

gga ttc atg aaa att ttg ggc gaa ggt ttc ctc tca agg ttc ccg tcc 403  
 Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu Ser Arg Phe Pro Ser  
 90 95 100

cgc atc atc aac acc cac cca gct tta ttg cct tct ttc cct ggt gcc 451  
 Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro Ser Phe Pro Gly Ala  
 105 110 115

cac gcg gtt cgc gat gct ttg gca tac ggt gtg aaa gtg tca ggt tcg 499  
 His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val Lys Val Ser Gly Ser  
 120 125 130

aca gtt cac ctt gtc gat gct ggt gtg gat acc ggc cca att att gct 547  
 Thr Val His Leu Val Asp Ala Gly Val Asp Thr Gly Pro Il Ile Ala  
 135 140 145

caa cga gca gtg ccg gta gaa gtg aat gat gat gaa tcc agc ctg cat 595

Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp Glu Ser Ser Leu His  
 150 155 160 165

gaa aga atc aag cag gtt gag cgt aaa ctc att gta gaa gtc ctg aac 643  
 Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile Val Glu Val Leu Asn  
 170 175 180

agc gtg gaa ttt tcg cgt cag ggt ggc gta caa ctc aac tgg aga ggc 691  
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 <213> Corynebacterium glutamicum

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Val Gly Val Val Ser Asp Val Glu Cys Pro Ala Leu Ser Arg Ala Ala  
 35 40 45

Asp Ala Gly Ile Asp Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala  
 50 55 60

Gln Trp Asn His Glu Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp  
 65 70 75 80

Leu Val Val Ser Ala Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu  
 85 90 95

Ser Arg Phe Pro Ser Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro  
 100 105 110

Ser Phe Pro Gly Ala His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val  
 115 120 125

Lys Val Ser Gly Ser Thr Val His Leu Val Asp Ala Gly Val Asp Thr  
 130 135 140

Gly Pro Ile Ile Ala Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp  
 145 150 155 160

Glu Ser Ser Leu His Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile  
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Val Glu Val Leu Asn Ser Val Glu Phe Ser Arg Gln Gly Gly Val Gln  
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Leu Asn Trp Arg Gly  
 195

<210> 909



<211> 1347  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1324)  
 <223> RXA01442

<400> 909

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tcg atc ggc acc cct ttg acc ccc aat gcc acg aaa gtg atg ctg ctg 163
Ser Ile Gly Thr Pro Leu Thr Pro Asn Ala Thr Lys Val Met Leu Leu
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Gly Ser Gly Glu Leu Gly Lys Glu Val Ala Ile Ala Phe Gln Arg Leu
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ggc ctg gaa gtc cat gca gtt gat cgc tac gaa cat gcc cca gcc cac 259
Gly Leu Glu Val His Ala Val Asp Arg Tyr Glu His Ala Pro Ala His
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cag gtc gct cac ttc tcc tat gtc atc gac atg aca gat gca gcc cag 307
Gln Val Ala His Phe Ser Tyr Val Ile Asp Met Thr Asp Ala Ala Gln
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gtg cgg gaa ttg gtg gag cgt gtg cgc cca gat ttt gtc att cct gaa 355
Val Arg Glu Leu Val Glu Arg Val Arg Pro Asp Phe Val Ile Pro Glu
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Ile Glu Ala Leu Ala Thr Asp Glu Leu Val Lys Ile Glu Glu Glu Gly
                        90                        95                        100

cta gct acc atc gtg ccc act gca cgt gca gcc aag ctg acc atg aac 451
Leu Ala Thr Ile Val Pro Thr Ala Arg Ala Ala Lys Leu Thr Met Asn
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cgc gaa ggc atc cgc aag ctg gcg gca gag gaa ctg ggt ctt cca acc 499
Arg Glu Gly Ile Arg Lys Leu Ala Ala Glu Glu Leu Gly Leu Pro Thr
                        120                        125                        130

tcc aac tat gag ttc tgc tcc act ttc gag gaa ttc tcc gca gct gct 547
Ser Asn Tyr Glu Phe Cys Ser Thr Phe Glu Glu Phe Ser Ala Ala Ala
                        135                        140                        145

gaa aag ctt ggt tac ccc aac gtg gtg aaa cca gtg atg agt tct tcc 595
Glu Lys Leu Gly Tyr Pro Asn Val Val Lys Pro Val Met Ser Ser Ser
                        150                        155                        160                        165

ggc aag ggc caa tct gtt ttg cgt agt tca gac gat ctg cag gca gca 643
Gly Lys Gly Gln Ser Val Leu Arg Ser Ser Asp Asp Leu Gln Ala Ala
                        170                        175                        180

tgg gat tat gcg atg agc ggt gca cgc gtg gcc aac tcc cgc gtc atc 691

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Trp	Asp	Tyr	Ala	Met	Ser	Gly	Ala	Arg	Val	Ala	Asn	Ser	Arg	Val	Ile	
			185					190					195			
gtg	gaa	gct	ttc	gtg	gaa	ttc	gat	tac	gag	atc	acc	ctg	ttg	aca	gta	739
Val	Glu	Ala	Phe	Val	Glu	Phe	Asp	Tyr	Glu	Ile	Thr	Leu	Leu	Thr	Val	
		200					205					210				
agg	tcc	atc	gat	ccc	acc	acc	tct	aag	cct	gcg	acc	tgg	ttc	tgt	gag	787
Arg	Ser	Ile	Asp	Pro	Thr	Thr	Ser	Lys	Pro	Ala	Thr	Trp	Phe	Cys	Glu	
	215					220					225					
ccc	att	ggg	cac	cg	caa	gaa	gac	ggc	gac	tac	gtg	gaa	tcc	tgg	cag	835
Pro	Ile	Gly	His	Arg	Gln	Glu	Asp	Gly	Asp	Tyr	Val	Glu	Ser	Trp	Gln	
230					235					240					245	
cca	atg	gag	atg	act	cct	cg	gcg	ctg	gaa	aac	gca	cg	tca	gta	gcc	883
Pro	Met	Glu	Met	Thr	Pro	Arg	Ala	Leu	Glu	Asn	Ala	Arg	Ser	Val	Ala	
				250					255					260		
gca	cg	atc	acc	aac	gca	ttg	ggc	gga	cg	ggc	gta	ttt	ggt	gtg	gag	931
Ala	Arg	Ile	Thr	Asn	Ala	Leu	Gly	Gly	Arg	Gly	Val	Phe	Gly	Val	Glu	
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ctc	ttt	gtc	tcc	ggc	gat	gac	gtg	tac	ttc	tct	gaa	gtc	tcc	cca	cg	979
Leu	Phe	Val	Ser	Gly	Asp	Asp	Val	Tyr	Phe	Ser	Glu	Val	Ser	Pro	Arg	
		280					285					290				
cca	cac	gac	acc	ggc	ctt	gtc	acc	ctt	gcc	acc	cag	cgt	ttc	tct	gaa	
1027																
Pro	His	Asp	Thr	Gly	Leu	Val	Thr	Leu	Ala	Thr	Gln	Arg	Phe	Ser	Glu	
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Phe	Glu	Leu	His	Ala	Lys	Ala	Ile	Leu	Gly	Leu	Pro	Val	Asp	Val	Thr	
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ctg	att	tct	cca	ggt	gcc	tcc	gct	gtc	atc	tac	ggt	ggc	atc	gaa	tct	
1123																
Leu	Ile	Ser	Pro	Gly	Ala	Ser	Ala	Val	Ile	Tyr	Gly	Gly	Ile	Glu	Ser	
				330					335					340		
gaa	ggc	gtg	agc	tac	acc	ggg	ttg	gct	gaa	gcg	ctg	gca	gtg	gct	gaa	
1171																
Glu	Gly	Val	Ser	Tyr	Thr	Gly	Leu	Ala	Glu	Ala	Leu	Ala	Val	Ala	Glu	
			345					350					355			
act	gat	ctt	cgt	atc	ttt	gcc	aag	cca	gag	gcc	ttc	acc	aag	cgt	cg	
1219																
Thr	Asp	Leu	Arg	Ile	Phe	Ala	Lys	Pro	Glu	Ala	Phe	Thr	Lys	Arg	Arg	
		360					365					370				
atg	ggt	gtt	gca	gtg	tcc	acc	gct	gag	gat	gtg	gct	gca	gcc	agg	gac	
1267																
Met	Gly	Val	Ala	Val	Ser	Thr	Ala	Glu	Asp	Val	Ala	Ala	Ala	Arg	Asp	
		375				380					385					
cg	gcc	act	ttg	gct	gcc	gc	gc	atc	aag	gtt	cat	cca	gga	aat	tcc	
1315																
Arg	Ala	Thr	Leu	Ala	Ala	Ala	Ala	Ile	Lys	Val	His	Pro	Gly	Asn	Ser	
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gca gag gct taacatgctg ggaaagcatc ggg

1347

Ala Glu Ala

<210> 910

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 910

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Lys	Val	Met	Leu	Leu	Gly	Ser	Gly	Glu	Leu	Gly	Lys	Glu	Val	Ala	Ile
			20					25					30		
Ala	Phe	Gln	Arg	Leu	Gly	Leu	Glu	Val	His	Ala	Val	Asp	Arg	Tyr	Glu
		35					40					45			
His	Ala	Pro	Ala	His	Gln	Val	Ala	His	Phe	Ser	Tyr	Val	Ile	Asp	Met
	50					55					60				
Thr	Asp	Ala	Ala	Gln	Val	Arg	Glu	Leu	Val	Glu	Arg	Val	Arg	Pro	Asp
	65				70					75				80	
Phe	Val	Ile	Pro	Glu	Ile	Glu	Ala	Leu	Ala	Thr	Asp	Glu	Leu	Val	Lys
				85				90						95	
Ile	Glu	Glu	Glu	Gly	Leu	Ala	Thr	Ile	Val	Pro	Thr	Ala	Arg	Ala	Ala
				100				105					110		
Lys	Leu	Thr	Met	Asn	Arg	Glu	Gly	Ile	Arg	Lys	Leu	Ala	Ala	Glu	Glu
		115					120					125			
Leu	Gly	Leu	Pro	Thr	Ser	Asn	Tyr	Glu	Phe	Cys	Ser	Thr	Phe	Glu	Glu
	130					135					140				
Phe	Ser	Ala	Ala	Ala	Glu	Lys	Leu	Gly	Tyr	Pro	Asn	Val	Val	Lys	Pro
	145				150					155				160	
Val	Met	Ser	Ser	Ser	Gly	Lys	Gly	Gln	Ser	Val	Leu	Arg	Ser	Ser	Asp
				165				170						175	
Asp	Leu	Gln	Ala	Ala	Trp	Asp	Tyr	Ala	Met	Ser	Gly	Ala	Arg	Val	Ala
			180					185					190		
Asn	Ser	Arg	Val	Ile	Val	Glu	Ala	Phe	Val	Glu	Phe	Asp	Tyr	Glu	Ile
		195					200					205			
Thr	Leu	Leu	Thr	Val	Arg	Ser	Ile	Asp	Pro	Thr	Thr	Ser	Lys	Pro	Ala
	210					215					220				
Thr	Trp	Phe	Cys	Glu	Pro	Ile	Gly	His	Arg	Gln	Glu	Asp	Gly	Asp	Tyr
	225				230					235				240	
Val	Glu	Ser	Trp	Gln	Pro	Met	Glu	Met	Thr	Pro	Arg	Ala	Leu	Glu	Asn
				245					250					255	

Ala Arg Ser Val Ala Ala Arg Ile Thr Asn Ala Leu Gly Gly Arg Gly  
 260 265 270

Val Phe Gly Val Glu Leu Phe Val Ser Gly Asp Asp Val Tyr Phe Ser  
 275 280 285

Glu Val Ser Pro Arg Pro His Asp Thr Gly Leu Val Thr Leu Ala Thr  
 290 295 300

Gln Arg Phe Ser Glu Phe Glu Leu His Ala Lys Ala Ile Leu Gly Leu  
 305 310 315 320

Pro Val Asp Val Thr Leu Ile Ser Pro Gly Ala Ser Ala Val Ile Tyr  
 325 330 335

Gly Gly Ile Glu Ser Glu Gly Val Ser Tyr Thr Gly Leu Ala Glu Ala  
 340 345 350

Leu Ala Val Ala Glu Thr Asp Leu Arg Ile Phe Ala Lys Pro Glu Ala  
 355 360 365

Phe Thr Lys Arg Arg Met Gly Val Ala Val Ser Thr Ala Glu Asp Val  
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Ala Ala Ala Arg Asp Arg Ala Thr Leu Ala Ala Ala Ile Lys Val  
 385 390 395 400

His Pro Gly Asn Ser Ala Glu Ala  
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<210> 911  
 <211> 2409  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(2386)  
 <223> RXN00537

<400> 911  
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 Met Ser Thr Phe Val  
 1 5

aat gac acc gtc gaa gac gca atc aag acc cct gag ctg gat cag cca 163  
 Asn Asp Thr Val Glu Asp Ala Ile Lys Thr Pro Glu Leu Asp Gln Pro  
 10 15 20

ttt gag gct ctt ggt ctg aaa gac gac gag tac gcg cgc atc aag gaa 211  
 Phe Glu Ala Leu Gly Leu Lys Asp Asp Glu Tyr Ala Arg Ile Lys Glu  
 25 30 35

atc ctt ggc cgc cgc cca acc gac gcc gag ctg acc gtt tac tcc gtc 259  
 Ile Leu Gly Arg Arg Pro Thr Asp Ala Glu Leu Thr Val Tyr Ser Val  
 40 45 50

atg tgg tcg gag cac tgc tcc tac aag tcc tcc aag gtt cac ctg cgt 307

Met	Trp	Ser	Glu	His	Cys	Ser	Tyr	Lys	Ser	Ser	Lys	Val	His	Leu	Arg	
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Tyr	Phe	Gly	Glu	Thr	Thr	Thr	Glu	Glu	Met	Ala	Ser	Lys	Ile	Leu	Ala	
70						75				80					85	
ggc	atc	ggc	gag	aac	gct	ggt	gtg	gtc	gac	atc	gga	gac	ggc	aac	gcc	403
Gly	Ile	Gly	Glu	Asn	Ala	Gly	Val	Val	Asp	Ile	Gly	Asp	Gly	Asn	Ala	
				90					95					100		
gtg	acc	ttc	cgc	gtg	gag	tcc	cac	aac	cac	cca	tcc	ttc	gta	gag	cca	451
Val	Thr	Phe	Arg	Val	Glu	Ser	His	Asn	His	Pro	Ser	Phe	Val	Glu	Pro	
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cac	cag	ggc	gct	gcg	acc	ggc	gtc	ggc	ggc	atc	gtc	cgc	gac	att	atg	499
His	Gln	Gly	Ala	Ala	Thr	Gly	Val	Gly	Gly	Ile	Val	Arg	Asp	Ile	Met	
		120					125					130				
gct	atg	ggc	gca	cgc	cca	atc	gct	gtg	atg	gat	cag	ctg	cgt	ttc	ggt	547
Ala	Met	Gly	Ala	Arg	Pro	Ile	Ala	Val	Met	Asp	Gln	Leu	Arg	Phe	Gly	
	135					140					145					
gca	ctg	gac	aac	cca	gac	acc	cag	cgt	gtg	ttt	cct	ggc	gtt	gtt	gac	595
Ala	Leu	Asp	Asn	Pro	Asp	Thr	Gln	Arg	Val	Phe	Pro	Gly	Val	Val	Asp	
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ggc	att	tcc	cat	tac	ggc	aac	tgc	ctc	ggc	ctg	cca	aac	atc	ggt	ggc	643
Gly	Ile	Ser	His	Tyr	Gly	Asn	Cys	Leu	Gly	Leu	Pro	Asn	Ile	Gly	Gly	
				170					175					180		
gaa	acc	gtc	ttc	gac	gat	tcc	tac	gca	ggt	aac	cca	ctg	gtc	aac	gca	691
Glu	Thr	Val	Phe	Asp	Asp	Ser	Tyr	Ala	Gly	Asn	Pro	Leu	Val	Asn	Ala	
			185					190					195			
ctg	tgc	gtg	ggt	acc	ctc	aag	gtg	gaa	gac	ctc	aag	ctt	gca	ttc	gca	739
Leu	Cys	Val	Gly	Thr	Leu	Lys	Val	Glu	Asp	Leu	Lys	Leu	Ala	Phe	Ala	
		200					205					210				
tcc	ggc	acc	ggc	aac	aag	gtg	atc	ctg	ttc	ggt	tcc	cgc	acc	ggc	ctt	787
Ser	Gly	Thr	Gly	Asn	Lys	Val	Ile	Leu	Phe	Gly	Ser	Arg	Thr	Gly	Leu	
	215					220					225					
gat	ggc	atc	ggt	ggc	gtg	tcc	gtc	ctg	ggt	tcc	gca	tcc	ttc	gaa	gaa	835
Asp	Gly	Ile	Gly	Gly	Val	Ser	Val	Leu	Gly	Ser	Ala	Ser	Phe	Glu	Glu	
230					235					240				245		
ggc	gaa	gag	cgc	aag	ctc	cca	gct	ggt	cag	ggt	ggc	gat	cct	ttc	gca	883
Gly	Glu	Glu	Arg	Lys	Leu	Pro	Ala	Val	Gln	Val	Gly	Asp	Pro	Phe	Ala	
				250					255					260		
gag	aag	gta	ctc	atc	gag	tgc	tgc	ctc	gag	ctg	tac	aag	gct	ggc	gtc	931
Glu	Lys	Val	Leu	Ile	Glu	Cys	Cys	Leu	Glu	Leu	Tyr	Lys	Ala	Gly	Val	
			265					270					275			
gtg	gtc	ggt	att	cag	gac	ctc	ggt	ggc	ggc	gga	ctt	gcg	tgt	gca	acc	979
Val	Val	Gly	Ile	Gln	Asp	Leu	Gly	Gly	Gly	Gly	Leu	Ala	Cys	Ala	Thr	
		280					285					290				
tct	gag	ctg	gca	gcc	gca	ggc	gac	ggc	ggc	atg	cgc	gtc	aac	cta	gac	
1027																

Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met Arg Val Asn Leu Asp  
 295 300 305  
 aac gtc cca ctg cgc gca gag aac atg tct gca gct gaa atc ctg gct  
 1075  
 Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala Ala Glu Ile Leu Ala  
 310 315 320 325  
 tcc gag tcc cag gag cgc atg tgt gct gtt gtc acc cct gaa aac gtt  
 1123  
 Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val Thr Pro Glu Asn Val  
 330 335 340  
 gag cgt ttc ctc gag atc tgt gca aag tgg gat gtc acc tgc gca gaa  
 1171  
 Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp Val Thr Cys Ala Glu  
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 atc ggc gaa gtt acc gac gag aag gac cgc tac gtt gtg gtc cac aac  
 1219  
 Ile Gly Glu Val Thr Asp Glu Lys Asp Arg Tyr Val Val Val His Asn  
 360 365 370  
 ggt gaa gtt gtt atc gac gca cct cca tca acc atc gat gaa ggc cct  
 1267  
 Gly Glu Val Val Ile Asp Ala Pro Pro Ser Thr Ile Asp Glu Gly Pro  
 375 380 385  
 gtc tac aac cgc cca gtt gct cgc cct gag aac cag gac gaa ctg cag  
 1315  
 Val Tyr Asn Arg Pro Val Ala Arg Pro Glu Asn Gln Asp Glu Leu Gln  
 390 395 400 405  
 ctc gaa ggc gag atc gct cgc cca gtc gac gtt gaa gag atc aag gct  
 1363  
 Leu Glu Gly Glu Ile Ala Arg Pro Val Asp Val Glu Glu Ile Lys Ala  
 410 415 420  
 gct tgg ctg aag ctt gtc gct tca cca gca ctt gca tcc cgc gcg ttt  
 1411  
 Ala Trp Leu Lys Leu Val Ala Ser Pro Ala Leu Ala Ser Arg Ala Phe  
 425 430 435  
 atc acc gag cag tac gac cgc tac gtc cgc ggc aac acc gtt cag gca  
 1459  
 Ile Thr Glu Gln Tyr Asp Arg Tyr Val Arg Gly Asn Thr Val Gln Ala  
 440 445 450  
 aag aac gcc aat gct ggc gtc ttg cgt atc gac gaa gag acc aac cgt  
 1507  
 Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp Glu Glu Thr Asn Arg  
 455 460 465  
 ggc gtt gcg atc tcc gcc gac gca tcc ggc cgt tac acc aag ctc gag  
 1555  
 Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg Tyr Thr Lys Leu Glu  
 470 475 480 485  
 cca aac act ggc gcg cag ctt gca ctg gct gag gct tac cgc aac gtg  
 1603  
 Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu Ala Tyr Arg Asn Val

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gtc tcc acc ggt gca cgc cca gtg gct gtc acc aac tgc ctg aac ttc 1651					
Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr Asn Cys Leu Asn Phe 505 510 515					
ggt tcc cca gaa aac gct ggt gtt atg tgg cag ttc aag gaa gca gtc 1699					
Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln Phe Lys Glu Ala Val 520 525 530					
cac ggt ctg gca gac gga tcc aag ctt ttg ggc att cca gtg tcc ggc 1747					
His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly Ile Pro Val Ser Gly 535 540 545					
ggt aac gtc tcc ttc tac aac cag act ggt gac gag ccc atc ctg cca 1795					
Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp Glu Pro Ile Leu Pro 550 555 560 565					
acc cca gtc gtg ggt gtt ttg gga gtc ttg gac aac gtc gag cag agc 1843					
Thr Pro Val Val Gly Val Leu Gly Val Leu Asp Asn Val Glu Gln Ser 570 575 580					
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Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp Leu Tyr Leu Leu Gly 585 590 595					
gag acc ttc gat gag ttc ggt ggc tcc atc tgg cag cag gtt tct ggc 1939					
Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp Gln Gln Val Ser Gly 600 605 610					
gct ggc ctc aac ggt ctg cca cca gta gtt gac ctg ctc aac gag cag 1987					
Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp Leu Leu Asn Glu Gln 615 620 625					
cgt ctt gca gac ctg ttc gtc ggt tct gat ctg ttt gct gca tcc cac 2035					
Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu Phe Ala Ala Ser His 630 635 640 645					
gat ctg tct gag ggc ggc ctt ggc cag acc ctc gca gag ctt gcg atc 2083					
Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu Ala Glu Leu Ala Ile 650 655 660					
cac cag aaa aag gga atg gat gtt gat ctc tcc cag atc cac cca tcc 2131					
His Gln Lys Lys Gly Met Asp Val Asp Leu Ser Gln Ile His Pro Ser 665 670 675					
ctg ttc acc tca ctg ttt gct gag tcc gct tcc cgc atc gtg gtt gca 2179					
Leu Phe Thr Ser Leu Phe Ala Glu Ser Ala Ser Arg Ile Val Val Ala 680 685 690					

acc aac cgc ggc gaa gag ttg gaa aag cgc gca gca gag ctg ggt gtt  
2227

Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala Ala Glu Leu Gly Val  
695 700 705

cca gtg ttc aag ctg ggc tgc acc aac gat tca gcc gtc atc gct gtc  
2275

Pro Val Phe Lys Leu Gly Cys Thr Asn Asp Ser Ala Val Ile Ala Val  
710 715 720 725

aag ggc gca gac gtt gag ttc act gtt tcc gtg gag gaa ctc cgc gaa  
2323

Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val Glu Glu Leu Arg Glu  
730 735 740

gca tgg acc aac act ttg cct gag gcc ttc ggt cac gca gtt gga gct  
2371

Ala Trp Thr Asn Thr Leu Pro Glu Ala Phe Gly His Ala Val Gly Ala  
745 750 755

aac gca gta gtt gca taattttctg ctgtgaagcc ggg  
2409

Asn Ala Val Val Ala  
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<210> 912

<211> 762

<212> PRT

<213> Corynebacterium glutamicum

<400> 912

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Glu Leu Asp Gln Pro Phe Glu Ala Leu Gly Leu Lys Asp Asp Glu Tyr  
20 25 30

Ala Arg Ile Lys Glu Ile Leu Gly Arg Arg Pro Thr Asp Ala Glu Leu  
35 40 45

Thr Val Tyr Ser Val Met Trp Ser Glu His Cys Ser Tyr Lys Ser Ser  
50 55 60

Lys Val His Leu Arg Tyr Phe Gly Glu Thr Thr Thr Glu Glu Met Ala  
65 70 75 80

Ser Lys Ile Leu Ala Gly Ile Gly Glu Asn Ala Gly Val Val Asp Ile  
85 90 95

Gly Asp Gly Asn Ala Val Thr Phe Arg Val Glu Ser His Asn His Pro  
100 105 110

Ser Phe Val Glu Pro His Gln Gly Ala Ala Thr Gly Val Gly Gly Ile  
115 120 125

Val Arg Asp Ile Met Ala Met Gly Ala Arg Pro Ile Ala Val Met Asp  
130 135 140

Gln Leu Arg Phe Gly Ala Leu Asp Asn Pro Asp Thr Gln Arg Val Phe



145		150		155		160
Pro Gly Val Val	Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu	165	170	175		
Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn	180	185	190			
Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu	195	200	205			
Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly	210	215	220			
Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser	225	230	235	240		
Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val Gln Val	245	250	255			
Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu	260	265	270			
Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly	275	280	285			
Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met	290	295	300			
Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala	305	310	315	320		
Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val	325	330	335			
Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp	340	345	350			
Val Thr Cys Ala Glu Ile Gly Glu Val Thr Asp Glu Lys Asp Arg Tyr	355	360	365			
Val Val Val His Asn Gly Glu Val Val Ile Asp Ala Pro Pro Ser Thr	370	375	380			
Ile Asp Glu Gly Pro Val Tyr Asn Arg Pro Val Ala Arg Pro Glu Asn	385	390	395	400		
Gln Asp Glu Leu Gln Leu Glu Gly Glu Ile Ala Arg Pro Val Asp Val	405	410	415			
Glu Glu Ile Lys Ala Ala Trp Leu Lys Leu Val Ala Ser Pro Ala Leu	420	425	430			
Ala Ser Arg Ala Phe Ile Thr Glu Gln Tyr Asp Arg Tyr Val Arg Gly	435	440	445			
Asn Thr Val Gln Ala Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp	450	455	460			
Glu Glu Thr Asn Arg Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg	465	470	475	480		

Tyr Thr Lys Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu  
 485 490 495  
 Ala Tyr Arg Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr  
 500 505 510  
 Asn Cys Leu Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln  
 515 520 525  
 Phe Lys Glu Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly  
 530 535 540  
 Ile Pro Val Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp  
 545 550 555 560  
 Glu Pro Ile Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp  
 565 570 575  
 Asn Val Glu Gln Ser Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp  
 580 585 590  
 Leu Tyr Leu Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp  
 595 600 605  
 Gln Gln Val Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp  
 610 615 620  
 Leu Leu Asn Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu  
 625 630 635 640  
 Phe Ala Ala Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu  
 645 650 655  
 Ala Glu Leu Ala Ile His Gln Lys Lys Gly Met Asp Val Asp Leu Ser  
 660 665 670  
 Gln Ile His Pro Ser Leu Phe Thr Ser Leu Phe Ala Glu Ser Ala Ser  
 675 680 685  
 Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala  
 690 695 700  
 Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr Asn Asp Ser  
 705 710 715 720  
 Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val  
 725 730 735  
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&lt;211&gt; 638

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (54) .. (638)

&lt;223&gt; FRXA02805

&lt;400&gt; 913

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 Val Phe  
 1

cct ggc gtt gtt gac ggc att tcc cat tac ggc aac tgc ctc ggc ctg 107  
 Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu  
 5 10 15

cca aac atc ggt ggc gaa acc gtc ttc gac gat tcc tac gca ggt aac 155  
 Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn  
 20 25 30

cca ctg gtc aac gca ctg tgc gtg ggt acc ctc aag gtg gaa gac ctc 203  
 Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu  
 35 40 45 50

aag ctt gca ttc gca tcc ggc acc ggc aac aag gtg atc ctg ttc ggt 251  
 Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly  
 55 60 65

tcc cgc acc ggc ctt gat ggc atc ggt ggc gtg tcc gtc ctg ggt tcc 299  
 Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser  
 70 75 80

gca tcc ttc gaa gaa ggc gaa gag cgc aag ctc cca gct gtt cag gtt 347  
 Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val Gln Val  
 85 90 95

ggc gat cct ttc gca gag aag gta ctc atc gag tgc tgc ctc gag ctg 395  
 Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu  
 100 105 110

tac aag gct ggc gtc gtg gtc ggt att cag gac ctc ggt ggc ggc gga 443  
 Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly  
 115 120 125 130

ctt gcg tgt gca acc tct gag ctg gca gcc gca ggc gac ggc ggc atg 491  
 Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met  
 135 140 145

cgc gtc aac cta gac aac gtc cca ctg cgc gca gag aac atg tct gca 539  
 Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala  
 150 155 160

gct gaa atc ctg gct tcc gag tcc cag gag cgc atg tgt gct gtt gtc 587  
 Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val  
 165 170 175

acc cct gaa aac gtt gag cgt ttc ctc gag atc tgt gca aag tgg gat 635  
 Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp  
 180 185 190

gtc 638  
 Val  
 195

<210> 914  
 <211> 195  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 914

Val	Phe	Pro	Gly	Val	Val	Asp	Gly	Ile	Ser	His	Tyr	Gly	Asn	Cys	Leu
1				5					10					15	
Gly	Leu	Pro	Asn	Ile	Gly	Gly	Glu	Thr	Val	Phe	Asp	Asp	Ser	Tyr	Ala
			20					25					30		
Gly	Asn	Pro	Leu	Val	Asn	Ala	Leu	Cys	Val	Gly	Thr	Leu	Lys	Val	Glu
		35					40					45			
Asp	Leu	Lys	Leu	Ala	Phe	Ala	Ser	Gly	Thr	Gly	Asn	Lys	Val	Ile	Leu
	50					55					60				
Phe	Gly	Ser	Arg	Thr	Gly	Leu	Asp	Gly	Ile	Gly	Gly	Val	Ser	Val	Leu
65					70					75					80
Gly	Ser	Ala	Ser	Phe	Glu	Glu	Gly	Glu	Glu	Arg	Lys	Leu	Pro	Ala	Val
				85					90					95	
Gln	Val	Gly	Asp	Pro	Phe	Ala	Glu	Lys	Val	Leu	Ile	Glu	Cys	Cys	Leu
			100					105					110		
Glu	Leu	Tyr	Lys	Ala	Gly	Val	Val	Val	Gly	Ile	Gln	Asp	Leu	Gly	Gly
		115					120					125			
Gly	Gly	Leu	Ala	Cys	Ala	Thr	Ser	Glu	Leu	Ala	Ala	Ala	Gly	Asp	Gly
	130					135						140			
Gly	Met	Arg	Val	Asn	Leu	Asp	Asn	Val	Pro	Leu	Arg	Ala	Glu	Asn	Met
145					150					155					160
Ser	Ala	Ala	Glu	Ile	Leu	Ala	Ser	Glu	Ser	Gln	Glu	Arg	Met	Cys	Ala
				165					170					175	
Val	Val	Thr	Pro	Glu	Asn	Val	Glu	Arg	Phe	Leu	Glu	Ile	Cys	Ala	Lys
			180					185					190		
Trp	Asp	Val													
		195													

<210> 915  
 <211> 697  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (23)..(697)

<223> FRXA00537

<400> 915

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	Val	Tyr	His	Arg	Ala	Val	Leu	Asn	Ala	Thr		

															1		5		10	
tcc	gcg	gca	aca	ccg	ttc	aag	caa	aag	aac	gcc	aat	gct	ggc	gtc	ttg	100				
Ser	Ala	Ala	Thr	Pro	Phe	Lys	Gln	Lys	Asn	Ala	Asn	Ala	Gly	Val	Leu					
				15			20			25										
cgt	atc	gac	gaa	gag	acc	anc	cgt	ggc	gtt	gcg	atc	tcc	gcc	gac	gca	148				
Arg	Ile	Asp	Glu	Glu	Thr	Xaa	Arg	Gly	Val	Ala	Ile	Ser	Ala	Asp	Ala					
				30			35			40										
tcc	ggc	cgt	tac	acc	aag	ctc	gag	cca	aac	act	ggc	gcg	cag	ctt	gca	196				
Ser	Gly	Arg	Tyr	Thr	Lys	Leu	Glu	Pro	Asn	Thr	Gly	Ala	Gln	Leu	Ala					
				45			50			55										
ctg	gct	gag	gct	tac	cgc	aac	gtg	gtc	tcc	acc	ggc	gca	cgc	cca	gtg	244				
Leu	Ala	Glu	Ala	Tyr	Arg	Asn	Val	Val	Ser	Thr	Gly	Ala	Arg	Pro	Val					
				60			65			70										
gct	gtc	acc	aac	tgc	ctg	aac	ttc	ggc	tcc	cca	gaa	aac	gct	ggc	gtt	292				
Ala	Val	Thr	Asn	Cys	Leu	Asn	Phe	Gly	Ser	Pro	Glu	Asn	Ala	Gly	Val					
				75			80			85			90							
atg	tgg	cag	ttc	aag	gaa	gca	gtc	cac	ggc	ctg	gca	gac	gga	tcc	aag	340				
Met	Trp	Gln	Phe	Lys	Glu	Ala	Val	His	Gly	Leu	Ala	Asp	Gly	Ser	Lys					
				95			100			105										
ctt	ttg	ggc	att	cca	gtg	tcc	ggc	ggc	aac	gtc	tcc	ttc	tac	aac	cag	388				
Leu	Leu	Gly	Ile	Pro	Val	Ser	Gly	Gly	Asn	Val	Ser	Phe	Tyr	Asn	Gln					
				110			115			120										
act	ggc	gac	gag	ccc	atc	ctg	cca	acc	cca	gtc	gtg	ggc	gtt	ttg	gga	436				
Thr	Gly	Asp	Glu	Pro	Ile	Leu	Pro	Thr	Pro	Val	Val	Gly	Val	Leu	Gly					
				125			130			135										
gtc	ttg	gac	aac	gtc	gag	cag	agc	atc	ggc	aac	gtc	ctc	cca	tcc	gag	484				
Val	Leu	Asp	Asn	Val	Glu	Gln	Ser	Ile	Gly	Asn	Val	Leu	Pro	Ser	Glu					
				140			145			150										
gac	aac	gat	ctc	tac	ctc	ctg	ggc	gag	acc	ttc	gat	gag	ttc	ggc	ggc	532				
Asp	Asn	Asp	Leu	Tyr	Leu	Leu	Gly	Glu	Thr	Phe	Asp	Glu	Phe	Gly	Gly					
				155			160			165			170							
tcc	atc	tgg	cag	cag	gtt	tct	ggc	gct	ggc	ctc	aac	ggc	ctg	cca	cca	580				
Ser	Ile	Trp	Gln	Gln	Val	Ser	Gly	Ala	Gly	Leu	Asn	Gly	Leu	Pro	Pro					
				175			180			185										
gta	gtt	gac	ctg	ctc	aac	gag	cag	cgt	ctt	gca	gac	ctg	ttc	gtc	ggc	628				
Val	Val	Asp	Leu	Leu	Asn	Glu	Gln	Arg	Leu	Ala	Asp	Leu	Phe	Val	Gly					
				190			195			200										
tct	gat	ctg	ttt	gct	gca	tcc	cac	gat	ctg	tct	gag	ggc	ggc	ctt	ggc	676				
Ser	Asp	Leu	Phe	Ala	Ala	Ser	His	Asp	Leu	Ser	Glu	Gly	Gly	Leu	Gly					
				205			210			215										
cag	acc	ctc	gca	gag	ctt	gcg										697				
Gln	Thr	Leu	Ala	Glu	Leu	Ala														
				220			225													

&lt;210&gt; 916

&lt;211&gt; 225

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 916

Val Tyr His Arg Ala Val Leu Asn Ala Thr Ser Ala Ala Thr Pro Phe  
 1 5 10 15

Lys Gln Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp Glu Glu Thr  
 20 25 30

Xaa Arg Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg Tyr Thr Lys  
 35 40 45

Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu Ala Tyr Arg  
 50 55 60

Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr Asn Cys Leu  
 65 70 75 80

Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln Phe Lys Glu  
 85 90 95

Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly Ile Pro Val  
 100 105 110

Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp Glu Pro Ile  
 115 120 125

Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp Asn Val Glu  
 130 135 140

Gln Ser Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp Leu Tyr Leu  
 145 150 155 160

Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp Gln Gln Val  
 165 170 175

Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp Leu Leu Asn  
 180 185 190

Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu Phe Ala Ala  
 195 200 205

Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu Ala Glu Leu  
 210 215 220

Ala

225

&lt;210&gt; 917

&lt;211&gt; 302

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (279)

&lt;223&gt; FRXA00561

&lt;400&gt; 917

ctc ttc cca gat cca ccc atc cct gtt cac ctc act tgt ttg ctg agt 48  
 Leu Phe Pro Asp Pro Pro Ile Pro Val His Leu Thr Cys Leu Leu Ser  
 1 5 10 15

ccc gct tcc cgc atc gtg gtt gca acc aac cgc ggc gaa gag ttg gaa 96  
 Pro Ala Ser Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu  
 20 25 30

aag cgc gca gca gag ctg ggt gtt cca gtg ttc aag ctg ggc tgc acc 144  
 Lys Arg Ala Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr  
 35 40 45

aac gat tca gcc gtc atc gct gtc aag ggc gca gac gtt gag ttc act 192  
 Asn Asp Ser Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr  
 50 55 60

gtt tcc gtg gag gaa ctc cgc gaa gca tgg acc aac act ttg cct gag 240  
 Val Ser Val Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu  
 65 70 75 80

gcc ttc ggt cac gca gtt gga gct aac gca gta gtt gca taattttctg 289  
 Ala Phe Gly His Ala Val Gly Ala Asn Ala Val Val Ala  
 85 90

ctgtgaagcc ggg 302

<210> 918  
 <211> 93  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 918  
 Leu Phe Pro Asp Pro Pro Ile Pro Val His Leu Thr Cys Leu Leu Ser  
 1 5 10 15

Pro Ala Ser Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu  
 20 25 30

Lys Arg Ala Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr  
 35 40 45

Asn Asp Ser Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr  
 50 55 60

Val Ser Val Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu  
 65 70 75 80

Ala Phe Gly His Ala Val Gly Ala Asn Ala Val Val Ala  
 85 90

<210> 919  
 <211> 792  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(769)  
 <223> RXA00541

&lt;400&gt; 919

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tcatcgaaga cttcgatgtg gtgggagttg aggtcgcgaa gtg agc gcc aaa atc 115  
 Val Ser Ala Lys Ile  
 1 5

ggg gtc att acc ttc cca ggc acc ctt gac gat gta gat gca gca cgc 163  
 Gly Val Ile Thr Phe Pro Gly Thr Leu Asp Asp Val Asp Ala Ala Arg  
 10 15 20

gct gct cgc atc gca ggt gca gaa gta atc agc ctg tgg cac gct gac 211  
 Ala Ala Arg Ile Ala Gly Ala Glu Val Ile Ser Leu Trp His Ala Asp  
 25 30 35

gag gat ctc aag ggc gtc gac gca gtt gtc gtt ccc ggt gga ttc tcc 259  
 Glu Asp Leu Lys Gly Val Asp Ala Val Val Val Pro Gly Gly Phe Ser  
 40 45 50

tac ggc gat tac ctg cgc acc ggt gca atc tct gca ctg gcg cca gta 307  
 Tyr Gly Asp Tyr Leu Arg Thr Gly Ala Ile Ser Ala Leu Ala Pro Val  
 55 60 65

atg cag tcc gtg att gag cag gcc ggt aag ggt atg cca gtc ttg ggc 355  
 Met Gln Ser Val Ile Glu Gln Ala Gly Lys Gly Met Pro Val Leu Gly  
 70 75 80 85

att tgc aac ggc ttc cag atc ctc acc gaa gca cgc ctg ctt cca ggc 403  
 Ile Cys Asn Gly Phe Gln Ile Leu Thr Glu Ala Arg Leu Leu Pro Gly  
 90 95 100

gcg ctg acc cgc aac aag ggt ctg cac ttt cac tgt gta gac gca cac 451  
 Ala Leu Thr Arg Asn Lys Gly Leu His Phe His Cys Val Asp Ala His  
 105 110 115

ctc gtt gta gag aac aac acc act gca tgg acc aac act ttg gaa aag 499  
 Leu Val Val Glu Asn Asn Thr Thr Ala Trp Thr Asn Thr Leu Glu Lys  
 120 125 130

ggg cag cag atc ctt att cct gca aag cac ggt gaa ggt cgc ttc cag 547  
 Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly Glu Gly Arg Phe Gln  
 135 140 145

gca gac gca gag acc atc gcc cag ctt gag ggt gaa ggc cgc gtg gtg 595  
 Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly Glu Gly Arg Val Val  
 150 155 160 165

ttc cgt tac acc gat aac ttc aac ggt tcc gtc aac gat atc gcc ggt 643  
 Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val Asn Asp Ile Ala Gly  
 170 175 180

atc act aat gaa act ggt cgc atc gtc ggt ctc atg ccg cac ccg gaa 691  
 Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu Met Pro His Pro Glu  
 185 190 195

cat gcc gtc gaa aag cta acc ggc cca tct att gat ggc ctg gag ctg 739  
 His Ala Val Glu Lys Leu Thr Gly Pro Ser Ile Asp Gly Leu Glu Leu  
 200 205 210

ttc ctg tcc gcc gtt ggc acc atc gcg gct taagaggagt aaatatgagc 789



Phe Leu Ser Ala Val Gly Thr Ile Ala Ala  
215 220

act

792

&lt;210&gt; 920

&lt;211&gt; 223

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 920

Val Ser Ala Lys Ile Gly Val Ile Thr Phe Pro Gly Thr Leu Asp Asp  
1 5 10 15

Val Asp Ala Ala Arg Ala Ala Arg Ile Ala Gly Ala Glu Val Ile Ser  
20 25 30

Leu Trp His Ala Asp Glu Asp Leu Lys Gly Val Asp Ala Val Val Val  
35 40 45

Pro Gly Gly Phe Ser Tyr Gly Asp Tyr Leu Arg Thr Gly Ala Ile Ser  
50 55 60

Ala Leu Ala Pro Val Met Gln Ser Val Ile Glu Gln Ala Gly Lys Gly  
65 70 75 80

Met Pro Val Leu Gly Ile Cys Asn Gly Phe Gln Ile Leu Thr Glu Ala  
85 90 95

Arg Leu Leu Pro Gly Ala Leu Thr Arg Asn Lys Gly Leu His Phe His  
100 105 110

Cys Val Asp Ala His Leu Val Val Glu Asn Asn Thr Thr Ala Trp Thr  
115 120 125

Asn Thr Leu Glu Lys Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly  
130 135 140

Glu Gly Arg Phe Gln Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly  
145 150 155 160

Glu Gly Arg Val Val Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val  
165 170 175

Asn Asp Ile Ala Gly Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu  
180 185 190

Met Pro His Pro Glu His Ala Val Glu Lys Leu Thr Gly Pro Ser Ile  
195 200 205

Asp Gly Leu Glu Leu Phe Leu Ser Ala Val Gly Thr Ile Ala Ala  
210 215 220

&lt;210&gt; 921

&lt;211&gt; 1014

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(991)

&lt;223&gt; RXA00620

&lt;400&gt; 921

ggtgatccat gtcaggaagc cagcgggtgaa accggcagtg aaaccagcgg tgaatgctaa 60

aattttccga acacacccga ggggtctaga cttgcctaac atg cgt cct gaa ctc 115  
 Met Arg Pro Glu Leu  
 1 5

tcc cag tac aag cac ctg tcg gca ggc aag gtc cgt gag atc tac gag 163  
 Ser Gln Tyr Lys His Leu Ser Ala Gly Lys Val Arg Glu Ile Tyr Glu  
 10 15 20

atc gac gac aag cac atc ctc atg gtg gct tcc gat cgt atc tct gca 211  
 Ile Asp Asp Lys His Ile Leu Met Val Ala Ser Asp Arg Ile Ser Ala  
 25 30 35

tac gat ttc atc ctc gat acc gaa att cca gac aag ggt cga gtg ctc 259  
 Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp Lys Gly Arg Val Leu  
 40 45 50

act gcg atg agc cag ttc ttc ttc gac acc atc gat ttt cct aat cac 307  
 Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile Asp Phe Pro Asn His  
 55 60 65

ctt gca ggt ccc gct gat gat cca cgt atc cca gaa gaa gtt ttg gga 355  
 Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro Glu Glu Val Leu Gly  
 70 75 80 85

cga gca atg gtg tgc aag aag ctc aac atg ctt cct ttt gaa tgc gtg 403  
 Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu Pro Phe Glu Cys Val  
 90 95 100

gtt cgt gga tac ctc act ggc tct gga ctt gtt gaa tac aag cag acc 451  
 Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val Glu Tyr Lys Gln Thr  
 105 110 115

agc tcc gtg tgt gga gtt gag ctc cca gaa ggc ctc gtt gaa tct tct 499  
 Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly Leu Val Glu Ser Ser  
 120 125 130

cag ctg cct gag cca atc ttt acc cca gcc acc aag gct gac atc ggc 547  
 Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr Lys Ala Asp Ile Gly  
 135 140 145

gac cac gac atc aat gtc tcc ttt gac gtt gtt gaa gaa cgt ctc ggc 595  
 Asp His Asp Ile Asn Val Ser Phe Asp Val Val Glu Glu Arg Leu Gly  
 150 155 160 165

gaa gct cgt gcg aac cag ttg cgc gat gcc tct att gct att tac aag 643  
 Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser Ile Ala Ile Tyr Lys  
 170 175 180

gct gct gct gag atc gcc cgt gac cgt ggc gtc atc ctt gcc gac acc 691  
 Ala Ala Ala Glu Ile Ala Arg Asp Arg Gly Val Ile Leu Ala Asp Thr  
 185 190 195

aaa ttt gag ttc ggc atc gat gaa gat ggc acc ctc gtg ctt ggt gat 739  
 Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr Leu Val Leu Gly Asp

200	205	210	
gaa gtc ctt acc cca gat tcc tcc cgc tac tgg cct ttg gaa ggc tat			787
Glu Val Leu Thr Pro Asp Ser Ser Arg Tyr Trp Pro Leu Glu Gly Tyr			
215	220	225	
gaa gca gga tct gtg caa cca agc ttt gat aag caa ttc gtg cgc aac			835
Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys Gln Phe Val Arg Asn			
230	235	240	245
tgg ctc acc ggc cct aaa tct ggc tgg gac aag gat tcc ggc ttg gag			883
Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys Asp Ser Gly Leu Glu			
	250	255	260
cca cca gct ctg cca ggt tcc gtt gtt gag gca acc cgc gag cgc tac			931
Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala Thr Arg Glu Arg Tyr			
	265	270	275
atc gag gcc tac gag ctg att tct ggt cag aag ttc tgc cag tgg att			979
Ile Glu Ala Tyr Glu Leu Ile Ser Gly Gln Lys Phe Cys Gln Trp Ile			
	280	285	290
ggt tct tgc gtc taagctgctt gattttccct aaa			
1014			
Gly Ser Cys Val			
295			

&lt;210&gt; 922

&lt;211&gt; 297

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 922

Met Arg Pro Glu Leu Ser Gln Tyr Lys His Leu Ser Ala Gly Lys Val			
1	5	10	15
Arg Glu Ile Tyr Glu Ile Asp Asp Lys His Ile Leu Met Val Ala Ser			
	20	25	30
Asp Arg Ile Ser Ala Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp			
	35	40	45
Lys Gly Arg Val Leu Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile			
	50	55	60
Asp Phe Pro Asn His Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro			
	65	70	75
Glu Glu Val Leu Gly Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu			
	85	90	95
Pro Phe Glu Cys Val Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val			
	100	105	110
Glu Tyr Lys Gln Thr Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly			
	115	120	125
Leu Val Glu Ser Ser Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr			
	130	135	140

Lys Ala Asp Ile Gly Asp His Asp Ile Asn Val Ser Phe Asp Val Val  
145 150 155 160

Glu Glu Arg Leu Gly Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser  
165 170 175

Ile Ala Ile Tyr Lys Ala Ala Ala Glu Ile Ala Arg Asp Arg Gly Val  
180 185 190

Ile Leu Ala Asp Thr Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr  
195 200 205

Leu Val Leu Gly Asp Glu Val Leu Thr Pro Asp Ser Ser Arg Tyr Trp  
210 215 220

Pro Leu Glu Gly Tyr Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys  
225 230 235 240

Gln Phe Val Arg Asn Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys  
245 250 255

Asp Ser Gly Leu Glu Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala  
260 265 270

Thr Arg Glu Arg Tyr Ile Glu Ala Tyr Glu Leu Ile Ser Gly Gln Lys  
275 280 285

Phe Cys Gln Trp Ile Gly Ser Cys Val  
290 295

<210> 923

<211> 1293

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1270)

<223> RXN00770

<400> 923

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cctcaagtta agatcggttag gcgatagggg ttgagcattt ttg ctc tcc ccg tat 115  
Leu Leu Ser Pro Tyr  
1 5

gcg tgg ggg ttg tcc cgc gca ctt tta gac agt tat gtt cct aat aag 163  
Ala Trp Gly Leu Ser Arg Ala Leu Leu Asp Ser Tyr Val Pro Asn Lys  
10 15 20

ttc caa acc cca gca gga gaa gcg aag tac acg atg agt gat cac cag 211  
Phe Gln Thr Pro Ala Gly Glu Ala Lys Tyr Thr Met Ser Asp His Gln  
25 30 35

gac acc acc gcc gaa ggc gtt tca tac gca gca gca gga gtc gac atc 259  
Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala Ala Gly Val Asp Ile  
40 45 50

gaa gcc ggc gat cgt gcc gtc gaa ctc ttt gca cca atg gcc aag cgc 307

Glu	Ala	Gly	Asp	Arg	Ala	Val	Glu	Leu	Phe	Ala	Pro	Met	Ala	Lys	Arg		
55						60					65						
gcc	acc	cgc	cca	gag	gtt	ctt	ggc	aac	ctc	gga	ggc	ttc	gca	gga	ctc	355	
Ala	Thr	Arg	Pro	Glu	Val	Leu	Gly	Asn	Leu	Gly	Gly	Phe	Ala	Gly	Leu	85	
70					75					80							
ttt	gag	ctc	gga	aaa	tac	aag	aag	cca	atc	ctc	gca	gca	gga	tct	gac	403	
Phe	Glu	Leu	Gly	Lys	Tyr	Lys	Lys	Pro	Ile	Leu	Ala	Ala	Gly	Ser	Asp	100	
				90					95								
gga	gtc	ggc	acc	aag	ctt	gtc	atc	gcc	cag	atg	atg	gac	aag	cac	gac	451	
Gly	Val	Gly	Thr	Lys	Leu	Val	Ile	Ala	Gln	Met	Met	Asp	Lys	His	Asp	115	
			105					110									
acc	atc	ggc	atc	gac	ctt	gtt	gca	atg	tgt	gtg	gat	gac	ctc	gtt	gtc	499	
Thr	Ile	Gly	Ile	Asp	Leu	Val	Ala	Met	Cys	Val	Asp	Asp	Leu	Val	Val		
		120					125					130					
acc	ggc	gca	gag	cca	ctg	ttc	ctc	cag	gac	tac	atc	gcc	atc	ggc	aag	547	
Thr	Gly	Ala	Glu	Pro	Leu	Phe	Leu	Gln	Asp	Tyr	Ile	Ala	Ile	Gly	Lys		
	135					140					145						
gtt	gtc	cca	gag	cac	gtt	gct	gag	atc	gtc	tcc	ggc	atc	gca	gaa	ggc	595	
Val	Val	Pro	Glu	His	Val	Ala	Glu	Ile	Val	Ser	Gly	Ile	Ala	Glu	Gly	165	
150					155					160							
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Cys	Val	Gln	Ala	Gly	Cys	Ala	Leu	Leu	Gly	Gly	Glu	Thr	Ala	Glu	His	180	
				170					175								
cca	ggt	gtt	atg	gaa	cca	gac	cac	tac	gat	gtc	tcc	gca	act	gca	gtc	691	
Pro	Gly	Val	Met	Glu	Pro	Asp	His	Tyr	Asp	Val	Ser	Ala	Thr	Ala	Val		
			185					190					195				
ggc	gtt	gtc	gaa	gca	gat	gaa	ctg	cta	gga	cca	gac	cgc	gtc	cgc	gca	739	
Gly	Val	Val	Glu	Ala	Asp	Glu	Leu	Leu	Gly	Pro	Asp	Arg	Val	Arg	Ala		
		200					205					210					
ggc	gac	gtc	ctc	atc	ggc	atg	gct	tcc	tcc	ggc	ctg	cac	tcc	aac	ggc	787	
Gly	Asp	Val	Leu	Ile	Gly	Met	Ala	Ser	Ser	Gly	Leu	His	Ser	Asn	Gly		
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tac	tcc	ctg	gct	cgc	cac	gtc	ctc	ctg	gaa	aag	gca	ggc	ctg	gcg	ctt	835	
Tyr	Ser	Leu	Ala	Arg	His	Val	Leu	Leu	Glu	Lys	Ala	Gly	Leu	Ala	Leu	245	
230					235					240							
gac	gga	cac	atc	gaa	gaa	ctc	gga	cgc	acc	ctc	ggc	gaa	gaa	ctt	ctc	883	
Asp	Gly	His	Ile	Glu	Glu	Leu	Gly	Arg	Thr	Leu	Gly	Glu	Glu	Leu	Leu		
				250					255					260			
gag	cca	acc	cgc	atc	tac	gcc	aag	gac	tgc	ctg	gca	ctg	atc	gca	gag	931	
Glu	Pro	Thr	Arg	Ile	Tyr	Ala	Lys	Asp	Cys	Leu	Ala	Leu	Ile	Ala	Glu		
			265				270						275				
tgc	gaa	gtt	cac	acc	ttc	tgc	cac	gtc	acc	ggc	ggc	ggc	ctc	gca	ggc	979	
Cys	Glu	Val	His	Thr	Phe	Cys	His	Val	Thr	Gly	Gly	Gly	Leu	Ala	Gly		
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1027																	

Asn Leu Glu Arg Val Val Pro Glu Gly Leu Val Ala Glu Met Ser Arg  
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gca act tgg acc cca ggc caa atc ttc cgc acc atc tcc tct gtg ggc  
 1075

Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr Ile Ser Ser Val Gly  
 310 315 320 325

aag gtt tcc cgc gaa gaa atg gaa aag acc ttc aac atg ggt gtc ggc  
 1123

Lys Val Ser Arg Glu Glu Met Glu Lys Thr Phe Asn Met Gly Val Gly  
 330 335 340

atg gtt gca gtc gtt gct gaa aag gac cgc gac cgc gcc ctg gca atg  
 1171

Met Val Ala Val Val Ala Glu Lys Asp Arg Asp Arg Ala Leu Ala Met  
 345 350 355

ctc acc gca cgt cac att gac tgc tgg gaa atc gga acc gta cgc aac  
 1219

Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile Gly Thr Val Arg Asn  
 360 365 370

ggt gaa gag gga gag cct cgc gtg atc ctc aac ggc gag cac cct ggc  
 1267

Gly Glu Glu Gly Glu Pro Arg Val Ile Leu Asn Gly Glu His Pro Gly  
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 1293

Tyr  
 390

<210> 924

<211> 390

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 924

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Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala  
 35 40 45

Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala  
 50 55 60

Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly  
 65 70 75 80

Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu  
 85 90 95

Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met  
 100 105 110

Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val  
 115 120 125  
 Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr  
 130 135 140  
 Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser  
 145 150 155 160  
 Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly  
 165 170 175  
 Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val  
 180 185 190  
 Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro  
 195 200 205  
 Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly  
 210 215 220  
 Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys  
 225 230 235 240  
 Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu Gly Arg Thr Leu  
 245 250 255  
 Gly Glu Glu Leu Leu Glu Pro Thr Arg Ile Tyr Ala Lys Asp Cys Leu  
 260 265 270  
 Ala Leu Ile Ala Glu Cys Glu Val His Thr Phe Cys His Val Thr Gly  
 275 280 285  
 Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu Gly Leu Val  
 290 295 300  
 Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr  
 305 310 315 320  
 Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu Lys Thr Phe  
 325 330 335  
 Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys Asp Arg Asp  
 340 345 350  
 Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile  
 355 360 365  
 Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val Ile Leu Asn  
 370 375 380  
 Gly Glu His Pro Gly Tyr  
 385 390

&lt;210&gt; 925

&lt;211&gt; 818

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (15) .. (818)

&lt;223&gt; FRXA00557

&lt;400&gt; 925

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Leu Leu Ser Pro Tyr Ala Trp Gly Leu Ser Arg Ala	
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ctt tta gac agt tat gtt cct aat aag ttc caa acc cca gca gga gaa	98
Leu Leu Asp Ser Tyr Val Pro Asn Lys Phe Gln Thr Pro Ala Gly Glu	
15 20 25	
gcg aag tac acg atg agt gat cac cag gac acc acc gcc gaa ggc gtt	146
Ala Lys Tyr Thr Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val	
30 35 40	
tca tac gca gca gca gga gtc gac atc gaa gcc ggc gat cgt gcc gtc	194
Ser Tyr Ala Ala Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val	
45 50 55 60	
gaa ctc ttt gca cca atg gcc aag cgc gcc acc cgc cca gag gtt ctt	242
Glu Leu Phe Ala Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu	
65 70 75	
ggc aac ctc gga ggc ttc gca gga ctc ttt gag ctc gga aaa tac aag	290
Gly Asn Leu Gly Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys	
80 85 90	
aag cca atc ctc gca gca gga tct gac gga gtc ggc acc aag ctt gtc	338
Lys Pro Ile Leu Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val	
95 100 105	
atc gcc cag atg atg gac aag cac gac acc atc ggc atc gac ctt gtt	386
Ile Ala Gln Met Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val	
110 115 120	
gca atg tgt gtg gat gac ctc gtt gtc acc ggc gca gag cca ctg ttc	434
Ala Met Cys Val Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe	
125 130 135 140	
ctc cag gac tac atc gcc atc ggc aag gtt gtc cca gag cac gtt gct	482
Leu Gln Asp Tyr Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala	
145 150 155	
gag atc gtc tcc ggt atc gca gaa ggc tgt gtc cag gca ggc tgt gct	530
Glu Ile Val Ser Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala	
160 165 170	
ctg ctc ggt ggc gaa acc gca gaa cac cca ggt gtt atg gaa cca gac	578
Leu Leu Gly Gly Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp	
175 180 185	
cac tac gat gtc tcc gca act gca gtc ggc gtt gtc gaa gca gat gaa	626
His Tyr Asp Val Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu	
190 195 200	
ctg cta gga cca gac cgc gtc cgc gca ggc gac gtc ctc atc ggc atg	674
Leu Leu Gly Pro Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met	
205 210 215 220	



gct tcc tcc ggt ctg cac tcc aac ggt tac tcc ctg gct cgc cac gtc 722  
 Ala Ser Ser Gly Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val  
                   225                   230                   235

ctc ctg gaa aag gca ggc ctg gcg ctt gac gga cac atc gaa gaa ctc 770  
 Leu Leu Glu Lys Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu  
                   240                   245                   250

gga cgc acc ccc ggt gaa gaa ctt ctc gag cca acc cgc atg tac gcc 818  
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<211> 268

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 926

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                   20                  25                  30

Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala  
                   35                  40                  45

Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala  
                   50                  55                  60

Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly  
   65                  70                  75                  80

Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu  
                   85                  90                  95

Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met  
                   100                  105                  110

Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val  
                   115                  120                  125

Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr  
                   130                  135                  140

Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser  
   145                  150                  155                  160

Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly  
                   165                  170                  175

Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val  
                   180                  185                  190

Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro  
                   195                  200                  205

Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly  
                   210                  215                  220

Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys  
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Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu Gly Arg Thr Pro  
 245 250 255

Gly Glu Glu Leu Leu Glu Pro Thr Arg Met Tyr Ala  
 260 265

<210> 927

<211> 338

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(315)

<223> FRXA00770

<400> 927

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ggg ctc gtc gca gaa atg tcc cga gca act tgg acc cca ggc caa atc 96  
 Gly Leu Val Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile  
 20 25 30

ttc cgc acc atc tcc tct gtg ggc aag gtt tcc cgc gaa gaa atg gaa 144  
 Phe Arg Thr Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu  
 35 40 45

aag acc ttc aac atg ggt gtc ggc atg gtt gca gtc gtt gct gaa aag 192  
 Lys Thr Phe Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys  
 50 55 60

gac cgc gac cgc gcc ctg gca atg ctc acc gca cgt cac att gac tgc 240  
 Asp Arg Asp Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys  
 65 70 75 80

tgg gaa atc gga acc gta cgc aac ggt gaa gag gga gag cct cgc gtg 288  
 Trp Glu Ile Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val  
 85 90 95

atc ctc aac ggc gag cac cct ggc tac taagcccaac tgtctgctct 335  
 Ile Leu Asn Gly Glu His Pro Gly Tyr  
 100 105

aag 338

<210> 928

<211> 105

<212> PRT

<213> Corynebacterium glutamicum

<400> 928

Val Thr Gly Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu  
 1 5 10 15

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			20					25					30		
Phe	Arg	Thr	Ile	Ser	Ser	Val	Gly	Lys	Val	Ser	Arg	Glu	Glu	Met	Glu
		35					40					45			
Lys	Thr	Phe	Asn	Met	Gly	Val	Gly	Met	Val	Ala	Val	Val	Ala	Glu	Lys
	50					55					60				
Asp	Arg	Asp	Arg	Ala	Leu	Ala	Met	Leu	Thr	Ala	Arg	His	Ile	Asp	Cys
65					70					75					80
Trp	Glu	Ile	Gly	Thr	Val	Arg	Asn	Gly	Glu	Glu	Gly	Glu	Pro	Arg	Val
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<213> Corynebacterium glutamicum
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<221> CDS
<222> (101) .. (1297)
<223> RXN02345
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															Val Thr Ser Thr Gly	
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aac caa gcc cac gct cca gga atg ccc atc gtc gca gta att ggt gac															163	
Asn Gln Ala His Ala Pro Gly Met Pro Ile Val Ala Val Ile Gly Asp																
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ggc caa tta gcc cgc atg atg cag acc tcc gcc atc gaa ctc gga caa															211	
Gly Gln Leu Ala Arg Met Met Gln Thr Ser Ala Ile Glu Leu Gly Gln																
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tca ctg cga gtt cta gct gga gcg ccg gat tcc tcc gca gct caa gta															259	
Ser Leu Arg Val Leu Ala Gly Ala Pro Asp Ser Ser Ala Ala Gln Val																
															40 45 50	
gct gct gat gtt gtt ctc ggc gat tac acc aac att gat gat ctg cgc															307	
Ala Ala Asp Val Val Leu Gly Asp Tyr Thr Asn Ile Asp Asp Leu Arg																
															55 60 65	
gtc gcc atc gaa ggc gcc gat gtg atg acc ttc gac cac gag cac gtc															355	
Val Ala Ile Glu Gly Ala Asp Val Met Thr Phe Asp His Glu His Val																
															70 75 80 85	
ccc aac gaa cac ctg cac caa ctc atc gca gaa ggc gtc aac gtt cag															403	
Pro Asn Glu His Leu His Gln Leu Ile Ala Glu Gly Val Asn Val Gln																
															90 95 100	
cca cgc cca gaa gcg ctg gtc aac gca caa gac aaa ctt gtc atg cgc															451	

Pro	Arg	Pro	Glu	Ala	Leu	Val	Asn	Ala	Gln	Asp	Lys	Leu	Val	Met	Arg		
			105					110					115				
aag	cgt	cta	cgt	gaa	ctc	ggc	gca	cca	gtc	cca	cca	ttt	gct	gcc	att	499	
Lys	Arg	Leu	Arg	Glu	Leu	Gly	Ala	Pro	Val	Pro	Pro	Phe	Ala	Ala	Ile		
		120					125					130					
gaa	tca	gtc	gaa	gat	gca	gtg	gga	ttc	ttc	gaa	gca	gtt	gat	ggc	caa	547	
Glu	Ser	Val	Glu	Asp	Ala	Val	Gly	Phe	Phe	Glu	Ala	Val	Asp	Gly	Gln		
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gtt	tgc	ctc	aaa	gca	cgc	cgt	ggc	gga	tac	gac	ggc	aag	ggc	gta	tgg	595	
Val	Cys	Leu	Lys	Ala	Arg	Arg	Gly	Gly	Tyr	Asp	Gly	Lys	Gly	Val	Trp		
150					155					160					165		
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Phe	Pro	Ala	Asp	Val	Ala	Glu	Leu	Gln	Ser	Leu	Val	Ala	Glu	Leu	Leu		
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Asp	Gly	Gly	Thr	Pro	Leu	Met	Ala	Glu	Lys	Lys	Val	Ala	Leu	Asn	Arg		
			185					190					195				
gaa	ctg	tcc	gcc	atg	gtt	gcc	cgc	acc	cca	agt	gga	gaa	acc	aaa	gcg	739	
Glu	Leu	Ser	Ala	Met	Val	Ala	Arg	Thr	Pro	Ser	Gly	Glu	Thr	Lys	Ala		
		200					205					210					
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Trp	Pro	Val	Val	Glu	Ser	Val	Gln	Lys	Asn	Gly	Val	Cys	Ala	Glu	Ala		
	215					220					225						
atc	gct	ccc	gca	cct	gaa	cta	tcc	gca	gaa	ctg	cag	gaa	tcc	acc	aga	835	
Ile	Ala	Pro	Ala	Pro	Glu	Leu	Ser	Ala	Glu	Leu	Gln	Glu	Ser	Thr	Arg		
230					235					240					245		
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Gly	Leu	Ala	Gln	Lys	Ile	Ala	Thr	Glu	Leu	Gly	Val	Thr	Gly	Val	Leu		
			250					255					260				
gca	gtg	gag	ctt	ttt	gaa	acc	ctc	gac	caa	aac	ggg	cag	cca	gag	atc	931	
Ala	Val	Glu	Leu	Phe	Glu	Thr	Leu	Asp	Gln	Asn	Gly	Gln	Pro	Glu	Ile		
			265				270					275					
ttt	gtc	aac	gag	ctc	gcc	atg	cgt	tca	cac	aac	acc	ggc	cac	tgg	act	979	
Phe	Val	Asn	Glu	Leu	Ala	Met	Arg	Ser	His	Asn	Thr	Gly	His	Trp	Thr		
		280					285					290					
caa	gat	ggc	tgc	gtg	acc	agc	caa	ttc	gag	cag	cac	ctc	cgc	gca	gtc		
1027																	
Gln	Asp	Gly	Cys	Val	Thr	Ser	Gln	Phe	Glu	Gln	His	Leu	Arg	Ala	Val		
	295					300					305						
ctc	gac	tac	cca	ctg	ggc	gct	acc	gac	act	ttg	gct	gat	tac	acc	gtg		
1075																	
Leu	Asp	Tyr	Pro	Leu	Gly	Ala	Thr	Asp	Thr	Leu	Ala	Asp	Tyr	Thr	Val		
310					315					320					325		
atg	gcc	aac	gtg	ctc	ggc	gac	acc	gac	cca	gag	atg	ccc	atg	gca			
1123																	
Met	Ala	Asn	Val	Leu	Gly	Ala	Asp	Thr	Asp	Pro	Glu	Met	Pro	Met	Ala		
			330				335						340				

acc cgc atg gtg gaa gtg ggg cgc aag tac cca gat gcc aag att cac  
1171

Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp Ala Lys Ile His  
345 350 355

ctc tac ggc aag gga cat cgc ccg gga cga aag att ggc cac gtc aac  
1219

Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile Gly His Val Asn  
360 365 370

atg gtg gga tcc gac ctt gaa aag acc cga gcc gaa gcc ctg gcc tgc  
1267

Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu Ala Leu Ala Cys  
375 380 385

gca tac ttc ctt gtc aac gct cgc tgg gat taggtctttt ctgagcgcta  
1317

Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp  
390 395

gca  
1320

<210> 930

<211> 399

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 930-

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Ile Glu Leu Gly Gln Ser Leu Arg Val Leu Ala Gly Ala Pro Asp Ser  
35 40 45

Ser Ala Ala Gln Val Ala Ala Asp Val Val Leu Gly Asp Tyr Thr Asn  
50 55 60

Ile Asp Asp Leu Arg Val Ala Ile Glu Gly Ala Asp Val Met Thr Phe  
65 70 75 80

Asp His Glu His Val Pro Asn Glu His Leu His Gln Leu Ile Ala Glu  
85 90 95

Gly Val Asn Val Gln Pro Arg Pro Glu Ala Leu Val Asn Ala Gln Asp  
100 105 110

Lys Leu Val Met Arg Lys Arg Leu Arg Glu Leu Gly Ala Pro Val Pro  
115 120 125

Pro Phe Ala Ala Ile Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu  
130 135 140

Ala Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp  
145 150 155 160

Gly Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu  
 165 170 175  
 Val Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys  
 180 185 190  
 Val Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser  
 195 200 205  
 Gly Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly  
 210 215 220  
 Val Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu  
 225 230 235 240  
 Gln Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly  
 245 250 255  
 Val Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn  
 260 265 270  
 Gly Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn  
 275 280 285  
 Thr Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln  
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 His Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu  
 305 310 315 320  
 Ala Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro  
 325 330 335  
 Glu Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro  
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 Asp Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys  
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Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp Gly	
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Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu Val	
35 40 45	
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Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val	
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Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly	
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Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val	
85 90 95	
tgt gca gaa gca atc gct ccc gca cct gaa cta tcc gca gaa ctg cag	336
Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln	
100 105 110	
gaa tcc acc aga gga ttg gcc cag aag atc gcc acg gaa ctc ggc gtc	384
Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val	
115 120 125	
act ggt gtc ttg gca gtg gag ctt ttt gaa acc ctc gac caa aac ggg	432
Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly	
130 135 140	
cag cca gag atc ttt gtc aac gag ctc gcc atg cgt tca cac aac acc	480
Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr	
145 150 155 160	
ggc cac tgg act caa gat ggc tgc gtg acc agc caa ttc gag cag cac	528
Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His	
165 170 175	
ctc cgc gca gtc ctc gac tac cca ctg ggt gct acc gac act ttg gct	576
Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala	
180 185 190	
gat tac acc gtg atg gcc aac gtg ctc ggt gcc gac acc gac cca gag	624
Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu	
195 200 205	
atg ccc atg gca acc cgc atg gtg gaa gtg ggg cgc aag tac cca gat	672
Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp	
210 215 220	
gcc aag att cac ctc tac ggc aag gga cat cgc ccg gga cga aag att	720
Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile	
225 230 235 240	
ggc cac gtc aac atg gtg gga tcc gac ctt gaa aag acc cga gcc gaa	768
Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu	
245 250 255	
gcc ctg gcc tgc gca tac ttc ctt gtc aac gct cgc tgg gat	810

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Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val  
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Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly  
 65 70 75 80

Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val  
 85 90 95

Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln  
 100 105 110

Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val  
 115 120 125

Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly  
 130 135 140

Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr  
 145 150 155 160

Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His  
 165 170 175

Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala  
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Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu  
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Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp  
 210 215 220

Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile  
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 Val Gly Pro Leu Val  
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 Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala  
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gca gag gta ctc gct gag ttt ggc att cct ttt gaa gtc gga gtt gtc 211  
 Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val  
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tct gca cac cgc acc cca gag aag atg ctc aac tac gca aag act gca 259  
 Ser Ala His Arg Thr Pro Glu Lys Met Leu Asn Tyr Ala Lys Thr Ala  
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cat gag cgc ggc atc aag acg atc atc gcg tgt gct ggc ggc gct gca 307  
 His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys Ala Gly Gly Ala Ala  
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cac ctg cca ggc atg gtg gct gca gca act cca ctt cca gtc atc ggt 355  
 His Leu Pro Gly Met Val Ala Ala Ala Thr Pro Leu Pro Val Ile Gly  
 70 75 80 85

gtt cca cgc gca ttg aag gat ctc gac ggt ttg gat tcc ttg ctg tcc 403  
 Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu Asp Ser Leu Leu Ser  
 90 95 100

atc gtc cag atg cca ggc ggc gtt cca gtc gcc act gtc tcc atc ggt 451  
 Ile Val Gln Met Pro Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly  
 105 110 115

ggc gcg aag aat gca ggc cta ctt gcc gtt cgt att ctc ggt gct ggt 499  
 Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly  
 120 125 130

gat cct tct ttg gtc acg aag atg gcc gat tac caa gag aat atg gcg 547  
 Asp Pro Ser Leu Val Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala  
 135 140 145

aag gaa gtt gaa gcc aag gac gaa gca ctg aag aag cgc ttg ctc ggc 595  
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 Glu Val Gly Val Val Ser Ala His Arg Thr Pro Glu Lys Met Leu Asn  
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 Tyr Ala Lys Thr Ala His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys  
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 Ala Gly Gly Ala Ala His Leu Pro Gly Met Val Ala Ala Ala Thr Pro  
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 Leu Pro Val Ile Gly Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu  
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 Asp Ser Leu Leu Ser Ile Val Gln Met Pro Gly Gly Val Pro Val Ala  
           100                  105                  110  
 Thr Val Ser Ile Gly Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg  
       115                  120                  125  
 Ile Leu Gly Ala Gly Asp Pro Ser Leu Val Thr Lys Met Ala Asp Tyr  
   130                  135                  140  
 Gln Glu Asn Met Ala Lys Glu Val Glu Ala Lys Asp Glu Ala Leu Lys  
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 Lys Arg Leu Leu Gly  
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   Val Gly Pro Leu Val  
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 Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala

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Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val				
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Ser Ala His Arg				
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Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly Gly Ala Lys Asn Ala				
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ggc cta ctt gcc gtt cgt att ctc ggt gct ggt gat cct tct ttg gtc				148
Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly Asp Pro Ser Leu Val				
30 35 40				
acg aag atg gcc gat tac caa gag aat atg gcg aag gaa gtt gaa gcc				196
Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala Lys Glu Val Glu Ala				
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aag gac gaa gca ctg aag aag cgc ttg ctc ggc taatgaatcc gatcgtggtg				249
Lys Asp Glu Ala Leu Lys Lys Arg Leu Leu Gly				
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                   20                  25                  30  
 Arg Ile Leu Gly Ala Gly Asp Pro Ser Leu Val Thr Lys Met Ala Asp  
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 Tyr Gln Glu Asn Met Ala Lys Glu Val Glu Ala Lys Asp Glu Ala Leu  
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 Ala Ile Val Arg Ala Thr Lys Gln Pro Phe Glu Ile Thr Thr Ile Asp  
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 Leu Asp Ala Pro Arg Pro Asp Glu Val Gln Ile Arg Val Ile Ala Ala  
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 Gly Val Arg His Thr Asp Ala Ile Val Arg Asp Gln Ile Tyr Pro Thr  
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 Phe Leu Pro Ala Val Phe Gly His Glu Gly Ala Gly Val Val Val Ala  
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 Val Gly Ser Ala Val Thr Ser Val Lys Pro Asp Asp Lys Val Val Leu  
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 gga ttc aac tct tgt ggc cag tgc ttg aag tgt ttg ggc ggt aag cct 403  
 Gly Phe Asn Ser Cys Gly Gln Cys Leu Lys Cys Leu Gly Gly Lys Pro

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Ala	Tyr	Cys	Glu	Lys	Phe	Tyr	Asp	Arg	Asn	Phe	Ala	Cys	Thr	Arg	Asp		
			105						110				115				
gcc	ggg	cac	act	act	ttg	ttt	acc	cg	t	gca	aca	aaa	gag	cag	gca	gag	499
Ala	Gly	His	Thr	Thr	Leu	Phe	Thr	Arg	Ala	Thr	Lys	Glu	Gln	Ala	Glu		
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gcc	atc	atc	gac	acc	ctt	gat	gat	gtt	ttc	tac	gat	gcg	gat	gcg	ggt	547	
Ala	Ile	Ile	Asp	Thr	Leu	Asp	Asp	Val	Phe	Tyr	Asp	Ala	Asp	Ala	Gly		
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Phe	Leu	Ala	Tyr	Pro	Ala	Thr	Pro	Pro	Glu	Ala	Ser	Gly	Val	Ser	Val		
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Leu	Val	Val	Ala	Ala	Gly	Thr	Ser	Asp	Leu	Pro	Gln	Ala	Lys	Glu	Ala		
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cta	cac	act	gcc	tcc	tac	ttg	ggg	cg	t	acc	tca	ctg	att	gtt	gat	691	
Leu	His	Thr	Ala	Ser	Tyr	Leu	Gly	Arg	Ser	Thr	Ser	Leu	Ile	Val	Asp		
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ttt	gga	gtg	gct	ggc	atc	cac	cg	ctg	ctt	tca	tac	gaa	gaa	gaa	ctc	739	
Phe	Gly	Val	Ala	Gly	Ile	His	Arg	Leu	Leu	Ser	Tyr	Glu	Glu	Glu	Leu		
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cg	g	gc	gg	gt	ct	at	gt	gc	g	ga	at	ga	gg	gc	ct	787	
Arg	Ala	Ala	Gly	Val	Leu	Ile	Val	Ala	Ala	Gly	Met	Asp	Gly	Ala	Leu		
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ccc	gga	gtt	gtc	gca	ggc	tta	gtg	tcc	gca	cct	gtc	gtc	gca	ctg	cca	835	
Pro	Gly	Val	Val	Ala	Gly	Leu	Val	Ser	Ala	Pro	Val	Val	Ala	Leu	Pro		
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acc	tcc	gtg	gga	tac	ggc	gca	ggt	gct	gga	gga	atc	gca	cca	ctt	ctg	883	
Thr	Ser	Val	Gly	Tyr	Gly	Ala	Gly	Ala	Gly	Gly	Ile	Ala	Pro	Leu	Leu		
				250			255							260			
acc	atg	ctt	aac	gcc	tgc	gcg	ccg	gga	gtt	gga	gtg	gtc	aac	att	gat	931	
Thr	Met	Leu	Asn	Ala	Cys	Ala	Pro	Gly	Val	Gly	Val	Val	Asn	Ile	Asp		
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aac	ggc	tat	gga	gca	gga	cac	ctg	gct	gcg	cag	att	gcg	gcg	agg		976	
Asn	Gly	Tyr	Gly	Ala	Gly	His	Leu	Ala	Ala	Gln	Ile	Ala	Ala	Arg			
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&lt;211&gt; 292

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 940

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Ile Thr Thr Ile Asp Leu Asp Ala Pro Arg Pro Asp Glu Val Gln Ile  
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 Arg Val Ile Ala Ala Gly Val Arg His Thr Asp Ala Ile Val Arg Asp  
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 Gln Ile Tyr Pro Thr Phe Leu Pro Ala Val Phe Gly His Glu Gly Ala  
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 Gly Val Val Val Ala Val Gly Ser Ala Val Thr Ser Val Lys Pro Asp  
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 Asp Lys Val Val Leu Gly Phe Asn Ser Cys Gly Gln Cys Leu Lys Cys  
                   85                  90                  95  
 Leu Gly Gly Lys Pro Ala Tyr Cys Glu Lys Phe Tyr Asp Arg Asn Phe  
                  100                 105                 110  
 Ala Cys Thr Arg Asp Ala Gly His Thr Thr Leu Phe Thr Arg Ala Thr  
           115                 120                 125  
 Lys Glu Gln Ala Glu Ala Ile Ile Asp Thr Leu Asp Asp Val Phe Tyr  
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 Asp Ala Asp Ala Gly Phe Leu Ala Tyr Pro Ala Thr Pro Pro Glu Ala  
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 Ser Gly Val Ser Val Leu Val Val Ala Ala Gly Thr Ser Asp Leu Pro  
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 Gln Ala Lys Glu Ala Leu His Thr Ala Ser Tyr Leu Gly Arg Ser Thr  
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 Ser Leu Ile Val Asp Phe Gly Val Ala Gly Ile His Arg Leu Leu Ser  
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 Tyr Glu Glu Glu Leu Arg Ala Ala Gly Val Leu Ile Val Ala Ala Gly  
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 Met Asp Gly Ala Leu Pro Gly Val Val Ala Gly Leu Val Ser Ala Pro  
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 Val Val Ala Leu Pro Thr Ser Val Gly Tyr Gly Ala Gly Ala Gly Gly  
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 Ile Ala Pro Leu Leu Thr Met Leu Asn Ala Cys Ala Pro Gly Val Gly  
           260                 265                 270  
 Val Val Asn Ile Asp Asn Gly Tyr Gly Ala Gly His Leu Ala Ala Gln  
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 Val Ala Asp Lys Lys  
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 Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala Ser Ala Glu Leu Ser  
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aac ctg tgg agt gcc gaa gag aag atc atc atg gag cgc cag ctc tgg 211  
 Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp  
 25 30 35

atc gcc gtg atg aaa gcc cag aaa gat ttg gga gtt gag atc cct gcc 259  
 Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly Val Glu Ile Pro Ala  
 40 45 50

gag gca att gaa tcc tat gaa gca gtg atc gac cag gtt gat ttg gca 307  
 Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp Gln Val Asp Leu Ala  
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agc atc gcc gat cgt gag cgc gtc acc cgc cac gat gtg aag gcc cgc 355  
 Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His Asp Val Lys Ala Arg  
 70 75 80 85

atc gaa gaa ttc aat gca ctg gct ggc cat gag cac atc cac aag ggc 403  
 Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu His Ile His Lys Gly  
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atg acc tcc cgc gac ctc acc gaa aat gtt gaa cag ctg cag atc cac 451  
 Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu Gln Leu Gln Ile His  
 105 110 115

cgc tcc ctt gag ctg gtc cgc aac aag ggc att gca gtt gtt gca gct 499  
 Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile Ala Val Val Ala Ala  
 120 125 130

atc gga tcc cgc gca gcg cag tac caa agc ctg gtc atg gct ggc cgt 547  
 Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu Val Met Ala Gly Arg  
 135 140 145

tcc cac aac gtg gca gcg cag gca act acc ttg ggc aag cgt ttc gca 595  
 Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu Gly Lys Arg Phe Ala  
 150 155 160 165

acc gca gct gat gaa atg ctc gtg gca ctt gag cgc gtc acc gaa ctg 643  
 Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu Arg Val Thr Glu Leu  
 170 175 180

ctc aac cgc tac cca ctt cgc gga atc aag ggc cca atg gga acc gcc 691  
 Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly Pro Met Gly Thr Ala  
 185 190 195

caa gac atg ctt gac ctc atg gaa ggc gac gag gct cgt ctc tcc gat 739

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Leu	Glu	Thr	Arg	Ile	Ala	Ala	His	Leu	Gly	Phe	Asp	Arg	Val	Phe	Asp	
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Ser	Val	Gly	Gln	Val	Tyr	Pro	Arg	Ser	Leu	Asp	Phe	Asp	Ala	Val	Ser	
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gct	ctg	gtt	cag	ctt	ggc	tcc	ggc	cca	tca	tcg	ctg	tcc	cac	acc	att	883
Ala	Leu	Val	Gln	Leu	Gly	Ser	Gly	Pro	Ser	Ser	Leu	Ser	His	Thr	Ile	
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cgt	ctc	atg	gcc	ggc	acc	gaa	act	gtt	acc	gaa	ggc	ttt	aag	gaa	ggc	931
Arg	Leu	Met	Ala	Gly	Thr	Glu	Thr	Val	Thr	Glu	Gly	Phe	Lys	Glu	Gly	
			265					270					275			
cag	gtc	ggc	tcc	tct	gca	atg	cct	cac	aag	atg	aac	gct	cgc	tcc	tgt	979
Gln	Val	Gly	Ser	Ser	Ala	Met	Pro	His	Lys	Met	Asn	Ala	Arg	Ser	Cys	
		280					285					290				
gag	cgc	gtg	ggc	ggc	ctg	cag	gtt	att	ctt	cgc	gga	tac	ctc	acc	atg	
		1027														
Glu	Arg	Val	Gly	Gly	Leu	Gln	Val	Ile	Leu	Arg	Gly	Tyr	Leu	Thr	Met	
		295				300					305					
gtt	gct	gat	ctt	tcc	ggc	cag	cag	tgg	aac	gaa	ggc	gat	gtc	ttc	tgc	
		1075														
Val	Ala	Asp	Leu	Ser	Gly	Gln	Gln	Trp	Asn	Glu	Gly	Asp	Val	Phe	Cys	
		310			315					320					325	
tcc	gtg	atc	cgc	cgc	gtt	gca	ctg	cca	gac	gca	ttc	ttc	gcg	att	gac	
		1123														
Ser	Val	Ile	Arg	Arg	Val	Ala	Leu	Pro	Asp	Ala	Phe	Phe	Ala	Ile	Asp	
				330					335					340		
gga	atg	ttt	gaa	act	ttc	ctg	aca	gtc	ctg	gat	gaa	ttc	ggc	gca	ttc	
		1171														
Gly	Met	Phe	Glu	Thr	Phe	Leu	Thr	Val	Leu	Asp	Glu	Phe	Gly	Ala	Phe	
			345					350					355			
cct	gcc	atg	atc	gag	cgc	gaa	ctt	gag	cgt	tac	ctg	cca	ttc	ctg	gca	
		1219														
Pro	Ala	Met	Ile	Glu	Arg	Glu	Leu	Glu	Arg	Tyr	Leu	Pro	Phe	Leu	Ala	
		360					365					370				
act	acc	cgt	atc	ctc	atg	gcc	gct	gtc	cgc	gca	ggc	gtt	ggc	cgc	gaa	
		1267														
Thr	Thr	Arg	Ile	Leu	Met	Ala	Ala	Val	Arg	Ala	Gly	Val	Gly	Arg	Glu	
		375				380					385					
acc	gca	cac	gaa	gta	atc	aag	gaa	aac	gct	gtc	gcg	gtt	gcc	ctc	aac	
		1315														
Thr	Ala	His	Glu	Val	Ile	Lys	Glu	Asn	Ala	Val	Ala	Val	Ala	Leu	Asn	
		390			395					400					405	
atg	cgc	gaa	aat	ggc	ggc	gac	cag	gac	ctt	atc	cag	cgc	ctc	gct	gct	
		1363														
Met	Arg	Glu	Asn	Gly	Gly	Asp	Gln	Asp	Leu	Ile	Gln	Arg	Leu	Ala	Ala	



410 415 420  
 gat gag cgc ctc cca atg agc gaa gct gac ctt gag gca gcg ctg gct  
 1411  
 Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu Glu Ala Ala Leu Ala  
 425 430 435  
 gac cgc cac gcc ttc atc ggt gcc gct gag tcc cag gtc tcc cgt gtg  
 1459  
 Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val  
 440 445 450  
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 1507  
 Leu Asp Arg Ile Gln Val Leu Val Asp Ala His Pro Gly Ala Ala Asp  
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 Tyr Arg Pro Gly Glu Ile Leu  
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 <211> 476  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 942  
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 Glu Arg Gln Leu Trp Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly  
 35 40 45  
 Val Glu Ile Pro Ala Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp  
 50 55 60  
 Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His  
 65 70 75 80  
 Asp Val Lys Ala Arg Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu  
 85 90 95  
 His Ile His Lys Gly Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu  
 100 105 110  
 Gln Leu Gln Ile His Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile  
 115 120 125  
 Ala Val Val Ala Ala Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu  
 130 135 140  
 Val Met Ala Gly Arg Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu  
 145 150 155 160  
 Gly Lys Arg Phe Ala Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu  
 165 170 175

Arg Val Thr Glu Leu Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly  
 180 185 190  
 Pro Met Gly Thr Ala Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu  
 195 200 205  
 Ala Arg Leu Ser Asp Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe  
 210 215 220  
 Asp Arg Val Phe Asp Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp  
 225 230 235 240  
 Phe Asp Ala Val Ser Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser  
 245 250 255  
 Leu Ser His Thr Ile Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu  
 260 265 270  
 Gly Phe Lys Glu Gly Gln Val Gly Ser Ser Ala Met Pro His Lys Met  
 275 280 285  
 Asn Ala Arg Ser Cys Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg  
 290 295 300  
 Gly Tyr Leu Thr Met Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu  
 305 310 315 320  
 Gly Asp Val Phe Cys Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala  
 325 330 335  
 Phe Phe Ala Ile Asp Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp  
 340 345 350  
 Glu Phe Gly Ala Phe Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr  
 355 360 365  
 Leu Pro Phe Leu Ala Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala  
 370 375 380  
 Gly Val Gly Arg Glu Thr Ala His Glu Val Ile Lys Glu Asn Ala Val  
 385 390 395 400  
 Ala Val Ala Leu Asn Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile  
 405 410 415  
 Gln Arg Leu Ala Ala Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu  
 420 425 430  
 Glu Ala Ala Leu Ala Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser  
 435 440 445  
 Gln Val Ser Arg Val Leu Asp Arg Ile Gln Val Leu Val Asp Ala His  
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 Pro Gly Ala Ala Asp Tyr Arg Pro Gly Glu Ile Leu  
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<210> 943  
 <211> 1683

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1660)

&lt;223&gt; RXA02622

&lt;400&gt; 943

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cagggtggcg tacaactcaa ctggagaggc taaatccttc atg agc gat gat cgt 115
                                         Met Ser Asp Asp Arg
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aag gca att aaa cgc gca cta att agc gtg tat gac aag act ggc ctg 163
Lys Ala Ile Lys Arg Ala Leu Ile Ser Val Tyr Asp Lys Thr Gly Leu
                        10                        15                        20

gag gat cta gcc cag gca ctt cac cgc gag aac gtg gaa att gtt tcc 211
Glu Asp Leu Ala Gln Ala Leu His Arg Glu Asn Val Glu Ile Val Ser
                        25                        30                        35

acc gga tcc act gcg gcg aag att gct gag ctt ggt att cct gtt acc 259
Thr Gly Ser Thr Ala Ala Lys Ile Ala Glu Leu Gly Ile Pro Val Thr
                        40                        45                        50

ccg gtt gag gag ctc acc ggt ttc cct gag tgc ctt gag ggc cgt gtg 307
Pro Val Glu Glu Leu Thr Gly Phe Pro Glu Cys Leu Glu Gly Arg Val
                        55                        60                        65

aag aca ctg cac cct aag gtt cac gct ggc atc ttg gcg gac acc cgc 355
Lys Thr Leu His Pro Lys Val His Ala Gly Ile Leu Ala Asp Thr Arg
                        70                        75                        80                        85

aag gaa gac cac ctg cgt cag ctc aag gaa ctt gag gtc gcc cca ttc 403
Lys Glu Asp His Leu Arg Gln Leu Lys Glu Leu Glu Val Ala Pro Phe
                        90                        95                        100

cag ctt gtc gtg gtg aac ctg tac cca ttt gct gag acc gtt gcg tcc 451
Gln Leu Val Val Val Asn Leu Tyr Pro Phe Ala Glu Thr Val Ala Ser
                        105                        110                        115

ggc gcc gat ttc gat gct tgc gtt gag cag atc gac atc gga ggc cca 499
Gly Ala Asp Phe Asp Ala Cys Val Glu Gln Ile Asp Ile Gly Gly Pro
                        120                        125                        130

tcc atg gtt cgt gct gcg gca aag aac cac cca tct gtc gct gtg gtt 547
Ser Met Val Arg Ala Ala Ala Lys Asn His Pro Ser Val Ala Val Val
                        135                        140                        145

gtt tca ccg aac cgc tac gag gat gtc cag gaa gct ttg aag acc ggt 595
Val Ser Pro Asn Arg Tyr Glu Asp Val Gln Glu Ala Leu Lys Thr Gly
150                        155                        160                        165

gga ttc tcc cgc gcg gag cgc acc aag ttg gct gct gag gct ttc cgc 643
Gly Phe Ser Arg Ala Glu Arg Thr Lys Leu Ala Ala Glu Ala Phe Arg
                        170                        175                        180

cac acc gca acc tac gat gtc acc gtt gca acc tgg atg agc gag cag 691
His Thr Ala Thr Tyr Asp Val Thr Val Ala Thr Trp Met Ser Glu Gln

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185				190				195				
ctg gct gcc gaa gat tct gag act gag ttc cca ggt tgg atc ggc acc	739											
Leu Ala Ala Glu Asp Ser Glu Thr Glu Phe Pro Gly Trp Ile Gly Thr												
200 205 210												
acc aac acc ttg tcc cgc agc ttg cgt tac ggt gag aac cct cac cag	787											
Thr Asn Thr Leu Ser Arg Ser Leu Arg Tyr Gly Glu Asn Pro His Gln												
215 220 225												
tct gca gct ttg tac gtg ggc aac acc cgc gga ctt gca cag gct aag	835											
Ser Ala Ala Leu Tyr Val Gly Asn Thr Arg Gly Leu Ala Gln Ala Lys												
230 235 240 245												
cag ttc cac ggc aag gaa atg agc tac aac aac tac acc gat tct gat	883											
Gln Phe His Gly Lys Glu Met Ser Tyr Asn Asn Tyr Thr Asp Ser Asp												
250 255 260												
gct gca tgg cgt gca gcg tgg gat cac gag cgt cct tgt gta gct atc	931											
Ala Ala Trp Arg Ala Ala Trp Asp His Glu Arg Pro Cys Val Ala Ile												
265 270 275												
atc aag cat gca aac cct tgt ggc att gct gtt tct gat gag tcc atc	979											
Ile Lys His Ala Asn Pro Cys Gly Ile Ala Val Ser Asp Glu Ser Ile												
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gca gcg gca cac cgc gag gca cac gca tgt gac tct gtg tcc gca ttc												
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Ala Ala Ala His Arg Glu Ala His Ala Cys Asp Ser Val Ser Ala Phe												
295 300 305												
ggt ggc gtc atc gcg tcc aac cgt gaa gtc agc gtt gag atg gct aac												
1075												
Gly Gly Val Ile Ala Ser Asn Arg Glu Val Ser Val Glu Met Ala Asn												
310 315 320 325												
cag gtt gca gag atc ttc act gag gtc atc atc gct cct tcc tat gaa												
1123												
Gln Val Ala Glu Ile Phe Thr Glu Val Ile Ile Ala Pro Ser Tyr Glu												
330 335 340												
gag ggc gct gtg gag atc ctg agc cag aag aag aac atc cgt att ctt												
1171												
Glu Gly Ala Val Glu Ile Leu Ser Gln Lys Lys Asn Ile Arg Ile Leu												
345 350 355												
cag gct gaa gca cct gtg cgt aag ggc ttt gag tcc cgt gag atc tcc												
1219												
Gln Ala Glu Ala Pro Val Arg Lys Gly Phe Glu Ser Arg Glu Ile Ser												
360 365 370												
ggc ggt ctg ctt gtt cag gaa cgc gac ttg atc cac gct gag ggc gac												
1267												
Gly Gly Leu Leu Val Gln Glu Arg Asp Leu Ile His Ala Glu Gly Asp												
375 380 385												
aac tcc gca aac tgg act ctt gct gcc ggc tct gct gtt tct cct gag												
1315												
Asn Ser Ala Asn Trp Thr Leu Ala Ala Gly Ser Ala Val Ser Pro Glu												
390 395 400 405												

gtt ctg aag gac ctg gag ttc gcg tgg act gca gtt cgt tcc gtg aag  
1363

Val Leu Lys Asp Leu Glu Phe Ala Trp Thr Ala Val Arg Ser Val Lys  
410 415 420

tcc aac gca att ctg ttg gct aag aac ggc gct acc gtt ggc gtt ggc  
1411

Ser Asn Ala Ile Leu Leu Ala Lys Asn Gly Ala Thr Val Gly Val Gly  
425 430 435

atg gga cag gtc aac cgc gtt gac tct gct cgc ttg gct gtc gac cgt  
1459

Met Gly Gln Val Asn Arg Val Asp Ser Ala Arg Leu Ala Val Asp Arg  
440 445 450

gca ggt gca gag cgc gct acc ggt tcc gtt gct gct tcc gat gcg ttc  
1507

Ala Gly Ala Glu Arg Ala Thr Gly Ser Val Ala Ala Ser Asp Ala Phe  
455 460 465

ttc cca ttc gct gat ggc ttt gag gtt ctc gct gag gct ggc atc act  
1555

Phe Pro Phe Ala Asp Gly Phe Glu Val Leu Ala Glu Ala Gly Ile Thr  
470 475 480 485

gct gtt gtg cag cct ggt gga tcc att cgc gac aac gag gtc att gag  
1603

Ala Val Val Gln Pro Gly Gly Ser Ile Arg Asp Asn Glu Val Ile Glu  
490 495 500

gca gcc aac aag gct ggc gtg acc atg tac ctg act ggt gcg cga cac  
1651

Ala Ala Asn Lys Ala Gly Val Thr Met Tyr Leu Thr Gly Ala Arg His  
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ttc gct cac taaagttttt aaagatttcg ctt  
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Phe Ala His  
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<211> 520

<212> PRT

<213> Corynebacterium glutamicum

<400> 944

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Val Glu Ile Val Ser Thr Gly Ser Thr Ala Ala Lys Ile Ala Glu Leu  
35 40 45

Gly Ile Pro Val Thr Pro Val Glu Glu Leu Thr Gly Phe Pro Glu Cys  
50 55 60

Leu Glu Gly Arg Val Lys Thr Leu His Pro Lys Val His Ala Gly Ile  
65 70 75 80

Leu Ala Asp Thr Arg Lys Glu Asp His Leu Arg Gln Leu Lys Glu Leu  
 85 90 95  
 Glu Val Ala Pro Phe Gln Leu Val Val Val Asn Leu Tyr Pro Phe Ala  
 100 105 110  
 Glu Thr Val Ala Ser Gly Ala Asp Phe Asp Ala Cys Val Glu Gln Ile  
 115 120 125  
 Asp Ile Gly Gly Pro Ser Met Val Arg Ala Ala Ala Lys Asn His Pro  
 130 135 140  
 Ser Val Ala Val Val Val Ser Pro Asn Arg Tyr Glu Asp Val Gln Glu  
 145 150 155 160  
 Ala Leu Lys Thr Gly Gly Phe Ser Arg Ala Glu Arg Thr Lys Leu Ala  
 165 170 175  
 Ala Glu Ala Phe Arg His Thr Ala Thr Tyr Asp Val Thr Val Ala Thr  
 180 185 190  
 Trp Met Ser Glu Gln Leu Ala Ala Glu Asp Ser Glu Thr Glu Phe Pro  
 195 200 205  
 Gly Trp Ile Gly Thr Thr Asn Thr Leu Ser Arg Ser Leu Arg Tyr Gly  
 210 215 220  
 Glu Asn Pro His Gln Ser Ala Ala Leu Tyr Val Gly Asn Thr Arg Gly  
 225 230 235 240  
 Leu Ala Gln Ala Lys Gln Phe His Gly Lys Glu Met Ser Tyr Asn Asn  
 245 250 255  
 Tyr Thr Asp Ser Asp Ala Ala Trp Arg Ala Ala Trp Asp His Glu Arg  
 260 265 270  
 Pro Cys Val Ala Ile Ile Lys His Ala Asn Pro Cys Gly Ile Ala Val  
 275 280 285  
 Ser Asp Glu Ser Ile Ala Ala Ala His Arg Glu Ala His Ala Cys Asp  
 290 295 300  
 Ser Val Ser Ala Phe Gly Gly Val Ile Ala Ser Asn Arg Glu Val Ser  
 305 310 315 320  
 Val Glu Met Ala Asn Gln Val Ala Glu Ile Phe Thr Glu Val Ile Ile  
 325 330 335  
 Ala Pro Ser Tyr Glu Glu Gly Ala Val Glu Ile Leu Ser Gln Lys Lys  
 340 345 350  
 Asn Ile Arg Ile Leu Gln Ala Glu Ala Pro Val Arg Lys Gly Phe Glu  
 355 360 365  
 Ser Arg Glu Ile Ser Gly Gly Leu Leu Val Gln Glu Arg Asp Leu Ile  
 370 375 380  
 His Ala Glu Gly Asp Asn Ser Ala Asn Trp Thr Leu Ala Ala Gly Ser  
 385 390 395 400

Ala Val Ser Pro Glu Val Leu Lys Asp Leu Glu Phe Ala Trp Thr Ala  
 405 410 415

Val Arg Ser Val Lys Ser Asn Ala Ile Leu Leu Ala Lys Asn Gly Ala  
 420 425 430

Thr Val Gly Val Gly Met Gly Gln Val Asn Arg Val Asp Ser Ala Arg  
 435 440 445

Leu Ala Val Asp Arg Ala Gly Ala Glu Arg Ala Thr Gly Ser Val Ala  
 450 455 460

Ala Ser Asp Ala Phe Phe Pro Phe Ala Asp Gly Phe Glu Val Leu Ala  
 465 470 475 480

Glu Ala Gly Ile Thr Ala Val Val Gln Pro Gly Gly Ser Ile Arg Asp  
 485 490 495

Asn Glu Val Ile Glu Ala Ala Asn Lys Ala Gly Val Thr Met Tyr Leu  
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Thr Gly Ala Arg His Phe Ala His  
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<210> 945  
 <211> 1641  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1618)  
 <223> RXN00488

<400> 945  
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 Met Thr Thr Gln Ser  
 1 5

cga gtt tct acc gga gga gac aac cca aac aag gtt gcc ctt gtt gga 163  
 Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly  
 10 15 20

tta acc ttt gat gac gta ctt ttg ctt cca gat gcg tcg gac gtt gtt 211  
 Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp Ala Ser Asp Val Val  
 25 30 35

cct tca gag gta gat acc tcg acg cag tta aca cgt aat att cgc ctt 259  
 Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr Arg Asn Ile Arg Leu  
 40 45 50

aac acc cct att ctt tct gcc gca atg gat act gtc acc gag gct cgc 307  
 Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr Val Thr Glu Ala Arg  
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atg gct atc ggc atg gca cgc cat ggc ggc att ggt gtt ttg cac cgc 355  
 Met Ala Ile Gly Met Ala Arg His Gly Gly Ile Gly Val Leu His Arg  
 70 75 80 85

aac ctg tct att caa gag cag gca gaa aac gtt gag ctg gtg aag cgt	403
Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val Glu Leu Val Lys Arg	
90 95 100	
tct gag tct gga atg gtc act gat cct gtt acc tgt act cct gac atg	451
Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr Cys Thr Pro Asp Met	
105 110 115	
agc atc caa gaa gtg gat gat ctg tgt gca cgc ttc cgc att tcc ggt	499
Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg Phe Arg Ile Ser Gly	
120 125 130	
ctg cct gtt gtt gat gag gcc gga aag ttg gtt ggt att tgc acc aac	547
Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn	
135 140 145	
cgc gat atg cgt ttt gaa agc gac atg aac cgt cgt gtc gct gaa gtt	595
Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg Arg Val Ala Glu Val	
150 155 160 165	
atg acc cca atg cct ttg gtt gtt gct gaa gag ggc gtc acc aag gag	643
Met Thr Pro Met Pro Leu Val Val Ala Glu Glu Gly Val Thr Lys Glu	
170 175 180	
cag gct ctt gct ttg ctg tct gca aac aag gtg gag aag ctt cct atc	691
Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val Glu Lys Leu Pro Ile	
185 190 195	
atc gca aag gac ggc aag ctt gtc ggt ctg atc acg gtg aag gac ttc	739
Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile Thr Val Lys Asp Phe	
200 205 210	
gtt aag act gag cag cac ccg aac gca tcc aag gat gca tca ggt cgt	787
Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys Asp Ala Ser Gly Arg	
215 220 225	
ctg ctg gtt gcg gct ggc atc ggc acg ggc gag gag tca ttc cag cga	835
Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu Glu Ser Phe Gln Arg	
230 235 240 245	
gct ggt gcg ctt gcc gac gcc ggc gtc gac att ttg gtc gta gac tct	883
Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile Leu Val Val Asp Ser	
250 255 260	
gca cac gcc cat agc cgt gga gtt ttg gac atg gtg tcc cgc gtg aag	931
Ala His Ala His Ser Arg Gly Val Leu Asp Met Val Ser Arg Val Lys	
265 270 275	
aag tcg ttc ccc aag gtc gat atc gtt ggc ggc aac ttg gcg acc cgc	979
Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly Asn Leu Ala Thr Arg	
280 285 290	
gag gct gcg cag gcc atg att gaa gct ggc gca gac gct atc aag gtg	
1027	
Glu Ala Ala Gln Ala Met Ile Glu Ala Gly Ala Asp Ala Ile Lys Val	
295 300 305	
ggt att ggc cca ggt tct att tgc acc act cgc gtt gtc gca ggt gtc	
1075	
Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg Val Val Ala Gly Val	



310 315 320 325  
 ggt gca cct cag atc act gcg atc atg gag gca gct gtt cca gct cac  
 1123  
 Gly Ala Pro Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His  
 330 335 340  
 aag gct ggc gtt cct atc atc gcc gat ggc ggc atg cag ttc tct ggt  
 1171  
 Lys Ala Gly Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly  
 345 350 355  
 gat atc gct aag gct ttg gct gct ggc gct aac tcc gtg atg ctg ggc  
 1219  
 Asp Ile Ala Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly  
 360 365 370  
 tcc atg ctg gct ggt acc gct gag gct cct ggt gag acc atc acc atc  
 1267  
 Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile  
 375 380 385  
 aac ggc aag cag tac aag cgt tac cgc ggc atg ggc tcc atg ggc gct  
 1315  
 Asn Gly Lys Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala  
 390 395 400 405  
 atg cag ggc cgt gga ctt agt ggt gag aag cgt tcc tac tcc aag gac  
 1363  
 Met Gln Gly Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp  
 410 415 420  
 cgt tac ttc cag tct gac gtt aag agc gaa gac aag ctc gtt cca gaa  
 1411  
 Arg Tyr Phe Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu  
 425 430 435  
 ggc atc gaa ggt cgc gtg cct ttc cgc ggt ccc atc gga gac atc att  
 1459  
 Gly Ile Glu Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile  
 440 445 450  
 cac cag cag gtc ggt gga ctt cgt gca gca atg ggc tac acc ggt tcc  
 1507  
 His Gln Gln Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser  
 455 460 465  
 tcc acc att gaa gag ctg cac aac gct cgt ttc gtg cag atc acc agc  
 1555  
 Ser Thr Ile Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser  
 470 475 480 485  
 gcg ggt ctg aag gaa tcc cac ccg cac cac atc cag cag act gtg gaa  
 1603  
 Ala Gly Leu Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu  
 490 495 500  
 gct cct aac tac cac tagattttgc tcacttaaagc agc  
 1641  
 Ala Pro Asn Tyr His  
 505

&lt;210&gt; 946

&lt;211&gt; 506

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 946

Met Thr Thr Gln Ser Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys  
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Val Ala Leu Val Gly Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp  
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Ala Ser Asp Val Val Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr  
 35 40 45

Arg Asn Ile Arg Leu Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr  
 50 55 60

Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile  
 65 70 75 80

Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val  
 85 90 95

Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr  
 100 105 110

Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg  
 115 120 125

Phe Arg Ile Ser Gly Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val  
 130 135 140

Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg  
 145 150 155 160

Arg Val Ala Glu Val Met Thr Pro Met Pro Leu Val Val Ala Glu Glu  
 165 170 175

Gly Val Thr Lys Glu Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val  
 180 185 190

Glu Lys Leu Pro Ile Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile  
 195 200 205

Thr Val Lys Asp Phe Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys  
 210 215 220

Asp Ala Ser Gly Arg Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu  
 225 230 235 240

Glu Ser Phe Gln Arg Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile  
 245 250 255

Leu Val Val Asp Ser Ala His Ala His Ser Arg Gly Val Leu Asp Met  
 260 265 270

Val Ser Arg Val Lys Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly  
 275 280 285

Asn Leu Ala Thr Arg Glu Ala Ala Gln Ala Met Ile Glu Ala Gly Ala  
 290 295 300  
 Asp Ala Ile Lys Val Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg  
 305 310 315 320  
 Val Val Ala Gly Val Gly Ala Pro Gln Ile Thr Ala Ile Met Glu Ala  
 325 330 335  
 Ala Val Pro Ala His Lys Ala Gly Val Pro Ile Ile Ala Asp Gly Gly  
 340 345 350  
 Met Gln Phe Ser Gly Asp Ile Ala Lys Ala Leu Ala Ala Gly Ala Asn  
 355 360 365  
 Ser Val Met Leu Gly Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly  
 370 375 380  
 Glu Thr Ile Thr Ile Asn Gly Lys Gln Tyr Lys Arg Tyr Arg Gly Met  
 385 390 395 400  
 Gly Ser Met Gly Ala Met Gln Gly Arg Gly Leu Ser Gly Glu Lys Arg  
 405 410 415  
 Ser Tyr Ser Lys Asp Arg Tyr Phe Gln Ser Asp Val Lys Ser Glu Asp  
 420 425 430  
 Lys Leu Val Pro Glu Gly Ile Glu Gly Arg Val Pro Phe Arg Gly Pro  
 435 440 445  
 Ile Gly Asp Ile Ile His Gln Gln Val Gly Gly Leu Arg Ala Ala Met  
 450 455 460  
 Gly Tyr Thr Gly Ser Ser Thr Ile Glu Glu Leu His Asn Ala Arg Phe  
 465 470 475 480  
 Val Gln Ile Thr Ser Ala Gly Leu Lys Glu Ser His Pro His His Ile  
 485 490 495  
 Gln Gln Thr Val Glu Ala Pro Asn Tyr His  
 500 505

<210> 947  
 <211> 574  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(574)  
 <223> FRXA00492

<400> 947  
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 tagataattg tggacacact atgaggagga actgtcgcac atg aca acc cag agc 115  
 Met Thr Thr Gln Ser  
 1 5

cga gtt tct acc gga gga gac aac cca aac aag gtt gcc ctt gtt gga 163  
 Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly  
                   10                  15                  20

tta acc ttt gat gac gta ctt ttg ctt cca gat gcg tcg gac gtt gtt 211  
 Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp Ala Ser Asp Val Val  
                   25                  30                  35

cct tca gag gta gat acc tcg acg cag tta aca cgt aat att cgc ctt 259  
 Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr Arg Asn Ile Arg Leu  
                   40                  45                  50

aac acc cct att ctt tct gcc gca atg gat act gtc acc gag gct cgc 307  
 Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr Val Thr Glu Ala Arg  
                   55                  60                  65

atg gct atc ggc atg gca cgc cat ggc ggc att ggt gtt ttg cac cgc 355  
 Met Ala Ile Gly Met Ala Arg His Gly Gly Ile Gly Val Leu His Arg  
                   70                  75                  80                  85

aac ctg tct att caa gag cag gca gaa aac gtt gag ctg gtg aag cgt 403  
 Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val Glu Leu Val Lys Arg  
                   90                  95                  100

tct gag tct gga atg gtc act gat cct gtt acc tgt act cct gac atg 451  
 Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr Cys Thr Pro Asp Met  
                   105                  110                  115

agc atc caa gaa gtg gat gat ctg tgt gca cgc ttc cgc att tcc ggt 499  
 Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg Phe Arg Ile Ser Gly  
                   120                  125                  130

ctg cct gtt gtt gat gag gcc gga aag ttg gtt ggt att tgc acc aac 547  
 Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn  
                   135                  140                  145

cgc gat atg cgt ttt gaa agc gac atg 574  
 Arg Asp Met Arg Phe Glu Ser Asp Met  
 150                  155

&lt;210&gt; 948

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 948

Met Thr Thr Gln Ser Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys  
   1                  5                  10                  15

Val Ala Leu Val Gly Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp  
                   20                  25                  30

Ala Ser Asp Val Val Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr  
                   35                  40                  45

Arg Asn Ile Arg Leu Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr  
                   50                  55                  60

Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile  
   65                  70                  75                  80

Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val  
                             85                            90                            95

Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr  
                             100                            105                            110

Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg  
                             115                            120                            125

Phe Arg Ile Ser Gly Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val  
                             130                            135                            140

Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met  
                             145                            150                            155

<210> 949  
 <211> 557  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(534)  
 <223> FRXA00488

<400> 949  
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 Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His Lys Ala Gly  
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gtt cct atc atc gcc gat ggc ggc atg cag ttc tct ggt gat atc gct 96  
 Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly Asp Ile Ala  
                             20                            25                            30

aag gct ttg gct gct ggc gct aac tcc gtg atg ctg ggc tcc atg ctg 144  
 Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu  
                             35                            40                            45

gct ggt acc gct gag gct cct ggt gag acc atc acc atc aac ggc aag 192  
 Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys  
                             50                            55                            60

cag tac aag cgt tac cgc ggc atg ggc tcc atg ggc gct atg cag ggc 240  
 Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala Met Gln Gly  
     65                            70                            75                            80

cgt gga ctt agt ggt gag aag cgt tcc tac tcc aag gac cgt tac ttc 288  
 Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp Arg Tyr Phe  
                             85                            90                            95

cag tct gac gtt aag agc gaa gac aag ctc gtt cca gaa ggc atc gaa 336  
 Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu  
                             100                            105                            110

ggt cgc gtg cct ttc cgc ggt ccc atc gga gac atc att cac cag cag 384  
 Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln  
                             115                            120                            125

gtc ggt gga ctt cgt gca gca atg ggc tac acc ggt tcc tcc acc att 432

Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser Ser Thr Ile  
 130 135 140

gaa gag ctg cac aac gct cgt ttc gtg cag atc acc agc gcg ggt ctg 480  
 Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser Ala Gly Leu  
 145 150 155 160

aag gaa tcc cac ccg cac cac atc cag cag act gtg gaa gct cct aac 528  
 Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn  
 165 170 175

tac cac tagattttgc tcacttaaagc agc 557  
 Tyr His

<210> 950  
 <211> 178  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 950  
 Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His Lys Ala Gly  
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Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly Asp Ile Ala  
 20 25 30

Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu  
 35 40 45

Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys  
 50 55 60

Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala Met Gln Gly  
 65 70 75 80

Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp Arg Tyr Phe  
 85 90 95

Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu  
 100 105 110

Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln  
 115 120 125

Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser Ser Thr Ile  
 130 135 140

Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser Ala Gly Leu  
 145 150 155 160

Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn  
 165 170 175

Tyr His

<210> 951  
 <211> 1554

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1531)

&lt;223&gt; RXA02469

&lt;400&gt; 951

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gccgtgttca gggataactg attaatacaac taggagaccc atg cgt ttt ctt aac 115
                                   Met Arg Phe Leu Asn
                                   1                               5

aat tcc aat ccg ccc tat gag ctg aca tat tcc gat gtg ttt atg gtg 163
Asn Ser Asn Pro Pro Tyr Glu Leu Thr Tyr Ser Asp Val Phe Met Val
                        10                               15                               20

cct tcg cgt tct gac gta ggc tcc cgc atg tcc gtg gat ctg cgc acc 211
Pro Ser Arg Ser Asp Val Gly Ser Arg Met Ser Val Asp Leu Arg Thr
                        25                               30                               35

aat gac gga act gga aca acc atc ccg ctc gtt gtg gca aac atg act 259
Asn Asp Gly Thr Gly Thr Thr Ile Pro Leu Val Val Ala Asn Met Thr
                        40                               45                               50

gct gtt gct ggc cga cgc atg gct gag acc att gcg cgc cgc ggt ggc 307
Ala Val Ala Gly Arg Arg Met Ala Glu Thr Ile Ala Arg Arg Gly Gly
                        55                               60                               65

atg gcg att ctt ccg cag gat gtg ccc gcc gat att gct gca gag act 355
Met Ala Ile Leu Pro Gln Asp Val Pro Ala Asp Ile Ala Ala Glu Thr
                        70                               75                               80                               85

atc gcg aat gtg aag aaa gcg gac ctg gtt ttt gat acc cca att acc 403
Ile Ala Asn Val Lys Lys Ala Asp Leu Val Phe Asp Thr Pro Ile Thr
                        90                               95                               100

gta aaa ccg cac cac acc gtg ggt tat gca cgc aac ttg atc cac aag 451
Val Lys Pro His His Thr Val Gly Tyr Ala Arg Asn Leu Ile His Lys
                        105                               110                               115

cgt gcg cac ggt gca gcc att gtt ttg gag ggc gat cag ccg gtc ggc 499
Arg Ala His Gly Ala Ala Ile Val Leu Glu Gly Asp Gln Pro Val Gly
                        120                               125                               130

atc gtc acc gac aag gac ctc gaa ggc gca gac aac ttc act cag gtg 547
Ile Val Thr Asp Lys Asp Leu Glu Gly Ala Asp Asn Phe Thr Gln Val
                        135                               140                               145

ggc acc ctc atg tcc acc tcc cta ttg acg ctg cct gag gat att tcc 595
Gly Thr Leu Met Ser Thr Ser Leu Leu Thr Leu Pro Glu Asp Ile Ser
                        150                               155                               160                               165

ccc gaa gac gcc ttc gga atc ctc cac gaa cac agc cgc aaa ctc gcc 643
Pro Glu Asp Ala Phe Gly Ile Leu His Glu His Ser Arg Lys Leu Ala
                        170                               175                               180

ccc gtc gtc gcg gct gac ggc tca ctc cgc ggc atc ctc acc cgc acc 691
Pro Val Val Ala Ala Asp Gly Ser Leu Arg Gly Ile Leu Thr Arg Thr

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185	190	195	
ggc gcc ctg cgc gcc acc atg tac aag ccg gct atc gac gcc aac ggc Gly Ala Leu Arg Ala Thr Met Tyr Lys Pro Ala Ile Asp Ala Asn Gly 200 205 210			739
cgc ctg cga gtc ggc gcc gcc atc ggc atc aac ggc gac atc gaa gga Arg Leu Arg Val Gly Ala Ala Ile Gly Ile Asn Gly Asp Ile Glu Gly 215 220 225			787
cgc acc aaa acg ctt ctc gac gcc ggc gcc gac gtt cta gtc gtc gac Arg Thr Lys Thr Leu Leu Asp Ala Gly Ala Asp Val Leu Val Val Asp 230 235 240 245			835
aca gca cac ggc cac caa tcc acc atg atc agc gcc ctc aaa cgc atc Thr Ala His Gly His Gln Ser Thr Met Ile Ser Ala Leu Lys Arg Ile 250 255 260			883
cgc gca ctc gac gtc aac gtc ccc atc gtt gct ggc aac gtg gtc acc Arg Ala Leu Asp Val Asn Val Pro Ile Val Ala Gly Asn Val Val Thr 265 270 275			931
gcc gat ggt gtc cgc gac cta gtt gaa gca ggc gca aac atc atc aag Ala Asp Gly Val Arg Asp Leu Val Glu Ala Gly Ala Asn Ile Ile Lys 280 285 290			979
gta ggc gtt gga cca ggc gca atg tgc acc acc cgc atg caa acc ggc 1027 Val Gly Val Gly Pro Gly Ala Met Cys Thr Thr Arg Met Gln Thr Gly 295 300 305			
gtt ggc cga cca cag ttc tcc gca gtg ctg gaa tgc gca gcc gaa gcc 1075 Val Gly Arg Pro Gln Phe Ser Ala Val Leu Glu Cys Ala Ala Glu Ala 310 315 320 325			
cgc aaa ctc ggc gca cac gta tgg gca gac ggc gga gtc cgc gac ccc 1123 Arg Lys Leu Gly Ala His Val Trp Ala Asp Gly Gly Val Arg Asp Pro 330 335 340			
cgc gac gtc gcc ctg gca ctc gca gct ggc gcc tcc aac gtg atg gtc 1171 Arg Asp Val Ala Leu Ala Leu Ala Ala Gly Ala Ser Asn Val Met Val 345 350 355			
gga tcc tgg ttc tcc gga acc tac gaa tcc ccc ggc gac ctc cgc ttc 1219 Gly Ser Trp Phe Ser Gly Thr Tyr Glu Ser Pro Gly Asp Leu Arg Phe 360 365 370			
gaa tcc gac gga cgc atg tac aaa gaa tcc ttc ggt atg gca tcc cgg 1267 Glu Ser Asp Gly Arg Met Tyr Lys Glu Ser Phe Gly Met Ala Ser Arg 375 380 385			
cgc gcc gtg gaa agc cga aac caa aag gtc gaa gct ttc gaa aaa gca 1315 Arg Ala Val Glu Ser Arg Asn Gln Lys Val Glu Ala Phe Glu Lys Ala 390 395 400 405			



cgc cgc gca atg ttc gaa gaa ggc atc tcc act gcc cgc atc tac att  
1363

Arg Arg Ala Met Phe Glu Glu Gly Ile Ser Thr Ala Arg Ile Tyr Ile  
410 415 420

gac aaa cgc cac ggc gga gtc gag gac ctg gta gat caa atc atc tcc  
1411

Asp Lys Arg His Gly Gly Val Glu Asp Leu Val Asp Gln Ile Ile Ser  
425 430 435

ggt gtc cgc tcc tca ttc acc tac gca ggc gcc gat tcg att gaa acc  
1459

Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala Asp Ser Ile Glu Thr  
440 445 450

ttc ttc gaa cgc gcc acc gtc gga gtt caa tcc acc gaa ggc tac gca  
1507

Phe Phe Glu Arg Ala Thr Val Gly Val Gln Ser Thr Glu Gly Tyr Ala  
455 460 465

gaa gga aag cca cgc gct tcg cgt taagtgttgt tgtgcctttg aga  
1554

Glu Gly Lys Pro Arg Ala Ser Arg  
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<210> 952

<211> 477

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 952

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Asp Val Phe Met Val Pro Ser Arg Ser Asp Val Gly Ser Arg Met Ser  
20 25 30

Val Asp Leu Arg Thr Asn Asp Gly Thr Gly Thr Thr Ile Pro Leu Val  
35 40 45

Val Ala Asn Met Thr Ala Val Ala Gly Arg Arg Met Ala Glu Thr Ile  
50 55 60

Ala Arg Arg Gly Gly Met Ala Ile Leu Pro Gln Asp Val Pro Ala Asp  
65 70 75 80

Ile Ala Ala Glu Thr Ile Ala Asn Val Lys Lys Ala Asp Leu Val Phe  
85 90 95

Asp Thr Pro Ile Thr Val Lys Pro His His Thr Val Gly Tyr Ala Arg  
100 105 110

Asn Leu Ile His Lys Arg Ala His Gly Ala Ala Ile Val Leu Glu Gly  
115 120 125

Asp Gln Pro Val Gly Ile Val Thr Asp Lys Asp Leu Glu Gly Ala Asp  
130 135 140

Asn Phe Thr Gln Val Gly Thr Leu Met Ser Thr Ser Leu Leu Thr Leu  
145 150 155 160

Pro Glu Asp Ile Ser Pro Glu Asp Ala Phe Gly Ile Leu His Glu His  
 165 170 175  
 Ser Arg Lys Leu Ala Pro Val Val Ala Ala Asp Gly Ser Leu Arg Gly  
 180 185 190  
 Ile Leu Thr Arg Thr Gly Ala Leu Arg Ala Thr Met Tyr Lys Pro Ala  
 195 200 205  
 Ile Asp Ala Asn Gly Arg Leu Arg Val Gly Ala Ala Ile Gly Ile Asn  
 210 215 220  
 Gly Asp Ile Glu Gly Arg Thr Lys Thr Leu Leu Asp Ala Gly Ala Asp  
 225 230 235 240  
 Val Leu Val Val Asp Thr Ala His Gly His Gln Ser Thr Met Ile Ser  
 245 250 255  
 Ala Leu Lys Arg Ile Arg Ala Leu Asp Val Asn Val Pro Ile Val Ala  
 260 265 270  
 Gly Asn Val Val Thr Ala Asp Gly Val Arg Asp Leu Val Glu Ala Gly  
 275 280 285  
 Ala Asn Ile Ile Lys Val Gly Val Gly Pro Gly Ala Met Cys Thr Thr  
 290 295 300  
 Arg Met Gln Thr Gly Val Gly Arg Pro Gln Phe Ser Ala Val Leu Glu  
 305 310 315 320  
 Cys Ala Ala Glu Ala Arg Lys Leu Gly Ala His Val Trp Ala Asp Gly  
 325 330 335  
 Gly Val Arg Asp Pro Arg Asp Val Ala Leu Ala Leu Ala Ala Gly Ala  
 340 345 350  
 Ser Asn Val Met Val Gly Ser Trp Phe Ser Gly Thr Tyr Glu Ser Pro  
 355 360 365  
 Gly Asp Leu Arg Phe Glu Ser Asp Gly Arg Met Tyr Lys Glu Ser Phe  
 370 375 380  
 Gly Met Ala Ser Arg Arg Ala Val Glu Ser Arg Asn Gln Lys Val Glu  
 385 390 395 400  
 Ala Phe Glu Lys Ala Arg Arg Ala Met Phe Glu Glu Gly Ile Ser Thr  
 405 410 415  
 Ala Arg Ile Tyr Ile Asp Lys Arg His Gly Gly Val Glu Asp Leu Val  
 420 425 430  
 Asp Gln Ile Ile Ser Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala  
 435 440 445  
 Asp Ser Ile Glu Thr Phe Phe Glu Arg Ala Thr Val Gly Val Gln Ser  
 450 455 460  
 Thr Glu Gly Tyr Ala Glu Gly Lys Pro Arg Ala Ser Arg  
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<210> 953  
 <211> 1692  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1669)  
 <223> RXN00487

<400> 953

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                                   Val Ser Leu Gln Thr
                                   1                               5

aat cat cgc cca gta ctc gtc gtt gac ttc ggc gca cag tac gcg cag      163
Asn His Arg Pro Val Leu Val Val Asp Phe Gly Ala Gln Tyr Ala Gln
                                   10                               15                               20

ctg atc gca cgt cgt gtg cgt gag gcc ggc atc tac tcc gaa gtc atc      211
Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile Tyr Ser Glu Val Ile
                                   25                               30                               35

ccg cac acc gcc acc gca gac gat gtg cgc gct aaa aat gca gca gcc      259
Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala Lys Asn Ala Ala Ala
                                   40                               45                               50

ctc gtc ctt tcc ggt ggc cca tcc tcc gtg tat gcc gag gga gca cca      307
Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr Ala Glu Gly Ala Pro
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tcc ctt gac gct gag att ctt gat ctc gga ttg cca gta ttt ggc att      355
Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu Pro Val Phe Gly Ile
                                   70                               75                               80                               85

tgc tac ggc ttc caa gcc atg acc cac gcg ctt ggt ggc acc gtt gcc      403
Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu Gly Gly Thr Val Ala
                                   90                               95                               100

aac acc ggt aag cgc gaa tac gga cgc acc gac atc aac gtt gcc ggt      451
Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp Ile Asn Val Ala Gly
                                   105                               110                               115

ggc gtc ctc cac gaa ggc ctc gaa gcc tgc cac aag gtg tgg atg agc      499
Gly Val Leu His Glu Gly Leu Glu Ala Cys His Lys Val Trp Met Ser
                                   120                               125                               130

cac ggc gac gcc gtc tct gaa gcc cca gaa ggt ttc gta gtc acc gcg      547
His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly Phe Val Val Thr Ala
                                   135                               140                               145

tcc tcc gaa ggt gcg cct gtc gca gct ttc gaa aac aag gaa cgc aaa      595
Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu Asn Lys Glu Arg Lys
                                   150                               155                               160                               165

atg gct ggc gtg cag tac cac cca gag gta ttg cac tca cca cac ggc      643
Met Ala Gly Val Gln Tyr His Pro Glu Val Leu His Ser Pro His Gly
                                   170                               175                               180

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cag gca gtt ctg acc cgc ttc ctc act gag atc gca ggt cta gag cag 691  
 Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln  
 185 190 195

aac tgg acc gca gca aac atc gct gaa gaa ctc atc gaa aag gtc cgc 739  
 Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu Ile Glu Lys Val Arg  
 200 205 210

gag cag atc ggc gaa gat ggc cgc gct att tgt ggc cta tcc ggt ggt 787  
 Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys Gly Leu Ser Gly Gly  
 215 220 225

gtg gac tcc gct gtt gcc ggt gct ttg gtg cag cgc gcc att ggt gac 835  
 Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln Arg Ala Ile Gly Asp  
 230 235 240 245

cgt ttg acc tgt gtc ttt gtt gac cac ggt ctg ctg cgt gcc ggt gag 883  
 Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu  
 250 255 260

cgc gag cag gtg gaa aaa gac ttc gtc gca gca acc ggc gcc aag ctg 931  
 Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala Thr Gly Ala Lys Leu  
 265 270 275

gtt acc gtt gat gag cgc cag gca ttc cta tcc aag ctg gcc gga gtt 979  
 Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val  
 280 285 290

acc gaa cca gaa gca aag cgc aag gct atc ggc gct gag ttc atc cgc  
 1027  
 Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly Ala Glu Phe Ile Arg  
 295 300 305

tcc ttc gag cgc gca gtt gcc ggt gtg ctg gaa gaa gct cca gaa ggt  
 1075  
 Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly  
 310 315 320 325

tcc acc gtg gac ttc ctg gtt cag ggc acc ctg tac cca gac gtc gtg  
 1123  
 Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val  
 330 335 340

gaa tcc ggt ggt gga tct ggt acc gca aac atc aag agc cac cac aac  
 1171  
 Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn  
 345 350 355

gtc ggt gga ctg cca gac gat gtg gaa ttc aag ctt gtt gag cca ctg  
 1219  
 Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu  
 360 365 370

cgt gac ctc ttc aaa gac gaa gtc cgt gcc gtt ggc cgt gaa ctt ggc  
 1267  
 Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly  
 375 380 385

ctg cct gag gaa atc gtt ggc cgc cag cca ttc cca gga cca gga ctt  
 1315

Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe Pro Gly Pro Gly Leu  
 390 395 400 405

ggt atc cgc atc atc ggt gaa gtc acc gaa gat cgc cta gaa acc ctc  
 1363

Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp Arg Leu Glu Thr Leu  
 410 415 420

cgc cac gct gac ctg atc gcc cgc acc gag ctc acc gaa gcc gga ctt  
 1411

Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu Thr Glu Ala Gly Leu  
 425 430 435

gac ggc gtg atc tgg cag tgc cca gta gtc ctc ctg gca gat gtc cgc  
 1459

Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg  
 440 445 450

tct gtt ggt gtt caa ggc gat ggc cgc acc tac gga cac cca atc gtg  
 1507

Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr Gly His Pro Ile Val  
 455 460 465

ctg cgc cca gtg tct tcc gaa gac gca atg acc gcc gac tgg acc cgc  
 1555

Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr Ala Asp Trp Thr Arg  
 470 475 480 485

ctg cca tac gag gtt ctg gag aag atc tcc acc cgc atc acc aac gaa  
 1603

Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr Arg Ile Thr Asn Glu  
 490 495 500

gtt cca gat gtg aac cgc gtg gtg ctg gac gta acc tcc aag cca cca  
 1651

Val Pro Asp Val Asn Arg Val Val Leu Asp Val Thr Ser Lys Pro Pro  
 505 510 515

gga acc atc gaa tgg gag taggccttaa atgagccttc gtt  
 1692

Gly Thr Ile Glu Trp Glu  
 520

<210> 954

<211> 523

<212> PRT

<213> Corynebacterium glutamicum

<400> 954

Val Ser Leu Gln Thr Asn His Arg Pro Val Leu Val Val Asp Phe Gly  
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Ala Gln Tyr Ala Gln Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile  
 20 25 30

Tyr Ser Glu Val Ile Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala  
 35 40 45

Lys Asn Ala Ala Ala Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr  
 50 55 60

Ala Glu Gly Ala Pro Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu  
 65 70 75 80  
 Pro Val Phe Gly Ile Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu  
 85 90 95  
 Gly Gly Thr Val Ala Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp  
 100 105 110  
 Ile Asn Val Ala Gly Gly Val Leu His Glu Gly Leu Glu Ala Cys His  
 115 120 125  
 Lys Val Trp Met Ser His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly  
 130 135 140  
 Phe Val Val Thr Ala Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu  
 145 150 155 160  
 Asn Lys Glu Arg Lys Met Ala Gly Val Gln Tyr His Pro Glu Val Leu  
 165 170 175  
 His Ser Pro His Gly Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile  
 180 185 190  
 Ala Gly Leu Glu Gln Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu  
 195 200 205  
 Ile Glu Lys Val Arg Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys  
 210 215 220  
 Gly Leu Ser Gly Gly Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln  
 225 230 235 240  
 Arg Ala Ile Gly Asp Arg Leu Thr Cys Val Phe Val Asp His Gly Leu  
 245 250 255  
 Leu Arg Ala Gly Glu Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala  
 260 265 270  
 Thr Gly Ala Lys Leu Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser  
 275 280 285  
 Lys Leu Ala Gly Val Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly  
 290 295 300  
 Ala Glu Phe Ile Arg Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu  
 305 310 315 320  
 Glu Ala Pro Glu Gly Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu  
 325 330 335  
 Tyr Pro Asp Val Val Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile  
 340 345 350  
 Lys Ser His His Asn Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys  
 355 360 365  
 Leu Val Glu Pro Leu Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val  
 370 375 380

Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe  
385 390 395 400

Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp  
405 410 415

Arg Leu Glu Thr Leu Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu  
420 425 430

Thr Glu Ala Gly Leu Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu  
435 440 445

Leu Ala Asp Val Arg Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr  
450 455 460

Gly His Pro Ile Val Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr  
465 470 475 480

Ala Asp Trp Thr Arg Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr  
485 490 495

Arg Ile Thr Asn Glu Val Pro Asp Val Asn Arg Val Val Leu Asp Val  
500 505 510

Thr Ser Lys Pro Pro Gly Thr Ile Glu Trp Glu  
515 520

<210> 955

<211> 1486

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1486)

<223> FRXA00487

<400> 955

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agaatcttat ttggaggctc gtctagtaga gtgagttctt gtg agc ctt cag aca 115  
Val Ser Leu Gln Thr  
1 5

aat cat cgc cca gta ctc gtc gtt gac ttc ggc gca cag tac gcg cag 163  
Asn His Arg Pro Val Leu Val Val Asp Phe Gly Ala Gln Tyr Ala Gln  
10 15 20

ctg atc gca cgt cgt gtg cgt gag gcc ggc atc tac tcc gaa gtc atc 211  
Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile Tyr Ser Glu Val Ile  
25 30 35

ccg cac acc gcc acc gca gac gat gtg cgc gct aaa aat gca gca gcc 259  
Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala Lys Asn Ala Ala Ala  
40 45 50

ctc gtc ctt tcc ggt ggc cca tcc tcc gtg tat gcc gag gga gca cca 307  
Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr Ala Glu Gly Ala Pro  
55 60 65

tcc ctt gac gct gag att ctt gat ctc gga ttg cca gta ttt ggc att	355
Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu Pro Val Phe Gly Ile	
70 75 80 85	
tgc tac ggc ttc caa gcc atg acc cac gcg ctt ggt ggc acc gtt gcc	403
Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu Gly Gly Thr Val Ala	
90 95 100	
aac acc ggt aag cgc gaa tac gga cgc acc gac atc aac gtt gcc ggt	451
Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp Ile Asn Val Ala Gly	
105 110 115	
ggc gtc ctc cac gaa ggc ctc gaa gcc tgc cac aag gtg tgg atg agc	499
Gly Val Leu His Glu Gly Leu Glu Ala Cys His Lys Val Trp Met Ser	
120 125 130	
cac ggc gac gcc gtc tct gaa gcc cca gaa ggt ttc gta gtc acc gcg	547
His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly Phe Val Val Thr Ala	
135 140 145	
tcc tcc gaa ggt gcg cct gtc gca gct ttc gaa aac aag gaa cgc aaa	595
Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu Asn Lys Glu Arg Lys	
150 155 160 165	
atg gct ggc gtg cag tac cac cca gag gta ttg cac tca cca cac ggc	643
Met Ala Gly Val Gln Tyr His Pro Glu Val Leu His Ser Pro His Gly	
170 175 180	
cag gca gtt ctg acc cgc ttc ctc act gag atc gca ggt cta gag cag	691
Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln	
185 190 195	
aac tgg acc gca gca aac atc gct gaa gaa ctc atc gaa aag gtc cgc	739
Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu Ile Glu Lys Val Arg	
200 205 210	
gag cag atc ggc gaa gat ggc cgc gct att tgt ggc cta tcc ggt ggt	787
Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys Gly Leu Ser Gly Gly	
215 220 225	
gtg gac tcc gct gtt gcc ggt gct ttg gtg cag cgc gcc att ggt gac	835
Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln Arg Ala Ile Gly Asp	
230 235 240 245	
cgt ttg acc tgt gtc ttt gtt gac cac ggt ctg ctg cgt gcc ggt gag	883
Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu	
250 255 260	
cgc gag cag gtg gaa aaa gac ttc gtc gca gca acc ggc gcc aag ctg	931
Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala Thr Gly Ala Lys Leu	
265 270 275	
gtt acc gtt gat gag cgc cag gca ttc cta tcc aag ctg gcc gga gtt	979
Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val	
280 285 290	
acc gaa cca gaa gca aag cgc aag gct atc ggc gct gag ttc atc cgc	
1027	
Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly Ala Glu Phe Ile Arg	
295 300 305	



tcc ttc gag cgc gca gtt gcc ggt gtg ctg gaa gaa gct cca gaa ggt  
1075

Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly  
310 315 320 325

tcc acc gtg gac ttc ctg gtt cag ggc acc ctg tac cca gac gtc gtg  
1123

Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val  
330 335 340

gaa tcc ggt ggt gga tct ggt acc gca aac atc aag agc cac cac aac  
1171

Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn  
345 350 355

gtc ggt gga ctg cca gac gat gtg gaa ttc aag ctt gtt gag cca ctg  
1219

Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu  
360 365 370

cgt gac ctc ttc aaa gac gaa gtc cgt gcc gtt ggc cgt gaa ctt ggc  
1267

Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly  
375 380 385

ctg cct gag gaa atc gtt ggc cgc cag cca ttc cca gga cca gga ctt  
1315

Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe Pro Gly Pro Gly Leu  
390 395 400 405

ggt atc cgc atc atc ggt gaa gtc acc gaa gat cgc cta gaa acc ctc  
1363

Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp Arg Leu Glu Thr Leu  
410 415 420

cgc cac gct gac ctg atc gcc cgc acc gag ctc acc gaa gcc gga ctt  
1411

Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu Thr Glu Ala Gly Leu  
425 430 435

gac ggc gtg atc tgg cag tgc cca gta gtc ctc ctg gca gat gtc cgc  
1459

Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg  
440 445 450

tct gtt ggt gtt caa ggc gat ggc cgc  
1486

Ser Val Gly Val Gln Gly Asp Gly Arg  
455 460

<210> 956

<211> 462

<212> PRT

<213> Corynebacterium glutamicum

<400> 956

Val Ser Leu Gln Thr Asn His Arg Pro Val Leu Val Val Asp Phe Gly  
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Ala Gln Tyr Ala Gln Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile

20					25					30					
Tyr	Ser	Glu	Val	Ile	Pro	His	Thr	Ala	Thr	Ala	Asp	Asp	Val	Arg	Ala
		35					40					45			
Lys	Asn	Ala	Ala	Ala	Leu	Val	Leu	Ser	Gly	Gly	Pro	Ser	Ser	Val	Tyr
		50					55					60			
Ala	Glu	Gly	Ala	Pro	Ser	Leu	Asp	Ala	Glu	Ile	Leu	Asp	Leu	Gly	Leu
		65					70					75			80
Pro	Val	Phe	Gly	Ile	Cys	Tyr	Gly	Phe	Gln	Ala	Met	Thr	His	Ala	Leu
				85					90					95	
Gly	Gly	Thr	Val	Ala	Asn	Thr	Gly	Lys	Arg	Glu	Tyr	Gly	Arg	Thr	Asp
			100					105					110		
Ile	Asn	Val	Ala	Gly	Gly	Val	Leu	His	Glu	Gly	Leu	Glu	Ala	Cys	His
		115					120					125			
Lys	Val	Trp	Met	Ser	His	Gly	Asp	Ala	Val	Ser	Glu	Ala	Pro	Glu	Gly
		130					135					140			
Phe	Val	Val	Thr	Ala	Ser	Ser	Glu	Gly	Ala	Pro	Val	Ala	Ala	Phe	Glu
		145					150					155			160
Asn	Lys	Glu	Arg	Lys	Met	Ala	Gly	Val	Gln	Tyr	His	Pro	Glu	Val	Leu
				165					170					175	
His	Ser	Pro	His	Gly	Gln	Ala	Val	Leu	Thr	Arg	Phe	Leu	Thr	Glu	Ile
			180					185					190		
Ala	Gly	Leu	Glu	Gln	Asn	Trp	Thr	Ala	Ala	Asn	Ile	Ala	Glu	Glu	Leu
		195					200					205			
Ile	Glu	Lys	Val	Arg	Glu	Gln	Ile	Gly	Glu	Asp	Gly	Arg	Ala	Ile	Cys
		210					215					220			
Gly	Leu	Ser	Gly	Gly	Val	Asp	Ser	Ala	Val	Ala	Gly	Ala	Leu	Val	Gln
		225					230					235			240
Arg	Ala	Ile	Gly	Asp	Arg	Leu	Thr	Cys	Val	Phe	Val	Asp	His	Gly	Leu
				245				250						255	
Leu	Arg	Ala	Gly	Glu	Arg	Glu	Gln	Val	Glu	Lys	Asp	Phe	Val	Ala	Ala
			260					265						270	
Thr	Gly	Ala	Lys	Leu	Val	Thr	Val	Asp	Glu	Arg	Gln	Ala	Phe	Leu	Ser
			275				280					285			
Lys	Leu	Ala	Gly	Val	Thr	Glu	Pro	Glu	Ala	Lys	Arg	Lys	Ala	Ile	Gly
		290					295					300			
Ala	Glu	Phe	Ile	Arg	Ser	Phe	Glu	Arg	Ala	Val	Ala	Gly	Val	Leu	Glu
		305					310					315			320
Glu	Ala	Pro	Glu	Gly	Ser	Thr	Val	Asp	Phe	Leu	Val	Gln	Gly	Thr	Leu
				325					330					335	
Tyr	Pro	Asp	Val	Val	Glu	Ser	Gly	Gly	Gly	Ser	Gly	Thr	Ala	Asn	Ile
			340					345						350	

Lys Ser His His Asn Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys  
 355 360 365  
 Leu Val Glu Pro Leu Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val  
 370 375 380  
 Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe  
 385 390 395 400  
 Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp  
 405 410 415  
 Arg Leu Glu Thr Leu Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu  
 420 425 430  
 Thr Glu Ala Gly Leu Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu  
 435 440 445  
 Leu Ala Asp Val Arg Ser Val Gly Val Gln Gly Asp Gly Arg  
 450 455 460

<210> 957  
 <211> 693  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(670)  
 <223> RXA02237

<400> 957  
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 gcacttctcg agcgtttcgg cttcgaggat taattcttca gtg tcg ggc gat aac 115  
 Val Ser Gly Asp Asn 5  
 1  
 caa cta gga cgg ctc gta att ctt gcg ggc ccc tca gcg gtc ggt aaa 163  
 Gln Leu Gly Arg Leu Val Ile Leu Ala Gly Pro Ser Ala Val Gly Lys 20  
 10 15  
 tcg act gtg gtt gat cgc ctc cgc aat gac gtt cca aac ctg tat ttc 211  
 Ser Thr Val Val Asp Arg Leu Arg Asn Asp Val Pro Asn Leu Tyr Phe 35  
 25 30  
 agt gtg tcg atg acc act agg gca cct cgt cct ggt gaa gtc gat gga 259  
 Ser Val Ser Met Thr Thr Arg Ala Pro Arg Pro Gly Glu Val Asp Gly 50  
 40 45  
 cgt gac tac ttc tat gtc act gca cag gaa ttt cag gac aaa atc gac 307  
 Arg Asp Tyr Phe Tyr Val Thr Ala Gln Glu Phe Gln Asp Lys Ile Asp 65  
 55 60  
 tgt gga gag atg ctt gaa tgg gca gat atc cac ggc ggt ttg cag cgt 355  
 Cys Gly Glu Met Leu Glu Trp Ala Asp Ile His Gly Gly Leu Gln Arg 85  
 70 75 80  
 tca ggc act cca gca ggt ccc gtc aat gag gct cgc caa aat ggt cgg 403

Ser Gly Thr Pro Ala Gly Pro Val Asn Glu Ala Arg Gln Asn Gly Arg  
 90 95 100  
 cca gta ttg gtt gag gtt gat ctt gca gga gcc cga aac atc gct agc 451  
 Pro Val Leu Val Glu Val Asp Leu Ala Gly Ala Arg Asn Ile Ala Ser  
 105 110 115  
 tta att cca gat gca gaa acc atc ttc ctt gct cca cct tca tgg gaa 499  
 Leu Ile Pro Asp Ala Glu Thr Ile Phe Leu Ala Pro Pro Ser Trp Glu  
 120 125 130  
 gtt ttg gtt gaa cgc ctc act gga cgt ggc acc gaa agc gaa gac gtt 547  
 Val Leu Val Glu Arg Leu Thr Gly Arg Gly Thr Glu Ser Glu Asp Val  
 135 140 145  
 att gct cgc agg ctc gag acc gca cgc gaa gaa ttg gct gct cag agc 595  
 Ile Ala Arg Arg Leu Glu Thr Ala Arg Glu Glu Leu Ala Ala Gln Ser  
 150 155 160 165  
 gaa ttt aag cac gtc att atc aat gat gat gtg gat aca gcc gtc aag 643  
 Glu Phe Lys His Val Ile Ile Asn Asp Asp Val Asp Thr Ala Val Lys  
 170 175 180  
 gct att gag gat gtt ctc ctc ggc gct tagccaaaac atagagcggg 690  
 Ala Ile Glu Asp Val Leu Leu Gly Ala  
 185 190  
 agg 693  
  
 <210> 958  
 <211> 190  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 958  
 Val Ser Gly Asp Asn Gln Leu Gly Arg Leu Val Ile Leu Ala Gly Pro  
 1 5 10 15  
 Ser Ala Val Gly Lys Ser Thr Val Val Asp Arg Leu Arg Asn Asp Val  
 20 25 30  
 Pro Asn Leu Tyr Phe Ser Val Ser Met Thr Thr Arg Ala Pro Arg Pro  
 35 40 45  
 Gly Glu Val Asp Gly Arg Asp Tyr Phe Tyr Val Thr Ala Gln Glu Phe  
 50 55 60  
 Gln Asp Lys Ile Asp Cys Gly Glu Met Leu Glu Trp Ala Asp Ile His  
 65 70 75 80  
 Gly Gly Leu Gln Arg Ser Gly Thr Pro Ala Gly Pro Val Asn Glu Ala  
 85 90 95  
 Arg Gln Asn Gly Arg Pro Val Leu Val Glu Val Asp Leu Ala Gly Ala  
 100 105 110  
 Arg Asn Ile Ala Ser Leu Ile Pro Asp Ala Glu Thr Ile Phe Leu Ala  
 115 120 125  
 Pro Pro Ser Trp Glu Val Leu Val Glu Arg Leu Thr Gly Arg Gly Thr

130	135	140
Glu Ser Glu Asp Val 145	Ile Ala Arg Arg Leu 150	Glu Thr Ala Arg Glu Glu 155 160
Leu Ala Ala Gln Ser 165	Glu Phe Lys His Val 170	Ile Ile Asn Asp Asp Val 175
Asp Thr Ala Val Lys 180	Ala Ile Glu Asp Val 185	Leu Leu Gly Ala 190
<p>&lt;210&gt; 959</p> <p>&lt;211&gt; 1413</p> <p>&lt;212&gt; DNA</p> <p>&lt;213&gt; Corynebacterium glutamicum</p>		
<p>&lt;220&gt;</p> <p>&lt;221&gt; CDS</p> <p>&lt;222&gt; (101)..(1390)</p> <p>&lt;223&gt; RXA01446</p>		
<p>&lt;400&gt; 959</p> <p>gatgattaaa aacctcacat gggatagtaa gatgaaataa cgtctgtgtg cgcacacgcg 60</p> <p>tgcataactcc aacttcatgg atcggatgtg acgtaaacca atg gct gca atc gtt 115</p> <p>Met Ala Ala Ile Val 5</p> <p>1</p> <p>att gtc ggc gct caa tgg ggc gat gaa ggc aaa ggt aag gcc acg gat 163</p> <p>Ile Val Gly Ala Gln Trp Gly Asp Glu Gly Lys Gly Lys Ala Thr Asp 20</p> <p>10 15</p> <p>att ctc ggc gga ctc gtc gat tac gtg gtt aag ccc aat ggc ggt aac 211</p> <p>Ile Leu Gly Gly Leu Val Asp Tyr Val Val Lys Pro Asn Gly Gly Asn 35</p> <p>25 30</p> <p>aac gct gga cac act gtt gtg gtc ggc ggc gag aag tac gag cta aag 259</p> <p>Asn Ala Gly His Thr Val Val Val Gly Gly Glu Lys Tyr Glu Leu Lys 50</p> <p>40 45</p> <p>ctc ctt cct gcc ggc gtc ctc tcc gaa acg gcc acc cca att ttg ggc 307</p> <p>Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala Thr Pro Ile Leu Gly 65</p> <p>55 60</p> <p>aac ggc gtt gtg atc aac ctt gag gca ctg ttc gaa gaa atc gac ggc 355</p> <p>Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe Glu Glu Ile Asp Gly 85</p> <p>70 75 80</p> <p>ctt gag gct cgc ggt gcg gat gca tcc cgc ctg cgc atc tct gca aac 403</p> <p>Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu Arg Ile Ser Ala Asn 100</p> <p>90 95</p> <p>gct cac ctg gtt gct cca tac cac cag gtg atg gac cgt gtt cag gaa 451</p> <p>Ala His Leu Val Ala Pro Tyr His Gln Val Met Asp Arg Val Gln Glu 115</p> <p>105 110</p> <p>cgc ttc ctg ggc aag cgc gca atc ggc acc acc ggc cgt ggc atc ggc 499</p> <p>Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr Gly Arg Gly Ile Gly 130</p> <p>120 125</p>		

cca acc tac gcg gac aaa gta tcc cgc gtg gga atc cgt gtt caa gac 547  
 Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly Ile Arg Val Gln Asp  
 135 140 145

att ttc gac gaa tcc atc ctt cgt caa aaa gtc gaa tcc gcc ctg gat 595  
 Ile Phe Asp Glu Ser Ile Leu Arg Gln Lys Val Glu Ser Ala Leu Asp  
 150 155 160 165

tac aaa aac cag gtg ctg gtg aag atg tac aac cgc aag gcc atc gtc 643  
 Tyr Lys Asn Gln Val Leu Val Lys Met Tyr Asn Arg Lys Ala Ile Val  
 170 175 180

gct gag gaa atc gtg cag tac ttc ctc tcc tac gct gat cgt ctg cgc 691  
 Ala Glu Glu Ile Val Gln Tyr Phe Leu Ser Tyr Ala Asp Arg Leu Arg  
 185 190 195

ccc atg gtc atc gat gcc acc ttg gtg ctc aac gag gca ctt gat cag 739  
 Pro Met Val Ile Asp Ala Thr Leu Val Leu Asn Glu Ala Leu Asp Gln  
 200 205 210

ggc aag cac gtt ctt atg gaa ggt ggc cag gca acc atg ctc gac gtg 787  
 Gly Lys His Val Leu Met Glu Gly Gly Gln Ala Thr Met Leu Asp Val  
 215 220 225

gac cac ggc acc tac cca ttc gtc acc tcc tcc aac cca acc gcc ggt 835  
 Asp His Gly Thr Tyr Pro Phe Val Thr Ser Ser Asn Pro Thr Ala Gly  
 230 235 240 245

ggc gca agt gtt ggt tca ggt atc ggc cca acc aag atc acc agc tcc 883  
 Gly Ala Ser Val Gly Ser Gly Ile Gly Pro Thr Lys Ile Thr Ser Ser  
 250 255 260

ttg ggt atc atc aag gcc tac acc act cgt gtt ggt gcc ggc cca ttc 931  
 Leu Gly Ile Ile Lys Ala Tyr Thr Thr Arg Val Gly Ala Gly Pro Phe  
 265 270 275

cca act gag ctg ttt gat aag tgg ggc gag tac ctg cag acc gtc ggt 979  
 Pro Thr Glu Leu Phe Asp Lys Trp Gly Glu Tyr Leu Gln Thr Val Gly  
 280 285 290

ggc gag gtc ggc gtg aac acc ggc cgt aag cgt cgc tgt ggc tgg tac  
 1027  
 Gly Glu Val Gly Val Asn Thr Gly Arg Lys Arg Arg Cys Gly Trp Tyr  
 295 300 305

gac tcc gtg att gct cgt tac gca tcc cgc gtc aac gga ttc acc gac  
 1075  
 Asp Ser Val Ile Ala Arg Tyr Ala Ser Arg Val Asn Gly Phe Thr Asp  
 310 315 320 325

tac ttc ctg acc aag cta gac gtg ctc acc ggc atc ggt gaa atc cca  
 1123  
 Tyr Phe Leu Thr Lys Leu Asp Val Leu Thr Gly Ile Gly Glu Ile Pro  
 330 335 340

atc tgc gta gct tac gac gtt gat ggt gtt cgc cac gat gaa atg cca  
 1171  
 Ile Cys Val Ala Tyr Asp Val Asp Gly Val Arg His Asp Glu Met Pro  
 345 350 355

ctg acc cag tca gag ttc cac cac gca acc cca atc ttt gaa acc atg  
1219

Leu Thr Gln Ser Glu Phe His His Ala Thr Pro Ile Phe Glu Thr Met  
360 365 370

cct gca tgg gac gaa gac atc acc gac tgc aag acc ttc gag gat ctt  
1267

Pro Ala Trp Asp Glu Asp Ile Thr Asp Cys Lys Thr Phe Glu Asp Leu  
375 380 385

cca caa aag gcc cag gac tac gtc cga cgt ctg gaa gaa ctc tct ggt  
1315

Pro Gln Lys Ala Gln Asp Tyr Val Arg Arg Leu Glu Glu Leu Ser Gly  
390 395 400 405

gct cgc ttc tcc tac atc ggt gtt gga cct ggt cgc gat cag acc atc  
1363

Ala Arg Phe Ser Tyr Ile Gly Val Gly Pro Gly Arg Asp Gln Thr Ile  
410 415 420

gtc ctg cat gac gta cta gct gac aac tagtactgat aaacatcagt  
1410

Val Leu His Asp Val Leu Ala Asp Asn  
425 430

gag  
1413

<210> 960

<211> 430

<212> PRT

<213> Corynebacterium glutamicum

<400> 960

Met Ala Ala Ile Val Ile Val Gly Ala Gln Trp Gly Asp Glu Gly Lys  
1 5 10 15

Gly Lys Ala Thr Asp Ile Leu Gly Gly Leu Val Asp Tyr Val Val Lys  
20 25 30

Pro Asn Gly Gly Asn Asn Ala Gly His Thr Val Val Val Gly Gly Glu  
35 40 45

Lys Tyr Glu Leu Lys Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala  
50 55 60

Thr Pro Ile Leu Gly Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe  
65 70 75 80

Glu Glu Ile Asp Gly Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu  
85 90 95

Arg Ile Ser Ala Asn Ala His Leu Val Ala Pro Tyr His Gln Val Met  
100 105 110

Asp Arg Val Gln Glu Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr  
115 120 125

Gly Arg Gly Ile Gly Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly  
130 135 140

Ile Arg Val Gln Asp Ile Phe Asp Glu Ser Ile Leu Arg Gln Lys Val  
 145 150 155 160  
 Glu Ser Ala Leu Asp Tyr Lys Asn Gln Val Leu Val Lys Met Tyr Asn  
 165 170 175  
 Arg Lys Ala Ile Val Ala Glu Glu Ile Val Gln Tyr Phe Leu Ser Tyr  
 180 185 190  
 Ala Asp Arg Leu Arg Pro Met Val Ile Asp Ala Thr Leu Val Leu Asn  
 195 200 205  
 Glu Ala Leu Asp Gln Gly Lys His Val Leu Met Glu Gly Gly Gln Ala  
 210 215 220  
 Thr Met Leu Asp Val Asp His Gly Thr Tyr Pro Phe Val Thr Ser Ser  
 225 230 235 240  
 Asn Pro Thr Ala Gly Gly Ala Ser Val Gly Ser Gly Ile Gly Pro Thr  
 245 250 255  
 Lys Ile Thr Ser Ser Leu Gly Ile Ile Lys Ala Tyr Thr Thr Arg Val  
 260 265 270  
 Gly Ala Gly Pro Phe Pro Thr Glu Leu Phe Asp Lys Trp Gly Glu Tyr  
 275 280 285  
 Leu Gln Thr Val Gly Gly Glu Val Gly Val Asn Thr Gly Arg Lys Arg  
 290 295 300  
 Arg Cys Gly Trp Tyr Asp Ser Val Ile Ala Arg Tyr Ala Ser Arg Val  
 305 310 315 320  
 Asn Gly Phe Thr Asp Tyr Phe Leu Thr Lys Leu Asp Val Leu Thr Gly  
 325 330 335  
 Ile Gly Glu Ile Pro Ile Cys Val Ala Tyr Asp Val Asp Gly Val Arg  
 340 345 350  
 His Asp Glu Met Pro Leu Thr Gln Ser Glu Phe His His Ala Thr Pro  
 355 360 365  
 Ile Phe Glu Thr Met Pro Ala Trp Asp Glu Asp Ile Thr Asp Cys Lys  
 370 375 380  
 Thr Phe Glu Asp Leu Pro Gln Lys Ala Gln Asp Tyr Val Arg Arg Leu  
 385 390 395 400  
 Glu Glu Leu Ser Gly Ala Arg Phe Ser Tyr Ile Gly Val Gly Pro Gly  
 405 410 415  
 Arg Asp Gln Thr Ile Val Leu His Asp Val Leu Ala Asp Asn  
 420 425 430

&lt;210&gt; 961

&lt;211&gt; 1551

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1528)

&lt;223&gt; RXA00619

&lt;400&gt; 961

tcaaaggaag acaccattga aggtgtgctgc aaaatcggag aattcatcaa aaaatagcag 60

cgactagggtt agtttcggtt cgtggggaat aataatttgc gtg gct gat aaa aag 115  
Val Ala Asp Lys Lys  
1 5

aag atc gca aac gtc ctg tcg aac cgt tac gcc tcc gcg gaa ctt tct 163  
Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala Ser Ala Glu Leu Ser  
10 15 20

aac ctg tgg agt gcc gaa gag aag atc atc atg gag cgc cag ctc tgg 211  
Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp  
25 30 35

atc gcc gtg atg aaa gcc cag aaa gat ttg gga gtt gag atc cct gcc 259  
Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly Val Glu Ile Pro Ala  
40 45 50

gag gca att gaa tcc tat gaa gca gtg atc gac cag gtt gat ttg gca 307  
Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp Gln Val Asp Leu Ala  
55 60 65

agc atc gcc gat cgt gag cgc gtc acc cgc cac gat gtg aag gcc cgc 355  
Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His Asp Val Lys Ala Arg  
70 75 80 85

atc gaa gaa ttc aat gca ctg gct ggc cat gag cac atc cac aag ggc 403  
Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu His Ile His Lys Gly  
90 95 100

atg acc tcc cgc gac ctc acc gaa aat gtt gaa cag ctg cag atc cac 451  
Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu Gln Leu Gln Ile His  
105 110 115

cgc tcc ctt gag ctg gtc cgc aac aag ggc att gca gtt gtt gca gct 499  
Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile Ala Val Val Ala Ala  
120 125 130

atc gga tcc cgc gca gcg cag tac caa agc ctg gtc atg gct ggc cgt 547  
Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu Val Met Ala Gly Arg  
135 140 145

tcc cac aac gtg gca gcg cag gca act acc ttg ggc aag cgt ttc gca 595  
Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu Gly Lys Arg Phe Ala  
150 155 160 165

acc gca gct gat gaa atg ctc gtg gca ctt gag cgc gtc acc gaa ctg 643  
Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu Arg Val Thr Glu Leu  
170 175 180

ctc aac cgc tac cca ctt cgc gga atc aag ggc cca atg gga acc gcc 691  
Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly Pro Met Gly Thr Ala  
185 190 195

caa gac atg ctt gac ctc atg gaa ggc gac gag gct cgt ctc tcc gat 739

Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu Ala Arg Leu Ser Asp  
 200 205 210  
 ctg gaa acc cgc atc gca gca cac ctc ggc ttt gat cgc gtc ttc gac 787  
 Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe Asp Arg Val Phe Asp  
 215 220 225  
 tcc gtc ggc cag gtc tac cca cgt tcc ctt gac ttc gat gca gta tct 835  
 Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp Phe Asp Ala Val Ser  
 230 235 240 245  
 gct ctg gtt cag ctt ggc tcc ggc cca tca tcg ctg tcc cac acc att 883  
 Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser Leu Ser His Thr Ile  
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 Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu Gly Phe Lys Glu Gly  
 265 270 275  
 cag gtc ggt tcc tct gca atg cct cac aag atg aac gct cgc tcc tgt 979  
 Gln Val Gly Ser Ser Ala Met Pro His Lys Met Asn Ala Arg Ser Cys  
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 Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg Gly Tyr Leu Thr Met  
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 310 315 320 325  
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 Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala Phe Phe Ala Ile Asp  
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 1171  
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 345 350 355  
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 1219  
 Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr Leu Pro Phe Leu Ala  
 360 365 370  
 act acc cgt atc ctc atg gcc gct gtc cgc gca ggc gtt ggc cgc gaa  
 1267  
 Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala Gly Val Gly Arg Glu  
 375 380 385  
 acc gca cac gaa gta atc aag gaa aac gct gtc gcg gtt gcc ctc aac  
 1315  
 Thr Ala His Glu Val Ile Lys Glu Asn Ala Val Ala Val Ala Leu Asn  
 390 395 400 405  
 atg cgc gaa aat ggc ggt gac cag gac ctt atc cag cgc ctc gct gct  
 1363  
 Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile Gln Arg Leu Ala Ala

410 415 420  
 gat gag cgc ctc cca atg agc gaa gct gac ctt gag gca gcg ctg gct  
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 Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu Glu Ala Ala Leu Ala  
 425 430 435  
 gac cgc cac gcc ttc atc ggt gcc gct gag tcc cag gtc tcc cgt gtg  
 1459  
 Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val  
 440 445 450  
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 1507  
 Leu Asp Arg Ile Gln Val Leu Val Asp Ala His Pro Gly Ala Ala Asp  
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<210> 962  
 <211> 476  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 962  
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 Glu Arg Gln Leu Trp Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly  
 35 40 45  
 Val Glu Ile Pro Ala Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp  
 50 55 60  
 Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His  
 65 70 75 80  
 Asp Val Lys Ala Arg Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu  
 85 90 95  
 His Ile His Lys Gly Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu  
 100 105 110  
 Gln Leu Gln Ile His Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile  
 115 120 125  
 Ala Val Val Ala Ala Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu  
 130 135 140  
 Val Met Ala Gly Arg Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu  
 145 150 155 160  
 Gly Lys Arg Phe Ala Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu  
 165 170 175

Arg Val Thr Glu Leu Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly  
 180 185 190  
 Pro Met Gly Thr Ala Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu  
 195 200 205  
 Ala Arg Leu Ser Asp Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe  
 210 215 220  
 Asp Arg Val Phe Asp Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp  
 225 230 235 240  
 Phe Asp Ala Val Ser Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser  
 245 250 255  
 Leu Ser His Thr Ile Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu  
 260 265 270  
 Gly Phe Lys Glu Gly Gln Val Gly Ser Ser Ala Met Pro His Lys Met  
 275 280 285  
 Asn Ala Arg Ser Cys Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg  
 290 295 300  
 Gly Tyr Leu Thr Met Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu  
 305 310 315 320  
 Gly Asp Val Phe Cys Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala  
 325 330 335  
 Phe Phe Ala Ile Asp Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp  
 340 345 350  
 Glu Phe Gly Ala Phe Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr  
 355 360 365  
 Leu Pro Phe Leu Ala Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala  
 370 375 380  
 Gly Val Gly Arg Glu Thr Ala His Glu Val Ile Lys Glu Asn Ala Val  
 385 390 395 400  
 Ala Val Ala Leu Asn Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile  
 405 410 415  
 Gln Arg Leu Ala Ala Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu  
 420 425 430  
 Glu Ala Ala Leu Ala Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser  
 435 440 445  
 Gln Val Ser Arg Val Leu Asp Arg Ile Gln Val Leu Val Asp Ala His  
 450 455 460  
 Pro Gly Ala Ala Asp Tyr Arg Pro Gly Glu Ile Leu  
 465 470 475

&lt;210&gt; 963

&lt;211&gt; 666

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(643)

&lt;223&gt; RXA00688

&lt;400&gt; 963

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gccagctcct gcaaagcaac tacgaaggac ttctaaaata atg cga ctc gta ctc 115
                                         Met Arg Leu Val Leu
                                         1           5

ctc gga cct ccc ggt gct ggt aag ggc acc cag gct gca att ctc tct 163
Leu Gly Pro Pro Gly Ala Gly Lys Gly Thr Gln Ala Ala Ile Leu Ser
                        10                15                20

gag aag ctt ggc att cct cac att tct act ggc gat ctt ttc cgc gcc 211
Glu Lys Leu Gly Ile Pro His Ile Ser Thr Gly Asp Leu Phe Arg Ala
                        25                30                35

aac att ggc gaa ggt acc cct ctg ggt atc gag gcc aag cag tac atc 259
Asn Ile Gly Glu Gly Thr Pro Leu Gly Ile Glu Ala Lys Gln Tyr Ile
                        40                45                50

gac gct ggc aag ctg gtt cca acc gac gtg act gca cgt atg gtt gct 307
Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr Ala Arg Met Val Ala
                        55                60                65

tcc cgc ctt gct gag tcc gat gct gca gaa ggc ttc ctt ttg gat ggt 355
Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly Phe Leu Leu Asp Gly
                        70                75                80                85

ttc cca cgc acc gtt gag cag gct gac atc ttg gct aac ctg ctt tcc 403
Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu Ala Asn Leu Leu Ser
                        90                95                100

gaa gct ggc cag acc ctc gat ggt gtt gtt aac tac cag gtt tct gaa 451
Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn Tyr Gln Val Ser Glu
                        105                110                115

gac gtc gtc gtg gag cgc atg ctg tcc cgt ggt cgc gct gat gac aac 499
Asp Val Val Val Glu Arg Met Leu Ser Arg Gly Arg Ala Asp Asp Asn
                        120                125                130

gaa gag acc atc cgc acc cgt ctc ggt gtc tac cgc gac gag act gct 547
Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr Arg Asp Glu Thr Ala
                        135                140                145

cct ctg atc gat cac tac ggt gac aag atc atc aac att gag gct gaa 595
Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile Asn Ile Glu Ala Glu
                        150                155                160                165

ggc gaa gtc gaa gag atc aac gct cgt acc ctc aag gca ctg ggc aaa 643
Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu Lys Ala Leu Gly Lys
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 964  
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 Ala Ala Ile Leu Ser Glu Lys Leu Gly Ile Pro His Ile Ser Thr Gly  
                   20                  25                  30  
 Asp Leu Phe Arg Ala Asn Ile Gly Glu Gly Thr Pro Leu Gly Ile Glu  
           35                  40                  45  
 Ala Lys Gln Tyr Ile Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr  
       50                  55                  60  
 Ala Arg Met Val Ala Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly  
   65                  70                  75                  80  
 Phe Leu Leu Asp Gly Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu  
                   85                  90                  95  
 Ala Asn Leu Leu Ser Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn  
                   100                  105                  110  
 Tyr Gln Val Ser Glu Asp Val Val Val Glu Arg Met Leu Ser Arg Gly  
           115                  120                  125  
 Arg Ala Asp Asp Asn Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr  
       130                  135                  140  
 Arg Asp Glu Thr Ala Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile  
   145                  150                  155                  160  
 Asn Ile Glu Ala Glu Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu  
                   165                  170                  175  
 Lys Ala Leu Gly Lys  
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<210> 965  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(508)  
 <223> RXA00266

<400> 965  
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   Met Thr Glu Arg Thr  
   1                  5

ctc atc ctt atc aag cca gac ggt gtt acc aac gga cac gtc ggc gaa 163  
 Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn Gly His Val Gly Glu  
                   10                                  15                                  20

atc atc gca cgt att gag cgc aag ggc ctg aag ctc gct gct ctg gat 211  
 Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys Leu Ala Ala Leu Asp  
                   25                                  30                                  35

ctg cgt gtt gca gac cgc gag acc gct gaa aag cac tac gaa gag cac 259  
 Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys His Tyr Glu Glu His  
                   40                                  45                                  50

gct gac aag cca ttc ttc ggt gag ctc gtt gaa ttc atc acc tct gca 307  
 Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu Phe Ile Thr Ser Ala  
                   55                                  60                                  65

cct ctg atc gca ggc atc gtc gaa ggc gag cgt gca atc gat gca tgg 355  
 Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg Ala Ile Asp Ala Trp  
                   70                                  75                                  80                                  85

cgt cag ctt gct ggt ggc acc gac cca gtt gct aag gca acc cca ggc 403  
 Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala Lys Ala Thr Pro Gly  
                   90                                  95                                  100

acc atc cgc ggc gat ttc gca ctg act gtt gga gag aac gtt gtt cac 451  
 Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly Glu Asn Val Val His  
                   105                                  110                                  115

ggt tct gat tcc cca gag tcc gct gag cgc gag atc tcc atc tgg ttc 499  
 Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu Ile Ser Ile Trp Phe  
                   120                                  125                                  130

cct aac ctg taattttttac ggtagaaaa aaa 531  
 Pro Asn Leu  
                   135

&lt;210&gt; 966

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 966

Met Thr Glu Arg Thr Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn  
           1                                  5                                  10                                  15

Gly His Val Gly Glu Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys  
                   20                                  25                                  30

Leu Ala Ala Leu Asp Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys  
                   35                                  40                                  45

His Tyr Glu Glu His Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu  
           50                                  55                                  60

Phe Ile Thr Ser Ala Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg  
           65                                  70                                  75                                  80

Ala Ile Asp Ala Trp Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala  
                   85                                  90                                  95

Lys Ala Thr Pro Gly Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly  
 100 105 110

Glu Asn Val Val His Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu  
 115 120 125

Ile Ser Ile Trp Phe Pro Asn Leu  
 130 135

<210> 967

<211> 1245

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1222)

<223> RXA00489

<400> 967

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gtcttcgtcg tatacgacca tttaaggagg gcccgtcaca atg cgt gac cac gtt 115  
 Met Arg Asp His Val  
 1 5

gaa atc ggt atc ggc cgt gag gca cga cgc acc tac agc ttg gac gat 163  
 Glu Ile Gly Ile Gly Arg Glu Ala Arg Arg Thr Tyr Ser Leu Asp Asp  
 10 15 20

att tct gtc gtt tct agc cgc cgc acc cgt tca tcc aaa gat gtc gac 211  
 Ile Ser Val Val Ser Ser Arg Arg Thr Arg Ser Ser Lys Asp Val Asp  
 25 30 35

acc act tgg cat att gac gcc tac aag ttt gat ctg ccg ttc atg aat 259  
 Thr Thr Trp His Ile Asp Ala Tyr Lys Phe Asp Leu Pro Phe Met Asn  
 40 45 50

cac cca agt gat gca ttg gca agc cct gag ttt gtc att gaa atg ggc 307  
 His Pro Ser Asp Ala Leu Ala Ser Pro Glu Phe Val Ile Glu Met Gly  
 55 60 65

aag cag ggt ggc ctt ggc gtg atc aac gct gag ggt ctg tgg ggt cgc 355  
 Lys Gln Gly Gly Leu Gly Val Ile Asn Ala Glu Gly Leu Trp Gly Arg  
 70 75 80 85

cat gct gat ctc gat gag gcg atc gca aag gtg att gct gcg tat gag 403  
 His Ala Asp Leu Asp Glu Ala Ile Ala Lys Val Ile Ala Ala Tyr Glu  
 90 95 100

gaa ggc gac cag gct gca gcc act cgc act ctt cag gag ctg cac gca 451  
 Glu Gly Asp Gln Ala Ala Ala Thr Arg Thr Leu Gln Glu Leu His Ala  
 105 110 115

gcg cca ctg gat act gag ctg ctg agt gag cgc att gcg cag gtt cgt 499  
 Ala Pro Leu Asp Thr Glu Leu Leu Ser Glu Arg Ile Ala Gln Val Arg  
 120 125 130

gat tcc ggt gag atc gtt gct gtg cgc gtg tct cca caa aat gtt cgt 547  
 Asp Ser Gly Glu Ile Val Ala Val Arg Val Ser Pro Gln Asn Val Arg



135	140	145	
gag atc gca cca atc gtc atc aag gca ggt gct gat ctg ctg gtt atc Glu Ile Ala Pro Ile Val Ile Lys Ala Gly Ala Asp Leu Leu Val Ile 150 155 160 165			595
cag ggc acc ctg atc tct gca gag cac gtc aac acc ggt gga gag gcc Gln Gly Thr Leu Ile Ser Ala Glu His Val Asn Thr Gly Gly Glu Ala 170 175 180			643
ctg aac cta aag gaa ttc atc ggt tct ttg gat gtt cct gtc atc gct Leu Asn Leu Lys Glu Phe Ile Gly Ser Leu Asp Val Pro Val Ile Ala 185 190 195			691
ggt ggc gtg aac gat tac acc acc gcg ttg cac atg atg cgt acc ggt Gly Gly Val Asn Asp Tyr Thr Thr Ala Leu His Met Met Arg Thr Gly 200 205 210			739
gct gtg ggc atc atc gtc ggt ggc ggc gag aac acc aac agc cta gca Ala Val Gly Ile Ile Val Gly Gly Gly Glu Asn Thr Asn Ser Leu Ala 215 220 225			787
ttg ggc atg gag gta tcc atg gcc act gcg att gct gat gtc gct gcg Leu Gly Met Glu Val Ser Met Ala Thr Ala Ile Ala Asp Val Ala Ala 230 235 240 245			835
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cct cgt ttc cca cgc ggt gtg gtt act gag tcc gtg gac ttg gat gag 1075 Pro Arg Phe Pro Arg Gly Val Val Thr Glu Ser Val Asp Leu Asp Glu 310 315 320 325			
gca gca cca agc ttg gag cag att ctg cat ggt ccg tct acg atg ccg 1123 Ala Ala Pro Ser Leu Glu Gln Ile Leu His Gly Pro Ser Thr Met Pro 330 335 340			
tgg ggt gtg gaa aac ttc gaa ggt gga tta aag cgt gcg ctg gct aag 1171 Trp Gly Val Glu Asn Phe Glu Gly Gly Leu Lys Arg Ala Leu Ala Lys 345 350 355			
tgt ggc tac acc gat ttg aag agc ttc caa aag gta agc ctg cac gtt 1219 Cys Gly Tyr Thr Asp Leu Lys Ser Phe Gln Lys Val Ser Leu His Val			

360

365

370

aac taggtgtgtg tactcgctc ttc  
1245  
Asn

&lt;210&gt; 968

&lt;211&gt; 374

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 968

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Tyr	Ser	Leu	Asp	Asp	Ile	Ser	Val	Val	Ser	Ser	Arg	Arg	Thr	Arg	Ser
			20					25					30		
Ser	Lys	Asp	Val	Asp	Thr	Thr	Trp	His	Ile	Asp	Ala	Tyr	Lys	Phe	Asp
		35					40					45			
Leu	Pro	Phe	Met	Asn	His	Pro	Ser	Asp	Ala	Leu	Ala	Ser	Pro	Glu	Phe
	50					55					60				
Val	Ile	Glu	Met	Gly	Lys	Gln	Gly	Gly	Leu	Gly	Val	Ile	Asn	Ala	Glu
65					70					75					80
Gly	Leu	Trp	Gly	Arg	His	Ala	Asp	Leu	Asp	Glu	Ala	Ile	Ala	Lys	Val
				85					90					95	
Ile	Ala	Ala	Tyr	Glu	Glu	Gly	Asp	Gln	Ala	Ala	Ala	Thr	Arg	Thr	Leu
			100					105					110		
Gln	Glu	Leu	His	Ala	Ala	Pro	Leu	Asp	Thr	Glu	Leu	Leu	Ser	Glu	Arg
		115					120					125			
Ile	Ala	Gln	Val	Arg	Asp	Ser	Gly	Glu	Ile	Val	Ala	Val	Arg	Val	Ser
	130					135					140				
Pro	Gln	Asn	Val	Arg	Glu	Ile	Ala	Pro	Ile	Val	Ile	Lys	Ala	Gly	Ala
145					150					155					160
Asp	Leu	Leu	Val	Ile	Gln	Gly	Thr	Leu	Ile	Ser	Ala	Glu	His	Val	Asn
			165						170					175	
Thr	Gly	Gly	Glu	Ala	Leu	Asn	Leu	Lys	Glu	Phe	Ile	Gly	Ser	Leu	Asp
			180					185					190		
Val	Pro	Val	Ile	Ala	Gly	Gly	Val	Asn	Asp	Tyr	Thr	Thr	Ala	Leu	His
		195					200					205			
Met	Met	Arg	Thr	Gly	Ala	Val	Gly	Ile	Ile	Val	Gly	Gly	Gly	Glu	Asn
	210					215					220				
Thr	Asn	Ser	Leu	Ala	Leu	Gly	Met	Glu	Val	Ser	Met	Ala	Thr	Ala	Ile
225					230					235					240
Ala	Asp	Val	Ala	Ala	Ala	Arg	Arg	Asp	Tyr	Leu	Asp	Glu	Thr	Gly	Gly
			245						250					255	

Arg Tyr Val His Ile Ile Ala Asp Gly Ser Ile Glu Asn Ser Gly Asp  
 260 265 270  
 Val Val Lys Ala Ile Ala Cys Gly Ala Asp Ala Val Val Leu Gly Ser  
 275 280 285  
 Pro Leu Ala Arg Ala Glu Glu Ala Ala Gly Lys Gly Tyr Phe Trp Pro  
 290 295 300  
 Ala Val Ala Ala His Pro Arg Phe Pro Arg Gly Val Val Thr Glu Ser  
 305 310 315 320  
 Val Asp Leu Asp Glu Ala Ala Pro Ser Leu Glu Gln Ile Leu His Gly  
 325 330 335  
 Pro Ser Thr Met Pro Trp Gly Val Glu Asn Phe Glu Gly Gly Leu Lys  
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 Val Gln Lys Asp Ser  
 1 5  
 gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163  
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu  
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 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn  
 25 30 35  
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 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr  
 40 45 50  
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 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly  
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 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg

70	75	80	85	
gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat				403
Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn	90	95	100	
tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg				451
Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro	105	110	115	
gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt				499
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly	120	125	130	
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac				547
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp	135	140	145	
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg				595
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro	150	155	160	165
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc				643
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile	170	175	180	
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg				691
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu	185	190	195	
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg				739
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met	200	205	210	
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca				787
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro	215	220	225	
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa				835
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu	230	235	240	245
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc				883
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile	250	255	260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca				931
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro	265	270	275	
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa				979
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu	280	285	290	
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc				1027
Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg	295	300	305	
atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att				1075

Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile  
310 315 320 325

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa  
1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu  
330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac  
1171

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp  
345 350 355

aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac  
1219

Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn  
360 365 370

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1267

Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser  
375 380 385

acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga  
1315

Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly  
390 395 400 405

tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg  
1363

Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu  
410 415 420

cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac  
1411

Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr  
425 430 435

ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa  
1459

Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu  
440 445 450

tac ctg gca gta gat cct gaa cgg ttg cgt acc cgt aaa ctg cgc agg  
1507

Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg  
455 460 465

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Thr Leu Gly Glu Val Pro Phe Arg  
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<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 970

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Lys	Glu	Thr	Leu
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Tyr	Pro	Lys	Leu
	50		60
Thr	Glu	Pro	Phe
	65		75
Leu	Ser	Lys	Pro
	85		95
Arg	Leu	Thr	Ser
	100		110
Ile	Arg	Ile	Pro
	115		125
Ala	Arg	Arg	Ala
	130		140
Asp	Glu	Val	His
	145		155
Gly	Pro	Glu	Leu
	165		175
Ala	Cys	Ala	Arg
	180		190
Gln	Lys	Tyr	Ile
	195		205
Val	His	Phe	Ala
	210		220
Gly	Leu	Ser	Leu
	225		235
Ser	Leu	Gly	Thr
	245		255
Arg	Tyr	Asp	Leu
	260		270
Ile	Gly	Val	Gly
	275		285
Val	Leu	Arg	Pro
	290		300
Asp	Ala	Arg	Met
	305		315
Arg	Glu	Asp	His
	325		335

Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu  
 340 345 350  
 Ile Tyr Gly Ser Asp Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser  
 355 360 365  
 Thr Asp Asp Arg Asn Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn  
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 Trp Leu Lys Gly Ser Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr  
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 405 410 415  
 Ser Val Ser Asp Leu Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln  
 420 425 430  
 Ala Gln Ala Phe Tyr Phe Asn Ser Lys Glu Ala His Val Met Cys Ala  
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 Val Gln Lys Asp Ser 5  
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 gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163  
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu 20  
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 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn 35  
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 aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259  
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr 50  
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 gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307  
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly 65  
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Tyr	Pro	Cys	Lys	Ile	Tyr	Val	Ser	Glu	Ser	Asp	Ile	Arg	Ile	Pro	Pro	
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Glu	Tyr	Ile	Arg	Gly	Ala	Pro	Ser	Ala	Thr	Glu	Ala	Arg	Arg	Ala	Gly	
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gat	gtt	gca	gat	atc	atc	cca	cgc	ccc	acc	ctg	gat	gaa	gtc	cac	gac	547
Asp	Val	Ala	Asp	Ile	Ile	Pro	Arg	Pro	Thr	Leu	Asp	Glu	Val	His	Asp	
	135					140					145					
gca	att	atc	gac	ggc	gac	tgg	cac	gcc	ttc	aac	ggc	ccc	gaa	ctc	ccg	595
Ala	Ile	Ile	Asp	Gly	Asp	Trp	His	Ala	Phe	Asn	Gly	Pro	Glu	Leu	Pro	
150					155					160					165	
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Leu	Phe	His	Phe	Gly	Pro	Gln	Arg	Phe	Asp	Ile	Ala	Cys	Ala	Arg	Ile	
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Glu	His	Tyr	Thr	Gly	Ile	Asn	Val	Glu	His	Val	Gln	Lys	Tyr	Ile	Leu	
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Phe	Thr	Asn	Tyr	Ala	Met	His	Thr	Thr	Glu	Phe	Val	His	Phe	Ala	Met	
		200					205					210				
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Ser	Glu	Leu	Thr	Ser	Glu	Asp	Ser	Arg	Tyr	Val	Gly	Leu	Ser	Leu	Pro	
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230					235					240					245	
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Thr	Leu	Asp	Leu	Thr	Ser	Arg	Phe	Gln	Met	Pro	Arg	Tyr	Asp	Leu	Ile	
				250					255					260		
acc	gaa	gcc	ggc	gac	ggc	att	acc	att	atc	aac	atc	ggc	gtg	ggc	cca	931
Thr	Glu	Ala	Gly	Asp	Gly	Ile	Thr	Ile	Ile	Asn	Ile	Gly	Val	Gly	Pro	
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tcc	aat	gca	aaa	act	atc	acc	gac	tgc	ctt	gct	gtg	ctc	cgc	cca	gaa	979
Ser	Asn	Ala	Lys	Thr	Ile	Thr	Asp	Cys	Leu	Ala	Val	Leu	Arg	Pro	Glu	
		280					285					290				
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1027																
Ala	Trp	Val	Met	Ile	Gly	His	Cys	Ala	Gly	Met	Asp	Ala	Arg	Met	Arg	
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1075

Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile  
310 315 320 325

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa  
1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu  
330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc  
1168

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1191

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<211> 356

<212> PRT

<213> Corynebacterium glutamicum

<400> 972

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35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg  
50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr  
65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu  
85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp  
100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu  
115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu  
130 135 140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn  
145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile  
165 170 175

Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val  
180 185 190

Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe  
 195 200 205  
 Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val  
 210 215 220  
 Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr  
 225 230 235 240  
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro  
 245 250 255  
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn  
 260 265 270  
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala  
 275 280 285  
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met  
 290 295 300  
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln  
 305 310 315 320  
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile  
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 Val Ser Lys Asp Thr  
 1 5  
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 Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr Leu  
 10 15 20  
 gtt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct atc 211  
 Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe Gly Phe Gly Ala Ile  
 25 30 35  
 ggc acc acc ctt ggt gag gca gtg ttc act acc gcc atg acc ggt tac 259

Gly	Thr	Thr	Leu	Gly	Glu	Ala	Val	Phe	Thr	Thr	Ala	Met	Thr	Gly	Tyr	
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Gln	Glu	Thr	Met	Thr	Asp	Pro	Ser	Tyr	His	Arg	Gln	Ile	Val	Val	Ala	
	55					60					65					
acc	gca	cca	cag	atc	ggc	aac	acc	ggc	tgg	aac	gat	gag	gac	aac	gag	355
Thr	Ala	Pro	Gln	Ile	Gly	Asn	Thr	Gly	Trp	Asn	Asp	Glu	Asp	Asn	Glu	
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Ser	Arg	Asp	Gly	Lys	Ile	Trp	Val	Ala	Gly	Leu	Val	Ile	Arg	Asp	Leu	
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gca	gca	cgt	gtg	tcc	aac	tgg	cgc	gcc	acc	acc	tcc	ttg	cag	cag	gaa	451
Ala	Ala	Arg	Val	Ser	Asn	Trp	Arg	Ala	Thr	Thr	Ser	Leu	Gln	Gln	Glu	
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Met	Ala	Gly	Gln	Gly	Ile	Val	Gly	Ile	Gly	Gly	Ile	Asp	Thr	Arg	Ala	
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Leu	Val	Arg	His	Leu	Arg	Asn	Glu	Gly	Ser	Ile	Ala	Ala	Gly	Ile	Phe	
	135					140					145					
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Lys	Asn	Gln	Pro	Ala	Met	Thr	Gly	Ala	Asn	Leu	Ser	Val	Glu	Val	Ser	
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gct	gat	gaa	acc	tac	gtc	atc	gaa	gct	gaa	ggc	gaa	gag	cgc	cac	acc	691
Ala	Asp	Glu	Thr	Tyr	Val	Ile	Glu	Ala	Glu	Gly	Glu	Glu	Arg	His	Thr	
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Val	Val	Ala	Tyr	Asp	Leu	Gly	Ile	Lys	Gln	Asn	Thr	Pro	Arg	Arg	Phe	
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Ser	Ala	Arg	Gly	Val	Arg	Thr	Val	Ile	Val	Pro	Ala	Glu	Thr	Pro	Phe	
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Glu	Asp	Ile	Lys	Gln	Tyr	Asn	Pro	Ser	Gly	Val	Phe	Ile	Ser	Asn	Gly	
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Pro	Gly	Asp	Pro	Ala	Ala	Ala	Asp	Val	Met	Val	Asp	Ile	Val	Arg	Glu	
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Val	Leu	Glu	Ala	Asp	Ile	Pro	Phe	Phe	Gly	Ile	Cys	Phe	Gly	Asn	Gln	
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 1302  
 Lys Lys Gly Ala  
 390

&lt;210&gt; 974

&lt;211&gt; 393

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 974

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 Gly Phe Gly Ala Ile Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr  
 35 40 45  
 Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg  
 50 55 60  
 Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn  
 65 70 75 80  
 Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu  
 85 90 95

Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr  
 100 105 110  
 Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly  
 115 120 125  
 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile  
 130 135 140  
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu  
 145 150 155 160  
 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu  
 165 170 175  
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly  
 180 185 190  
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn  
 195 200 205  
 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro  
 210 215 220  
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val  
 225 230 235 240  
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val  
 245 250 255  
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile  
 260 265 270  
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr  
 275 280 285  
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His  
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 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu  
 305 310 315 320  
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile  
 325 330 335  
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu  
 340 345 350  
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala  
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 Gly Pro Asn Asp Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met  
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 Asp Ala Asp Ala Gln Lys Lys Gly Ala  
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&lt;210&gt; 975

&lt;211&gt; 1059

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (1036)

&lt;223&gt; RXA00145

&lt;400&gt; 975

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				Met	Lys	His	Leu	Leu		
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Ser	Ile	Ser	Asp	Leu	Ser	Lys	Asp	Glu	Ile	Val	Gly	Leu	Leu	Asp	Glu	
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gcg	gat	cgc	ttt	aag	gag	gtg	ctc	gaa	gga	cgt	gaa	gta	aag	aag	ctg	211
Ala	Asp	Arg	Phe	Lys	Glu	Val	Leu	Glu	Gly	Arg	Glu	Val	Lys	Lys	Leu	
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ccc	acg	ctg	cgt	ggc	cgc	acc	att	ttt	acc	ttg	ttc	tat	gag	aac	tcc	259
Pro	Thr	Leu	Arg	Gly	Arg	Thr	Ile	Phe	Thr	Leu	Phe	Tyr	Glu	Asn	Ser	
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Thr	Arg	Thr	Arg	Ser	Ser	Phe	Glu	Thr	Ala	Gly	Lys	Trp	Met	Ser	Ala	
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gat	gtg	att	aac	att	tcg	gcc	tca	tca	tcc	agc	gtg	aag	aag	ggc	gag	355
Asp	Val	Ile	Asn	Ile	Ser	Ala	Ser	Ser	Ser	Ser	Val	Lys	Lys	Gly	Glu	
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tcg	ctg	aaa	gat	acc	ggc	ttg	act	ttg	tcg	gca	atc	ggc	gcg	gat	gcg	403
Ser	Leu	Lys	Asp	Thr	Gly	Leu	Thr	Leu	Ser	Ala	Ile	Gly	Ala	Asp	Ala	
				90				95						100		

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Ile	Ile	Met	Arg	His	Pro	Ala	Ser	Gly	Ala	Ala	Gln	Gln	Leu	Ala	Gln	
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ttc	gtc	gca	cca	ggc	ggc	aac	ggc	ccc	agc	gtg	atc	aac	gcg	ggc	gac	499
Phe	Val	Ala	Pro	Gly	Gly	Asn	Gly	Pro	Ser	Val	Ile	Asn	Ala	Gly	Asp	
		120				125						130				

ggc	tcg	cac	cag	cac	ccc	acc	cag	gcg	ctt	ctc	gac	gct	tta	acc	atc	547
Gly	Ser	His	Gln	His	Pro	Thr	Gln	Ala	Leu	Leu	Asp	Ala	Leu	Thr	Ile	
	135					140					145					

cgg	cag	cgc	acc	ggc	cgc	att	gag	gga	ctc	aaa	gtt	gtc	atc	gtg	ggc	595
Arg	Gln	Arg	Thr	Gly	Arg	Ile	Glu	Gly	Leu	Lys	Val	Val	Ile	Val	Gly	
	150				155					160					165	

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Asp	Cys	Leu	His	Ser	Arg	Val	Val	Arg	Ser	Asn	Val	Asp	Leu	Leu	Ser	
				170				175						180		

act	ttg	ggc	gca	gag	gta	gtg	ctg	gtt	gct	cct	ccg	aca	ctg	ctt	cct	691
Thr	Leu	Gly	Ala	Glu	Val	Val	Leu	Val	Ala	Pro	Pro	Thr	Leu	Leu	Pro	

185										190					195					
att ggt gtg gag aac tgg cca gtc cga ttc tcc tac gac atg gac gca	739																			
Ile Gly Val Glu Asn Trp Pro Val Arg Phe Ser Tyr Asp Met Asp Ala																				
200 205 210																				
gaa att gcc gac gcc gac gta gtg atg atg ctg cgc gtt cag caa gaa	787																			
Glu Ile Ala Asp Ala Asp Val Val Met Met Leu Arg Val Gln Gln Glu																				
215 220 225																				
cgc atg cag ggt ggt ttc ttc ccc tca cac cgt gag tac gca acg ctg	835																			
Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg Glu Tyr Ala Thr Leu																				
230 235 240 245																				
tac ggc atg tcc aaa gag cgc gaa gct cgc ctc aag gac tcc gcc atc	883																			
Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu Lys Asp Ser Ala Ile																				
250 255 260																				
atc atg cac ccc ggc ccc atg ctt cgt ggc atg gaa att aac ttc cag	931																			
Ile Met His Pro Gly Pro Met Leu Arg Gly Met Glu Ile Asn Phe Gln																				
265 270 275																				
gtg gca gac gca cca cgc acc gcg gta ctg cag cag gta agc aac ggt	979																			
Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln Gln Val Ser Asn Gly																				
280 285 290																				
gtg cac atg cgc atg gcc att ttg ttc gcc ctg gtc gca ggc tct gac																				
1027 Val His Met Arg Met Ala Ile Leu Phe Ala Leu Val Ala Gly Ser Asp																				
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Ala Thr Ile																				
310																				

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 <213> Corynebacterium glutamicum

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 Glu Val Lys Lys Leu Pro Thr Leu Arg Gly Arg Thr Ile Phe Thr Leu  
 35 40 45  
 Phe Tyr Glu Asn Ser Thr Arg Thr Arg Ser Ser Phe Glu Thr Ala Gly  
 50 55 60  
 Lys Trp Met Ser Ala Asp Val Ile Asn Ile Ser Ala Ser Ser Ser Ser  
 65 70 75 80  
 Val Lys Lys Gly Glu Ser Leu Lys Asp Thr Gly Leu Thr Leu Ser Ala  
 85 90 95

Ile Gly Ala Asp Ala Ile Ile Met Arg His Pro Ala Ser Gly Ala Ala  
 100 105 110  
 Gln Gln Leu Ala Gln Phe Val Ala Pro Gly Gly Asn Gly Pro Ser Val  
 115 120 125  
 Ile Asn Ala Gly Asp Gly Ser His Gln His Pro Thr Gln Ala Leu Leu  
 130 135 140  
 Asp Ala Leu Thr Ile Arg Gln Arg Thr Gly Arg Ile Glu Gly Leu Lys  
 145 150 155 160  
 Val Val Ile Val Gly Asp Cys Leu His Ser Arg Val Val Arg Ser Asn  
 165 170 175  
 Val Asp Leu Leu Ser Thr Leu Gly Ala Glu Val Val Leu Val Ala Pro  
 180 185 190  
 Pro Thr Leu Leu Pro Ile Gly Val Glu Asn Trp Pro Val Arg Phe Ser  
 195 200 205  
 Tyr Asp Met Asp Ala Glu Ile Ala Asp Ala Asp Val Val Met Met Leu  
 210 215 220  
 Arg Val Gln Gln Glu Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg  
 225 230 235 240  
 Glu Tyr Ala Thr Leu Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu  
 245 250 255  
 Lys Asp Ser Ala Ile Ile Met His Pro Gly Pro Met Leu Arg Gly Met  
 260 265 270  
 Glu Ile Asn Phe Gln Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln  
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 Val Ala Gly Ser Asp Ala Thr Ile  
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 Val Val Asp Ser Asn  
 1 5  
 acc cag tat cca gaa acc ggc gca ctg gca ccg gct cct gca gac tca 163



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Leu	Leu	Ile	Ser	Asn	Val	Leu	Val	Tyr	Gly	Glu	Gly	Glu	Pro	Thr	Asn	
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Val	Phe	Val	Lys	Asp	Gly	Val	Ile	Ala	Ala	Ile	Gly	Gly	Thr	His	Glu	
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Ala	Asp	Arg	Thr	Ile	Asp	Gly	Asn	Gly	Gly	Val	Leu	Leu	Pro	Gly	Phe	
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gtg	gac	atg	cac	gtt	cac	ctg	cgt	gag	cca	ggc	cgc	gaa	gac	act	gaa	355
Val	Asp	Met	His	Val	His	Leu	Arg	Glu	Pro	Gly	Arg	Glu	Asp	Thr	Glu	
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acc	att	gcc	act	ggc	tct	gcc	gcc	gca	gcc	aag	ggc	gga	ttc	acc	gca	403
Thr	Ile	Ala	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Lys	Gly	Gly	Phe	Thr	Ala	
				90					95					100		
gta	ttc	acc	atg	gcg	aac	acc	act	cca	gtg	atg	gat	cag	ccg	gtt	atc	451
Val	Phe	Thr	Met	Ala	Asn	Thr	Thr	Pro	Val	Met	Asp	Gln	Pro	Val	Ile	
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Ala	Glu	Ser	Val	Trp	Phe	Lys	Gly	Gln	Asn	Ile	Gly	Leu	Cys	Asp	Val	
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cat	cca	gtt	gga	tcc	atc	acc	aag	ggc	ctt	gag	ggc	aag	gag	ctt	act	547
His	Pro	Val	Gly	Ser	Ile	Thr	Lys	Gly	Leu	Glu	Gly	Lys	Glu	Leu	Thr	
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gag	ttc	ggc	atg	atg	gct	cgc	tct	gaa	gcc	aag	gtg	cgc	atg	ttc	tct	595
Glu	Phe	Gly	Met	Met	Ala	Arg	Ser	Glu	Ala	Lys	Val	Arg	Met	Phe	Ser	
	150				155					160					165	
gat	gat	ggc	aag	tgc	gtc	gat	gat	cct	cag	gtc	atg	cgc	cgc	gcg	ctg	643
Asp	Asp	Gly	Lys	Cys	Val	Asp	Asp	Pro	Gln	Val	Met	Arg	Arg	Ala	Leu	
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gaa	tac	gcc	aag	ggc	atg	gac	gtt	ttg	atc	gcc	cag	cac	gct	gag	gat	691
Glu	Tyr	Ala	Lys	Gly	Met	Asp	Val	Leu	Ile	Ala	Gln	His	Ala	Glu	Asp	
			185					190					195			
cac	cgc	ctg	act	gag	ggc	gct	tca	gca	cac	gag	ggc	gaa	aac	gca	gct	739
His	Arg	Leu	Thr	Glu	Gly	Ala	Ser	Ala	His	Glu	Gly	Glu	Asn	Ala	Ala	
		200					205					210				
cgt	ctg	ggc	ctg	cgc	ggc	tgg	cca	cgt	gtg	gct	gag	gaa	tcc	atc	gtg	787
Arg	Leu	Gly	Leu	Arg	Gly	Trp	Pro	Arg	Val	Ala	Glu	Glu	Ser	Ile	Val	
	215					220					225					
gtg	cgc	gat	gcc	atc	atg	gct	cgt	gac	tac	ggc	aac	cgc	gtg	cac	atc	835
Val	Arg	Asp	Ala	Ile	Met	Ala	Arg	Asp	Tyr	Gly	Asn	Arg	Val	His	Ile	
	230				235					240					245	
tgc	cac	gcc	tcc	act	gaa	ggc	acc	gtg	gag	ttg	ctt	cgt	tgg	gct	aag	883
Cys	His	Ala	Ser	Thr	Glu	Gly	Thr	Val	Glu	Leu	Leu	Arg	Trp	Ala	Lys	

250								255				260				
tcc	cag	ggc	att	cca	atc	acc	gcg	gaa	gtc	acc	ccg	cac	cac	ctc	acc	931
Ser	Gln	Gly	Ile	Pro	Ile	Thr	Ala	Glu	Val	Thr	Pro	His	His	Leu	Thr	
			265					270					275			
ttg	acc	gat	gag	cgc	ctg	gaa	acc	tac	gac	gcg	gtc	aac	aaa	gtc	aat	979
Leu	Thr	Asp	Glu	Arg	Leu	Glu	Thr	Tyr	Asp	Ala	Val	Asn	Lys	Val	Asn	
		280					285					290				
ccg	cca	ctg	cgc	gaa	agc	cgc	gat	gcc	gaa	gcg	ctc	aag	aag	gcg	ctt	
1027																
Pro	Pro	Leu	Arg	Glu	Ser	Arg	Asp	Ala	Glu	Ala	Leu	Lys	Lys	Ala	Leu	
	295					300					305					
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1075																
Leu	Asp	Gly	Thr	Ile	Asp	Val	Val	Ala	Thr	Asp	His	Ala	Pro	His	Gly	
310					315					320					325	
tcc	gaa	gat	aag	tgc	tgt	gaa	ttc	gaa	aac	gcc	aag	cca	ggc	atg	ctc	
1123																
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				330					335					340		
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1171																
Gly	Leu	Glu	Thr	Ser	Leu	Ser	Ile	Ile	Val	Asp	Thr	Phe	Val	Ala	Thr	
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1267																
Ala	Glu	Ile	Thr	Arg	Leu	Pro	Gly	Gln	Gly	Arg	Pro	Ile	Ala	Glu	Gly	
		375				380					385					
gag	cca	gca	aac	ctc	gcg	att	gtt	gat	cca	gga	aaa	acc	tgg	aca	gca	
1315																
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390					395					400					405	
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1363																
Ser	Gly	Ala	Asp	Phe	Ala	Ser	Lys	Ala	Glu	Asn	Thr	Pro	Phe	Glu	Gly	
				410					415					420		
caa	gaa	ttc	agt	gcc	aag	gtc	aca	cac	acc	gtg	ctt	cgt	ggc	aag	gtg	
1411																
Gln	Glu	Phe	Ser	Ala	Lys	Val	Thr	His	Thr	Val	Leu	Arg	Gly	Lys	Val	
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1464

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Gly	Glu	Pro	Thr	Asn	Val	Phe	Val	Lys	Asp	Gly	Val	Ile	Ala	Ala	Ile
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Gly	Gly	Thr	His	Glu	Ala	Asp	Arg	Thr	Ile	Asp	Gly	Asn	Gly	Gly	Val
	50					55					60				
Leu	Leu	Pro	Gly	Phe	Val	Asp	Met	His	Val	His	Leu	Arg	Glu	Pro	Gly
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Arg	Glu	Asp	Thr	Glu	Thr	Ile	Ala	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Lys
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Gly	Gly	Phe	Thr	Ala	Val	Phe	Thr	Met	Ala	Asn	Thr	Thr	Pro	Val	Met
			100					105					110		
Asp	Gln	Pro	Val	Ile	Ala	Glu	Ser	Val	Trp	Phe	Lys	Gly	Gln	Asn	Ile
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Gly	Leu	Cys	Asp	Val	His	Pro	Val	Gly	Ser	Ile	Thr	Lys	Gly	Leu	Glu
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Gly	Lys	Glu	Leu	Thr	Glu	Phe	Gly	Met	Met	Ala	Arg	Ser	Glu	Ala	Lys
145					150					155					160
Val	Arg	Met	Phe	Ser	Asp	Asp	Gly	Lys	Cys	Val	Asp	Asp	Pro	Gln	Val
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Met	Arg	Arg	Ala	Leu	Glu	Tyr	Ala	Lys	Gly	Met	Asp	Val	Leu	Ile	Ala
			180					185					190		
Gln	His	Ala	Glu	Asp	His	Arg	Leu	Thr	Glu	Gly	Ala	Ser	Ala	His	Glu
		195					200					205			
Gly	Glu	Asn	Ala	Ala	Arg	Leu	Gly	Leu	Arg	Gly	Trp	Pro	Arg	Val	Ala
	210					215					220				
Glu	Glu	Ser	Ile	Val	Val	Arg	Asp	Ala	Ile	Met	Ala	Arg	Asp	Tyr	Gly
225					230					235					240
Asn	Arg	Val	His	Ile	Cys	His	Ala	Ser	Thr	Glu	Gly	Thr	Val	Glu	Leu
			245						250					255	
Leu	Arg	Trp	Ala	Lys	Ser	Gln	Gly	Ile	Pro	Ile	Thr	Ala	Glu	Val	Thr
			260					265						270	

Pro His His Leu Thr Leu Thr Asp Glu Arg Leu Glu Thr Tyr Asp Ala  
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Val Asn Lys Val Asn Pro Pro Leu Arg Glu Ser Arg Asp Ala Glu Ala  
 290 295 300

Leu Lys Lys Ala Leu Leu Asp Gly Thr Ile Asp Val Val Ala Thr Asp  
 305 310 315 320

His Ala Pro His Gly Ser Glu Asp Lys Cys Cys Glu Phe Glu Asn Ala  
 325 330 335

Lys Pro Gly Met Leu Gly Leu Glu Thr Ser Leu Ser Ile Ile Val Asp  
 340 345 350

Thr Phe Val Ala Thr Gly Leu Ala Asp Trp Arg Phe Val Ala Arg Val  
 355 360 365

Met Ser Glu Arg Pro Ala Glu Ile Thr Arg Leu Pro Gly Gln Gly Arg  
 370 375 380

Pro Ile Ala Glu Gly Glu Pro Ala Asn Leu Ala Ile Val Asp Pro Gly  
 385 390 395 400

Lys Thr Trp Thr Ala Ser Gly Ala Asp Phe Ala Ser Lys Ala Glu Asn  
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 <223> RXA02208

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atc	atc	gca	gtg	cac	gat	gat	tcc	ctc	tcc	cag	gaa	gtc	ttc	ggc	gtc	96
Ile	Ile	Ala	Val	His	Asp	Asp	Ser	Leu	Ser	Gln	Glu	Val	Phe	Gly	Val	
			20					25					30			
acc	ttc	cca	cga	cca	cta	ggc	ctc	gcc	gca	ggt	ttc	gac	aaa	aac	gca	144
Thr	Phe	Pro	Arg	Pro	Leu	Gly	Leu	Ala	Ala	Gly	Phe	Asp	Lys	Asn	Ala	
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tca	atg	gct	gat	gcc	tgg	ggt	gcc	gtt	gga	ttc	gga	tac	gcc	gaa	ctt	192
Ser	Met	Ala	Asp	Ala	Trp	Gly	Ala	Val	Gly	Phe	Gly	Tyr	Ala	Glu	Leu	
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Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu	
65 70 75 80	
ttc cgc ctg cct gcc gac aaa gct atc ttg aac cgc atg gga ttc aac	288
Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn	
85 90 95	
aac ctg ggt gca gca gaa gtc gca aaa aac ctg cgc aac cgg aaa tcc	336
Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser	
100 105 110	
acc gat gtc atc ggc atc aac atc ggt aaa acc aaa gtg gtt ccc gct	384
Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala	
115 120 125	
gaa cac gca gta gat gac tac cgc cgt tct gca tct ttg tta ggt gat	432
Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp	
130 135 140	
ctt gct gat tac ctg gtt gtc aac gtt tcc tcc ccc aac act ccg ggt	480
Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly	
145 150 155 160	
ctc cgc gat ctg cag gct gtg gaa tct ttg cga cca atc ctc gcc gca	528
Leu Arg Asp Leu Gln Ala Val Glu Ser Leu Arg Pro Ile Leu Ala Ala	
165 170 175	
gtg cag gaa tcc acc acc gtc cca gtc ttg gtg aaa atc gca cca gac	576
Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp	
180 185 190	
ctc tcc gac gaa gac atc gac gcc gta gct gac ctg gca gtt gag ctc	624
Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu	
195 200 205	
aaa ctc gcc gga atc gta gcc acc aat acc acc att tcc cgc gaa ggc	672
Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly	
210 215 220	
ctc aac act cct tca ggt gaa gtc gaa gcc atg ggt gct ggc gga atc	720
Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile	
225 230 235 240	
tcc ggt gct cca gta gca gcc cga tct ttg gag gta ctc aag cgc ctc	768
Ser Gly Ala Pro Val Ala Ala Arg Ser Leu Glu Val Leu Lys Arg Leu	
245 250 255	
tac gca cgg gta ggc aaa gag atg gtg ttg atc tct gtc ggt ggc atc	816
Tyr Ala Arg Val Gly Lys Glu Met Val Leu Ile Ser Val Gly Gly Ile	
260 265 270	
agc acc cct gag caa gcc tgg gaa cgc atc acc tcc ggc gca acc ctt	864
Ser Thr Pro Glu Gln Ala Trp Glu Arg Ile Thr Ser Gly Ala Thr Leu	
275 280 285	
ctg cag gga tac acc cca ttc atc tac ggt ggc ccc gat tgg atc aga	912
Leu Gln Gly Tyr Thr Pro Phe Ile Tyr Gly Gly Pro Asp Trp Ile Arg	
290 295 300	
gat atc cac ctt ggt atc gcc aag cag ctg aaa gct cac ggt ctg cgc	960

Asp Ile His Leu Gly Ile Ala Lys Gln Leu Lys Ala His Gly Leu Arg  
 305 310 315 320

aac atc gct gac gct gtg ggc agc gaa ttg gag tgg aag aac  
 1002

Asn Ile Ala Asp Ala Val Gly Ser Glu Leu Glu Trp Lys Asn  
 325 330

taaacagacc aaacacacgt gcc  
 1025

<210> 980

<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 980

Leu Gly Val Val Asp Gly Val Ala Pro Leu Asn Arg Thr Met Glu Lys  
 1 5 10 15

Ile Ile Ala Val His Asp Asp Ser Leu Ser Gln Glu Val Phe Gly Val  
 20 25 30

Thr Phe Pro Arg Pro Leu Gly Leu Ala Ala Gly Phe Asp Lys Asn Ala  
 35 40 45

Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu  
 50 55 60

Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu  
 65 70 75 80

Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn  
 85 90 95

Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser  
 100 105 110

Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala  
 115 120 125

Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp  
 130 135 140

Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly  
 145 150 155 160

Leu Arg Asp Leu Gln Ala Val Glu Ser Leu Arg Pro Ile Leu Ala Ala  
 165 170 175

Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp  
 180 185 190

Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu  
 195 200 205

Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly  
 210 215 220

Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile

225		230		235		240
Ser Gly Ala Pro Val Ala Ala Arg Ser Leu Glu Val Leu Lys Arg Leu						
		245		250		255
Tyr Ala Arg Val Gly Lys Glu Met Val Leu Ile Ser Val Gly Gly Ile						
		260		265		270
Ser Thr Pro Glu Gln Ala Trp Glu Arg Ile Thr Ser Gly Ala Thr Leu						
		275		280		285
Leu Gln Gly Tyr Thr Pro Phe Ile Tyr Gly Gly Pro Asp Trp Ile Arg						
		290		295		300
Asp Ile His Leu Gly Ile Ala Lys Gln Leu Lys Ala His Gly Leu Arg						
		305		310		315
Asn Ile Ala Asp Ala Val Gly Ser Glu Leu Glu Trp Lys Asn						
		325		330		

<210> 981  
 <211> 675  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(652)  
 <223> RXA01660

<400> 981  
 gaaaactggt gtttttcggc cgtgtccacc ccaggttcta tgctgtaaca aacgcggggt 60  
 taaacctcaa tcatcaaatt aggggaagggc tgggaaatcc atg tca tct aat tcc 115  
 Met Ser Ser Asn Ser  
 1 5  
 att aac gca gaa gcg cgc gct gag ctt gct gaa ctg atc aaa gag cta 163  
 Ile Asn Ala Glu Ala Arg Ala Glu Leu Ala Glu Leu Ile Lys Glu Leu  
 10 15 20  
 gct gtc gtc cac ggt gaa gtc acc ttg tct tcg ggc aag aag gct gat 211  
 Ala Val Val His Gly Glu Val Thr Leu Ser Ser Gly Lys Lys Ala Asp  
 25 30 35  
 tac tac atc gat gtc cgt cgt gcc acc ttg cac gcg cgc gca tct cgc 259  
 Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His Ala Arg Ala Ser Arg  
 40 45 50  
 ctg atc ggt cag ctg ctg cgc gaa gcc acc gct gac tgg gac tat gac 307  
 Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala Asp Trp Asp Tyr Asp  
 55 60 65  
 gca gtt ggc ggc ctg acc ttg ggc gct gac ccg gtt gcc acc gcc atc 355  
 Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro Val Ala Thr Ala Ile  
 70 75 80 85  
 atg cac gcc gac ggc cgc gat atc aac gcg ttt gtg gtg cgc aag gag 403  
 Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe Val Val Arg Lys Glu  
 90 95 100

gcc aag aag cac ggc atg cag cgt cgc att gag ggc cct gac ctg acg 451  
 Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu Gly Pro Asp Leu Thr  
 105 110 115

ggc aag aag gtg ctc gtg gtg gaa gat acc acc acc acc gga aat tcc 499  
 Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr Thr Thr Gly Asn Ser  
 120 125 130

cct ctg aca gct gtt gcc gcg ttg cgt gaa gct ggc att gag gtt gtg 547  
 Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala Gly Ile Glu Val Val  
 135 140 145

ggc gtt gcc acc gtg gtc gat cgc gca acc ggt gca gat gag gtt atc 595  
 Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly Ala Asp Glu Val Ile  
 150 155 160 165

gca gcg gaa ggc ctt cct tac cgc agc ttg ctg gga ctt tct gat ctt 643  
 Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu Gly Leu Ser Asp Leu  
 170 175 180

gga ctc aac taacaccccc ggccccacgg agt 675  
 Gly Leu Asn

&lt;210&gt; 982

&lt;211&gt; 184

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 982

Met Ser Ser Asn Ser Ile Asn Ala Glu Ala Arg Ala Glu Leu Ala Glu  
 1 5 10 15

Leu Ile Lys Glu Leu Ala Val Val His Gly Glu Val Thr Leu Ser Ser  
 20 25 30

Gly Lys Lys Ala Asp Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His  
 35 40 45

Ala Arg Ala Ser Arg Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala  
 50 55 60

Asp Trp Asp Tyr Asp Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro  
 65 70 75 80

Val Ala Thr Ala Ile Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe  
 85 90 95

Val Val Arg Lys Glu Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu  
 100 105 110

Gly Pro Asp Leu Thr Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr  
 115 120 125

Thr Thr Gly Asn Ser Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala  
 130 135 140

Gly Ile Glu Val Val Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly  
 145 150 155 160



Ala Asp Glu Val Ile Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu  
 165 170 175

Gly Leu Ser Asp Leu Gly Leu Asn  
 180

<210> 983

<211> 957

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(934)

<223> RXA02235

<400> 983

gtgtcaccgc agctgtccag ggcataagagg ccctgcgtga gggcggtgtc agcgtccgcg 60

cgctgcagga actcgaccac gcagtcaagg cttaagccct atg aca ttc ggc gag 115  
 Met Thr Phe Gly Glu  
 1 5

aag ctt ctg aac gcc gcc tcc acc cgt ggc agg cta tgc gtg ggc att 163  
 Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg Leu Cys Val Gly Ile  
 10 15 20

gat ccc cac gaa agc ctg ctg acg tcc tgg ggg ctg ccg gta aac gta 211  
 Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly Leu Pro Val Asn Val  
 25 30 35

gac gga ctt gcg gag ttc tcc cgc gcc tgc gtg gag gct ttc gcc gac 259  
 Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val Glu Ala Phe Ala Asp  
 40 45 50

acc gtg gca ttg gtg aag cct cag gtg gcg ttc tat gag cgt ttc ggt 307  
 Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe Tyr Glu Arg Phe Gly  
 55 60 65

tcc gct ggc ttt gcc atc ttg gaa gaa acc att cag acg ctg cgt gag 355  
 Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile Gln Thr Leu Arg Glu  
 70 75 80 85

cgt ggc tgt ttg gtg gtc tct gac gcc aaa cgc ggc gat att ggc tcc 403  
 Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg Gly Asp Ile Gly Ser  
 90 95 100

acc atg gct ggc tat gcc tca gcg tgg tta gat cca gcg tca ccg ctg 451  
 Thr Met Ala Gly Tyr Ala Ser Ala Trp Leu Asp Pro Ala Ser Pro Leu  
 105 110 115

tct agc gac gct gtg acg gtc tct ccc tac ctt ggt ttt cat tcc ttg 499  
 Ser Ser Asp Ala Val Thr Val Ser Pro Tyr Leu Gly Phe His Ser Leu  
 120 125 130

gac cca gtg ttc gaa ctt gcc gag caa cac ggc agg gga gtg ttt gtc 547  
 Asp Pro Val Phe Glu Leu Ala Glu Gln His Gly Arg Gly Val Phe Val  
 135 140 145

ttg gcc gcg acc tca aac cct gag gcc cgc gaa ctc cag gac cag caa 595  
 Leu Ala Ala Thr Ser Asn Pro Glu Ala Arg Glu Leu Gln Asp Gln Gln  
 150 155 160 165  
  
 aac gct gac ggc gtg agc att tcc cag cag atc gtg gat cag gca gcg 643  
 Asn Ala Asp Gly Val Ser Ile Ser Gln Gln Ile Val Asp Gln Ala Ala  
 170 175 180  
  
 gcg ctt aac gcg cct tat atg gcc cag ggc aag gct ggc aac att ggc 691  
 Ala Leu Asn Ala Pro Tyr Met Ala Gln Gly Lys Ala Gly Asn Ile Gly  
 185 190 195  
  
 gtc gtc atc ggc gcc acc ttg tcc aaa cca cca cgc tta tcg acg ctc 739  
 Val Val Ile Gly Ala Thr Leu Ser Lys Pro Pro Arg Leu Ser Thr Leu  
 200 205 210  
  
 ggg ggc gcc att ttg atg ccc ggc gtc ggc gcc cag ggc ggc acg gca 787  
 Gly Gly Ala Ile Leu Met Pro Gly Val Gly Ala Gln Gly Gly Thr Ala  
 215 220 225  
  
 agc gac gtt gat gag att gcg gga gac atg gct cat ctt gca ttc cca 835  
 Ser Asp Val Asp Glu Ile Ala Gly Asp Met Ala His Leu Ala Phe Pro  
 230 235 240 245  
  
 aat gtc tct aga agt att ttg gcg aca ggc cca gat atc gct gaa atg 883  
 Asn Val Ser Arg Ser Ile Leu Ala Thr Gly Pro Asp Ile Ala Glu Met  
 250 255 260  
  
 aag aat tct gtg gca aaa aat gct gca gac ttt cct ggt ttc ccc agg 931  
 Lys Asn Ser Val Ala Lys Asn Ala Ala Asp Phe Pro Gly Phe Pro Arg  
 265 270 275  
  
 tca tagtcgcgga aacggccctt aat 957  
 Ser

<210> 984  
 <211> 278  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 984  
 Met Thr Phe Gly Glu Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg  
 1 5 10 15  
  
 Leu Cys Val Gly Ile Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly  
 20 25 30  
  
 Leu Pro Val Asn Val Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val  
 35 40 45  
  
 Glu Ala Phe Ala Asp Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe  
 50 55 60  
  
 Tyr Glu Arg Phe Gly Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile  
 65 70 75 80  
  
 Gln Thr Leu Arg Glu Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg  
 85 90 95

Gly Asp Ile Gly Ser Thr Met Ala Gly Tyr Ala Ser Ala Trp Leu Asp  
 100 105 110  
 Pro Ala Ser Pro Leu Ser Ser Asp Ala Val Thr Val Ser Pro Tyr Leu  
 115 120 125  
 Gly Phe His Ser Leu Asp Pro Val Phe Glu Leu Ala Glu Gln His Gly  
 130 135 140  
 Arg Gly Val Phe Val Leu Ala Ala Thr Ser Asn Pro Glu Ala Arg Glu  
 145 150 155 160  
 Leu Gln Asp Gln Gln Asn Ala Asp Gly Val Ser Ile Ser Gln Gln Ile  
 165 170 175  
 Val Asp Gln Ala Ala Ala Leu Asn Ala Pro Tyr Met Ala Gln Gly Lys  
 180 185 190  
 Ala Gly Asn Ile Gly Val Val Ile Gly Ala Thr Leu Ser Lys Pro Pro  
 195 200 205  
 Arg Leu Ser Thr Leu Gly Gly Ala Ile Leu Met Pro Gly Val Gly Ala  
 210 215 220  
 Gln Gly Gly Thr Ala Ser Asp Val Asp Glu Ile Ala Gly Asp Met Ala  
 225 230 235 240  
 His Leu Ala Phe Pro Asn Val Ser Arg Ser Ile Leu Ala Thr Gly Pro  
 245 250 255  
 Asp Ile Ala Glu Met Lys Asn Ser Val Ala Lys Asn Ala Ala Asp Phe  
 260 265 270  
 Pro Gly Phe Pro Arg Ser  
 275

<210> 985  
 <211> 852  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(829)  
 <223> RXN01892

<400> 985  
 ggtctcagtg gcttcttggt tgctgtgatt ttttcaaggc gtaccccgtag gccgatgtta 60  
 aaagcgggtg gcacaacccc tactgaagga gaacaccact gtg acc acc tcg agt 115  
 Val Thr Thr Ser Ser  
 1 5  
 gaa caa ccc cgt aca gga tac aag cga gtg atg tta aag ctc gga ggt 163  
 Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met Leu Lys Leu Gly Gly  
 10 15 20  
 gaa atg ttt ggt ggt ggc aaa gtc ggc gtc gat cct gat gta gta gac 211  
 Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp Pro Asp Val Val Asp  
 25 30 35

aat gtt gca cgt cag atc gct gaa gtt gct aaa act gga gca gag att 259  
 Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys Thr Gly Ala Glu Ile  
 40 45 50

gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt cag 307  
 Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu Gln  
 55 60 65

cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc ggc 355  
 Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu Gly  
 70 75 80 85

aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat ggc 403  
 Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His Gly  
 90 95 100

gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca gaa 451  
 Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala Glu  
 105 110 115

cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc gtt 499  
 Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg Val  
 120 125 130

gtc atc ttc ggt gct ggc atg ggt atg ccg tac ttt tcc acg gac acc 547  
 Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp Thr  
 135 140 145

act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg atg 595  
 Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu Met  
 150 155 160 165

gct aag gct gtt gac ggt gtg tac agc gat gat cct cgt acc aac cca 643  
 Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp Pro Arg Thr Asn Pro  
 170 175 180

gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag aag 691  
 Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu Lys  
 185 190 195

ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac aac 739  
 Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp Asn  
 200 205 210

aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att gct 787  
 Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile Ala  
 215 220 225

cgc gcc atc agc ggt gaa cgt atc ggt act ctg gtc gag tcc 829  
 Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu Val Glu Ser  
 230 235 240

tgatacattt agtcttataa aca 852

&lt;210&gt; 986

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 986

Val Thr Thr Ser Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met  
 1 5 10 15  
 Leu Lys Leu Gly Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp  
 20 25 30  
 Pro Asp Val Val Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys  
 35 40 45  
 Thr Gly Ala Glu Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg  
 50 55 60  
 Gly Ala Glu Leu Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr  
 65 70 75 80  
 Met Gly Met Leu Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe  
 85 90 95  
 Leu Gly Gln His Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met  
 100 105 110  
 Ala Gln Val Ala Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu  
 115 120 125  
 Glu Lys Gly Arg Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr  
 130 135 140  
 Phe Ser Thr Asp Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys  
 145 150 155 160  
 Asp Val Leu Leu Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp  
 165 170 175  
 Pro Arg Thr Asn Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys  
 180 185 190  
 Glu Val Ile Glu Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser  
 195 200 205  
 Leu Cys Met Asp Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr  
 210 215 220  
 Glu Gly Asn Ile Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu  
 225 230 235 240  
 Val Glu Ser

&lt;210&gt; 987

&lt;211&gt; 798

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (47) .. (775)

&lt;223&gt; FRXA01892

&lt;400&gt; 987

atgttaaaag cggttggcac aaccctact gaaggagaac accacggtg acc acc tcg 58  
Val Thr Thr Ser  
1

agt gaa caa ccc cgt aca gga tac aaa cga gtg atg tta aag ctc gaa 106  
Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met Leu Lys Leu Glu  
5 10 15 20

ggt gaa atg ttt ggt ggt ggc aaa gtc ggc gtc gat cct gat gta gta 154  
Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp Pro Asp Val Val  
25 30 35

gac aat gtt gca cgt cag atc gct gaa gtt gct aaa act gga gca gag 202  
Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys Thr Gly Ala Glu  
40 45 50

att gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt 250  
Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu  
55 60 65

cag cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc 298  
Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu  
70 75 80

ggc aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat 346  
Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His  
85 90 95 100

ggc gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca 394  
Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala  
105 110 115

gaa cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc 442  
Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg  
120 125 130

gtt gtc atc ttc ggt gct ggc atg ggt atg ccg tac ttt tcc acg gac 490  
Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp  
135 140 145

acc act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg 538  
Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu  
150 155 160

atg	gct	aag	gct	gtt	gac	ggt	gtg	tac	agc	gat	gat	cct	cgt	acc	aac	586
Met	Ala	Lys	Ala	Val	Asp	Gly	Val	Tyr	Ser	Asp	Asp	Pro	Arg	Thr	Asn	
165					170					175					180	

cca gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag 634  
Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu  
185 190 195

aag ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac 682  
Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp  
200 205 210

aac aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att 730  
Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile  
215 220 225

gct cgc gcc atc agc ggt gaa cgt atc ggt act ctg gtc gag tcc 775

Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu Val Glu Ser  
 230 235 240

tgatacattt agtcttataa aca

798

<210> 988

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 988

Val Thr Thr Ser Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met  
 1 5 10 15

Leu Lys Leu Glu Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp  
 20 25 30

Pro Asp Val Val Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys  
 35 40 45

Thr Gly Ala Glu Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg  
 50 55 60

Gly Ala Glu Leu Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr  
 65 70 75 80

Met Gly Met Leu Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe  
 85 90 95

Leu Gly Gln His Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met  
 100 105 110

Ala Gln Val Ala Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu  
 115 120 125

Glu Lys Gly Arg Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr  
 130 135 140

Phe Ser Thr Asp Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys  
 145 150 155 160

Asp Val Leu Leu Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp  
 165 170 175

Pro Arg Thr Asn Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys  
 180 185 190

Glu Val Ile Glu Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser  
 195 200 205

Leu Cys Met Asp Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr  
 210 215 220

Glu Gly Asn Ile Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu  
 225 230 235 240

Val Glu Ser

<210> 989  
 <211> 798  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(775)  
 <223> RXA00105

<400> 989  
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cgaggagaat ggaacttact aacgctgtta tgatgacggc atg act gtt cca acg 115  
 Met Thr Val Pro Thr  
 1 5

cct tat gaa gac ctt ctt cgg aag att gct gaa gaa ggg tcc cac aag 163  
 Pro Tyr Glu Asp Leu Leu Arg Lys Ile Ala Glu Glu Gly Ser His Lys  
 10 15 20

gac gac cgc acc ggc acc ggc act act tct tta ttc gga caa caa atc 211  
 Asp Asp Arg Thr Gly Thr Gly Thr Thr Ser Leu Phe Gly Gln Gln Ile  
 25 30 35

cgc ttt gat ctc aat gaa ggt ttt ccc ctt ctg acc acc aag aag gtc 259  
 Arg Phe Asp Leu Asn Glu Gly Phe Pro Leu Leu Thr Thr Lys Lys Val  
 40 45 50

cat ttc cac tct gtt gtg ggt gag ctt ttg tgg ttc ctt cag ggg gat 307  
 His Phe His Ser Val Val Gly Glu Leu Leu Trp Phe Leu Gln Gly Asp  
 55 60 65

tcc aac gtc aaa tgg ctg cag gat aac aac atc cgc att tgg aat gaa 355  
 Ser Asn Val Lys Trp Leu Gln Asp Asn Asn Ile Arg Ile Trp Asn Glu  
 70 75 80 85

tgg gca gat gag gac ggc gag ctg ggc cct gtt tat ggt gtc cag tgg 403  
 Trp Ala Asp Glu Asp Gly Glu Leu Gly Pro Val Tyr Gly Val Gln Trp  
 90 95 100

cgt tct tgg cca acc cct gat ggt cgt cac att gac cag atc tca ggt 451  
 Arg Ser Trp Pro Thr Pro Asp Gly Arg His Ile Asp Gln Ile Ser Gly  
 105 110 115

gct tta gaa act ctg cga aac aac cct gat tca cgt cgc aat att gtc 499  
 Ala Leu Glu Thr Leu Arg Asn Asn Pro Asp Ser Arg Arg Asn Ile Val  
 120 125 130

tcg gcg tgg aat gtt tcc gag ctt gaa aac atg gct ctt ccc cct tgt 547  
 Ser Ala Trp Asn Val Ser Glu Leu Glu Asn Met Ala Leu Pro Pro Cys  
 135 140 145

cac ttg ctt ttc cag ctc tat gtc gcc gat ggc aaa ctg tct tgc cag 595  
 His Leu Leu Phe Gln Leu Tyr Val Ala Asp Gly Lys Leu Ser Cys Gln  
 150 155 160 165

ctc tac cag cgt tct gcg gac atg ttc ctg ggt gtg cct ttc aac atc 643  
 Leu Tyr Gln Arg Ser Ala Asp Met Phe Leu Gly Val Pro Phe Asn Ile  
 170 175 180



gca tct tat gca ctg ctc acc cac atg ttt gcc cag cag gca ggc ttg 691  
 Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala Gln Gln Ala Gly Leu  
                   185                                  190                                  195

gaa gtc ggc gag ttc att tgg act ggc ggc gac tgc cac att tat gac 739  
 Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp Cys His Ile Tyr Asp  
                   200                                  205                                  210

aac cac aag gaa cag gtc gcg gag cag ctg agc cga taagctcgcc 785  
 Asn His Lys Glu Gln Val Ala Glu Gln Leu Ser Arg  
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cctacccac ctt 798

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 <213> Corynebacterium glutamicum

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                   20                                  25                                  30

Phe Gly Gln Gln Ile Arg Phe Asp Leu Asn Glu Gly Phe Pro Leu Leu  
                   35                                  40                                  45

Thr Thr Lys Lys Val His Phe His Ser Val Val Gly Glu Leu Leu Trp  
           50                                  55                                  60

Phe Leu Gln Gly Asp Ser Asn Val Lys Trp Leu Gln Asp Asn Asn Ile  
           65                                  70                                  75                                  80

Arg Ile Trp Asn Glu Trp Ala Asp Glu Asp Gly Glu Leu Gly Pro Val  
                   85                                  90                                  95

Tyr Gly Val Gln Trp Arg Ser Trp Pro Thr Pro Asp Gly Arg His Ile  
                   100                                  105                                  110

Asp Gln Ile Ser Gly Ala Leu Glu Thr Leu Arg Asn Asn Pro Asp Ser  
                   115                                  120                                  125

Arg Arg Asn Ile Val Ser Ala Trp Asn Val Ser Glu Leu Glu Asn Met  
           130                                  135                                  140

Ala Leu Pro Pro Cys His Leu Leu Phe Gln Leu Tyr Val Ala Asp Gly  
           145                                  150                                  155                                  160

Lys Leu Ser Cys Gln Leu Tyr Gln Arg Ser Ala Asp Met Phe Leu Gly  
                   165                                  170                                  175

Val Pro Phe Asn Ile Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala  
                   180                                  185                                  190

Gln Gln Ala Gly Leu Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp  
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Cys His Ile Tyr Asp Asn His Lys Glu Gln Val Ala Glu Gln Leu Ser

210 215 220

Arg  
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Met Ile Val Ser Ile  
1 5

gag gga atc gac ggc gcc ggc aaa aac acc ctg gtt tcg gca tta acg 163  
Glu Gly Ile Asp Gly Ala Gly Lys Asn Thr Leu Val Ser Ala Leu Thr  
10 15 20

cag gtt att gat gca aaa gtc ctt gca ttc cca cgt tat gaa acc tcg 211  
Gln Val Ile Asp Ala Lys Val Leu Ala Phe Pro Arg Tyr Glu Thr Ser  
25 30 35

att cac gcc caa ttg gcc gcg gaa gca ctc cac ggc cgc atg ggc gac 259  
Ile His Ala Gln Leu Ala Ala Glu Ala Leu His Gly Arg Met Gly Asp  
40 45 50

ctc acc gac agc gcc tac gcc atg gcc acg ctt ttc gcc ctc gac cgc 307  
Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu Phe Ala Leu Asp Arg  
55 60 65

cac ttc gcg att gat gac tta aat gcg ccc ggc gtg gtg ctg ctc gac 355  
His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly Val Val Leu Leu Asp  
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cga tac gtc gcc tcc aac gcg gct tat acc gcc gcc aga ttg ctt gac 403  
Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala Ala Arg Leu Leu Asp  
90 95 100

gac gac gcc ccc cgc tgg gtt gcc gac ctg gaa ttc ggg cgg ctt ggg 451  
Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu Phe Gly Arg Leu Gly  
105 110 115

ctc cca cgt ccg acg ctt caa gtg ttg ttg gat acc ccc gcg gag gta 499  
Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp Thr Pro Ala Glu Val  
120 125 130

gcg caa gat agg gct aga cgt cga gaa gcg ctt gac tcc gcg cgt gcg 547  
Ala Gln Asp Arg Ala Arg Arg Arg Glu Ala Leu Asp Ser Ala Arg Ala  
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cgg gac cgc tat gaa tcg gat tcg gcg ctg cag caa cgc acc gcc gag 595  
Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln Gln Arg Thr Ala Glu

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His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu Ser Pro Trp Ile Val							
		170		175		180	
ggt gcc cct gat gaa gac ccc ggc cac gtt gcg cag aga atc gtg gaa							691
Val Ala Pro Asp Glu Asp Pro Gly His Val Ala Gln Arg Ile Val Glu							
		185		190		195	
ttc ctg ggt act ata aac taatcccaat tagcaggaag gat							732
Phe Leu Gly Thr Ile Asn							
		200					

&lt;210&gt; 992

&lt;211&gt; 203

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 992

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Val Ser Ala Leu Thr Gln Val Ile Asp Ala Lys Val Leu Ala Phe Pro																
			20				25							30		
Arg Tyr Glu Thr Ser Ile His Ala Gln Leu Ala Ala Glu Ala Leu His																
		35				40						45				
Gly Arg Met Gly Asp Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu																
		50				55					60					
Phe Ala Leu Asp Arg His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly																
		65			70				75						80	
Val Val Leu Leu Asp Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala																
				85				90						95		
Ala Arg Leu Leu Asp Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu																
			100					105					110			
Phe Gly Arg Leu Gly Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp																
		115					120					125				
Thr Pro Ala Glu Val Ala Gln Asp Arg Ala Arg Arg Arg Glu Ala Leu																
		130				135						140				
Asp Ser Ala Arg Ala Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln																
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Gln Arg Thr Ala Glu His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu																
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Ser Pro Trp Ile Val Val Ala Pro Asp Glu Asp Pro Gly His Val Ala																
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 Met Thr Glu Arg Thr  
 1 5

ctc atc ctt atc aag cca gac ggt gtt acc aac gga cac gtc ggc gaa 163  
 Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn Gly His Val Gly Glu  
 10 15 20

atc atc gca cgt att gag cgc aag ggc ctg aag ctc gct gct ctg gat 211  
 Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys Leu Ala Ala Leu Asp  
 25 30 35

ctg cgt gtt gca gac cgc gag acc gct gaa aag cac tac gaa gag cac 259  
 Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys His Tyr Glu Glu His  
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gct gac aag cca ttc ttc ggt gag ctc gtt gaa ttc atc acc tct gca 307  
 Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu Phe Ile Thr Ser Ala  
 55 60 65

cct ctg atc gca ggc atc gtc gaa ggc gag cgt gca atc gat gca tgg 355  
 Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg Ala Ile Asp Ala Trp  
 70 75 80 85

cgt cag ctt gct ggt ggc acc gac cca gtt gct aag gca acc cca ggc 403  
 Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala Lys Ala Thr Pro Gly  
 90 95 100

acc atc cgc ggc gat ttc gca ctg act gtt gga gag aac gtt gtt cac 451  
 Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly Glu Asn Val Val His  
 105 110 115

ggt tct gat tcc cca gag tcc gct gag cgc gag atc tcc atc tgg ttc 499  
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 Pro Asn Leu  
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Leu Ala Ala Leu Asp Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys	35	40	45
His Tyr Glu Glu His Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu	50	55	60
Phe Ile Thr Ser Ala Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg	65	70	75
Ala Ile Asp Ala Trp Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala	85	90	95
Lys Ala Thr Pro Gly Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly	100	105	110
Glu Asn Val Val His Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu	115	120	125
Ile Ser Ile Trp Phe Pro Asn Leu	130	135	

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 Val Thr Glu Ile Ser 5  
 1  
 aac atg cct gcc ggt ggc ctc atc gta gcc atc gac ggg ccg tct ggc 163  
 Asn Met Pro Ala Gly Gly Leu Ile Val Ala Ile Asp Gly Pro Ser Gly 20  
 10 15  
 acc gga aaa tcc acc aca tcc cgc gcg ctc gca acc cgt ctc tcg gcc 211  
 Thr Gly Lys Ser Thr Thr Ser Arg Ala Leu Ala Thr Arg Leu Ser Ala 35  
 25 30  
 aag tac cta gat act ggt gcg atg tac cgc gtc gca acg ctt cat gtg 259  
 Lys Tyr Leu Asp Thr Gly Ala Met Tyr Arg Val Ala Thr Leu His Val 50  
 40 45  
 ctt aac cag ggg att gac cct gca gat agc gca gcc gtg atc gct gca 307  
 Leu Asn Gln Gly Ile Asp Pro Ala Asp Ser Ala Ala Val Ile Ala Ala 65  
 55 60  
 acc gct gta ttg ccg ttg tcg att tct gac gat ccc gcc tcc act gag 355

Thr Ala Val Leu Pro Leu Ser Ile Ser Asp Asp Pro Ala Ser Thr Glu  
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 Val Leu Leu Ala Gly Val Asp Val Gln Lys Asp Ile Arg Gly Pro Glu 100  
 90 95  
 gtc acc caa aat gtc tcc gca gtg tcc gcg atc cct gag gtt cgt gaa 451  
 Val Thr Gln Asn Val Ser Ala Val Ser Ala Ile Pro Glu Val Arg Glu 115  
 105 110  
 aac ttg gtg gcg ttg cag cgc gca ctc gcc gcc aaa gca cat cgc tgc 499  
 Asn Leu Val Ala Leu Gln Arg Ala Leu Ala Ala Lys Ala His Arg Cys 130  
 120 125  
 gtc gtc gaa ggc aga gac atc gga acg gca gtg ctt gtc gac gcg ccc 547  
 Val Val Glu Gly Arg Asp Ile Gly Thr Ala Val Leu Val Asp Ala Pro 145  
 135 140  
 atc aag gcg ttt ctc acc gcc tca gcg gaa gtc cgc gcc cag cga cgc 595  
 Ile Lys Ala Phe Leu Thr Ala Ser Ala Glu Val Arg Ala Gln Arg Arg 165  
 150 155 160  
 ttt gac caa gac acc gca gca ggt cgc gac gta gat ttc gac gct gtg 643  
 Phe Asp Gln Asp Thr Ala Ala Gly Arg Asp Val Asp Phe Asp Ala Val 180  
 170 175  
 ctg gca gat gtt gtt cgc cgc gat gaa cta gat tcc acc cgt gcc gcc 691  
 Leu Ala Asp Val Val Arg Arg Asp Glu Leu Asp Ser Thr Arg Ala Ala 195  
 185 190  
 tca ccg ctg aaa cca gca gat gat gca cac atc gtg gac acc tct gat 739  
 Ser Pro Leu Lys Pro Ala Asp Asp Ala His Ile Val Asp Thr Ser Asp 210  
 200 205  
 atg acc atg gat caa gta ctt gat cac ctc atc cac cta gtg gaa gcc 787  
 Met Thr Met Asp Gln Val Leu Asp His Leu Ile His Leu Val Glu Ala 225  
 215 220  
 tcc gct gaa agg agc aac cag tgactgataa acacaccatg cct 831  
 Ser Ala Glu Arg Ser Asn Gln 235  
 230 235

&lt;210&gt; 996

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 996

Val Thr Glu Ile Ser Asn Met Pro Ala Gly Gly Leu Ile Val Ala Ile  
 1 5 10 15  
 Asp Gly Pro Ser Gly Thr Gly Lys Ser Thr Thr Ser Arg Ala Leu Ala  
 20 25 30  
 Thr Arg Leu Ser Ala Lys Tyr Leu Asp Thr Gly Ala Met Tyr Arg Val  
 35 40 45  
 Ala Thr Leu His Val Leu Asn Gln Gly Ile Asp Pro Ala Asp Ser Ala  
 50 55 60

Ala Val Ile Ala Ala Thr Ala Val Leu Pro Leu Ser Ile Ser Asp Asp  
65 70 75 80

Pro Ala Ser Thr Glu Val Leu Leu Ala Gly Val Asp Val Gln Lys Asp  
85 90 95

Ile Arg Gly Pro Glu Val Thr Gln Asn Val Ser Ala Val Ser Ala Ile  
100 105 110

Pro Glu Val Arg Glu Asn Leu Val Ala Leu Gln Arg Ala Leu Ala Ala  
115 120 125

Lys Ala His Arg Cys Val Val Glu Gly Arg Asp Ile Gly Thr Ala Val  
130 135 140

Leu Val Asp Ala Pro Ile Lys Ala Phe Leu Thr Ala Ser Ala Glu Val  
145 150 155 160

Arg Ala Gln Arg Arg Phe Asp Gln Asp Thr Ala Ala Gly Arg Asp Val  
165 170 175

Asp Phe Asp Ala Val Leu Ala Asp Val Val Arg Arg Asp Glu Leu Asp  
180 185 190

Ser Thr Arg Ala Ala Ser Pro Leu Lys Pro Ala Asp Asp Ala His Ile  
195 200 205

Val Asp Thr Ser Asp Met Thr Met Asp Gln Val Leu Asp His Leu Ile  
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Met Thr Ser Ser Arg  
1 5

aaa gtc cgt ccc acc aaa cac att ttc gtc acc ggt gga gtt gtt tcc 163  
Lys Val Arg Pro Thr Lys His Ile Phe Val Thr Gly Gly Val Val Ser  
10 15 20

tca ctc ggc aaa ggc ctg acc gca gca agc ctt ggt caa ttg ctg att 211  
Ser Leu Gly Lys Gly Leu Thr Ala Ala Ser Leu Gly Gln Leu Leu Ile  
25 30 35

gca cgg gga ctg tcg gtg acc atg cag aag ctg gat cca tac ctc aat 259

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Val	Asp	Pro	Gly	Thr	Met	Asn	Pro	Phe	Glu	His	Gly	Glu	Val	Phe	Val	
	55					60					65					
acc	gaa	gac	ggg	gca	gaa	aca	gac	ctg	gat	ttg	ggc	cac	tac	gag	cgt	355
Thr	Glu	Asp	Gly	Ala	Glu	Thr	Asp	Leu	Asp	Leu	Gly	His	Tyr	Glu	Arg	
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ttc	ctc	gat	cgc	aac	ctg	ggg	ctc	aac	gcc	aat	gtc	acc	acc	ggc	aag	403
Phe	Leu	Asp	Arg	Asn	Leu	Gly	Leu	Asn	Ala	Asn	Val	Thr	Thr	Gly	Lys	
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Val	Tyr	Ser	Thr	Val	Ile	Ala	Lys	Glu	Arg	Arg	Gly	Glu	Tyr	Leu	Gly	
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Lys	Thr	Val	Gln	Val	Ile	Pro	His	Ile	Thr	Asp	Glu	Ile	Lys	Ala	Arg	
		120					125					130				
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Ile	Leu	Ser	Met	Gly	Glu	Pro	Asp	Ala	His	Gly	Asn	Ala	Pro	Asp	Val	
	135					140					145					
gtg	atc	tct	gag	gtc	ggc	ggc	acc	gtc	ggc	gac	att	gaa	tcc	cag	cca	595
Val	Ile	Ser	Glu	Val	Gly	Gly	Thr	Val	Gly	Asp	Ile	Glu	Ser	Gln	Pro	
150					155					160					165	
ttc	ctt	gaa	gca	gct	cgc	cag	gta	cgc	cat	gaa	att	ggc	cgt	gaa	aac	643
Phe	Leu	Glu	Ala	Ala	Arg	Gln	Val	Arg	His	Glu	Ile	Gly	Arg	Glu	Asn	
				170					175					180		
tgc	ttc	ttc	atc	cac	tgt	tct	ttg	gtg	cca	tac	ttg	gct	acc	tca	ggc	691
Cys	Phe	Phe	Ile	His	Cys	Ser	Leu	Val	Pro	Tyr	Leu	Ala	Thr	Ser	Gly	
			185					190					195			
gag	ctg	aag	acc	aaa	ccc	acc	cag	cat	tct	gtc	gca	gag	ctg	cgc	ggc	739
Glu	Leu	Lys	Thr	Lys	Pro	Thr	Gln	His	Ser	Val	Ala	Glu	Leu	Arg	Gly	
		200					205					210				
atc	ggc	att	ttg	ccg	gat	gct	ctc	gtg	ctt	cgt	tgc	gat	cgg	gag	gtc	787
Ile	Gly	Ile	Leu	Pro	Asp	Ala	Leu	Val	Leu	Arg	Cys	Asp	Arg	Glu	Val	
	215					220					225					
cct	caa	ggc	ctg	aaa	gat	aag	atc	gcg	atg	atg	tgc	gat	ggt	gat	tat	835
Pro	Gln	Gly	Leu	Lys	Asp	Lys	Ile	Ala	Met	Met	Cys	Asp	Val	Asp	Tyr	
230					235					240					245	
gaa	ggc	ggt	gta	tct	tgc	cct	gat	tcc	agt	tct	att	tac	aac	att	cca	883
Glu	Gly	Val	Val	Ser	Cys	Pro	Asp	Ser	Ser	Ser	Ile	Tyr	Asn	Ile	Pro	
				250					255					260		
gat	gtc	ctc	tac	cgc	gag	cac	ctg	gac	acc	ttc	att	att	cgt	cgc	ctg	931
Asp	Val	Leu	Tyr	Arg	Glu	His	Leu	Asp	Thr	Phe	Ile	Ile	Arg	Arg	Leu	
			265					270					275			
ggc	ctt	ccg	ttc	cgt	gat	ggt	gac	tgg	agc	acc	tgg	cac	gat	ctg	ctg	979
Gly	Leu	Pro	Phe	Arg	Asp	Val	Asp	Trp	Ser	Thr	Trp	His	Asp	Leu	Leu	



280	285	290
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Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr Val Gly Ile Val Gly 295 300 305		
aag tac att gat ctt ccc gat gct tat ctc tca gtg gtg gaa gct gtt 1075		
Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser Val Val Glu Ala Val 310 315 320 325		
cgc gct gca ggc tac gcc aat tgg acg cgc acc aat atc aag tgg att 1123		
Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr Asn Ile Lys Trp Ile 330 335 340		
acc tca gat gat tgc gaa acc cca tct ggc gcc atg aaa gcg ctc agc 1171		
Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala Met Lys Ala Leu Ser 345 350 355		
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Gly Leu Asp Ala Ile Val Val Pro Gly Gly Phe Gly Ile Arg Gly Ile 360 365 370		
gaa ggc aaa atc ggt gcg att acg ttt gca cgt gag cac aag atc ccg 1267		
Glu Gly Lys Ile Gly Ala Ile Thr Phe Ala Arg Glu His Lys Ile Pro 375 380 385		
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cgc cag gca gga ctg gag cag gca tca tcc act gag ttt gac cca gct 1363		
Arg Gln Ala Gly Leu Glu Gln Ala Ser Ser Thr Glu Phe Asp Pro Ala 410 415 420		
gca acg cag cca gtg atc gcc acc atg gaa gag cag aaa gct gct gtg 1411		
Ala Thr Gln Pro Val Ile Ala Thr Met Glu Glu Gln Lys Ala Ala Val 425 430 435		
tcg ggt gaa gct gat ctg ggt ggc acc atg cgt ctt ggc gca tat cct 1459		
Ser Gly Glu Ala Asp Leu Gly Gly Thr Met Arg Leu Gly Ala Tyr Pro 440 445 450		
gca acc ctg gag gaa ggc tcc tta gta gcg gaa ctg tat ggc aca acg 1507		
Ala Thr Leu Glu Glu Gly Ser Leu Val Ala Glu Leu Tyr Gly Thr Thr 455 460 465		
gaa gtc tcc gag cgc cac cgt cac cgc tat gag gtc aat aat gcc tac 1555		
Glu Val Ser Glu Arg His Arg His Arg Tyr Glu Val Asn Asn Ala Tyr 470 475 480 485		

cgc gcc cag att gct gaa ggt tca gat ttg gtc ttc tcc gga acc tca  
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Arg Ala Gln Ile Ala Glu Gly Ser Asp Leu Val Phe Ser Gly Thr Ser  
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1651

Pro Asp Gly His Leu Val Glu Phe Val Glu Tyr Pro Lys Glu Val His  
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1699

Pro Tyr Leu Val Ala Thr Gln Ala His Pro Glu Tyr Lys Ser Arg Pro  
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Thr His Ala His Pro Leu Phe Tyr Gly Leu Val Lys Thr Ala Leu Glu  
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35 40 45

Asp Pro Tyr Leu Asn Val Asp Pro Gly Thr Met Asn Pro Phe Glu His  
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Gly Glu Val Phe Val Thr Glu Asp Gly Ala Glu Thr Asp Leu Asp Leu  
65 70 75 80

Gly His Tyr Glu Arg Phe Leu Asp Arg Asn Leu Gly Leu Asn Ala Asn  
85 90 95

Val Thr Thr Gly Lys Val Tyr Ser Thr Val Ile Ala Lys Glu Arg Arg  
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Gly Glu Tyr Leu Gly Lys Thr Val Gln Val Ile Pro His Ile Thr Asp  
115 120 125

Glu Ile Lys Ala Arg Ile Leu Ser Met Gly Glu Pro Asp Ala His Gly  
130 135 140

Asn Ala Pro Asp Val Val Ile Ser Glu Val Gly Gly Thr Val Gly Asp

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Ile Glu Ser Gln Pro Phe Leu Glu Ala Ala Arg Gln Val Arg His Glu						
		165		170		175
Ile Gly Arg Glu Asn Cys Phe Phe Ile His Cys Ser Leu Val Pro Tyr						
		180		185		190
Leu Ala Thr Ser Gly Glu Leu Lys Thr Lys Pro Thr Gln His Ser Val						
		195		200		205
Ala Glu Leu Arg Gly Ile Gly Ile Leu Pro Asp Ala Leu Val Leu Arg						
		210		215		220
Cys Asp Arg Glu Val Pro Gln Gly Leu Lys Asp Lys Ile Ala Met Met						
		225		230		240
Cys Asp Val Asp Tyr Glu Gly Val Val Ser Cys Pro Asp Ser Ser Ser						
		245		250		255
Ile Tyr Asn Ile Pro Asp Val Leu Tyr Arg Glu His Leu Asp Thr Phe						
		260		265		270
Ile Ile Arg Arg Leu Gly Leu Pro Phe Arg Asp Val Asp Trp Ser Thr						
		275		280		285
Trp His Asp Leu Leu Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr						
		290		295		300
Val Gly Ile Val Gly Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser						
		305		310		320
Val Val Glu Ala Val Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr						
		325		330		335
Asn Ile Lys Trp Ile Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala						
		340		345		350
Met Lys Ala Leu Ser Gly Leu Asp Ala Ile Val Val Pro Gly Gly Phe						
		355		360		365
Gly Ile Arg Gly Ile Glu Gly Lys Ile Gly Ala Ile Thr Phe Ala Arg						
		370		375		380
Glu His Lys Ile Pro Leu Leu Gly Leu Cys Leu Gly Leu Gln Cys Thr						
		385		390		400
Val Ile Glu Ala Ala Arg Gln Ala Gly Leu Glu Gln Ala Ser Ser Thr						
		405		410		415
Glu Phe Asp Pro Ala Ala Thr Gln Pro Val Ile Ala Thr Met Glu Glu						
		420		425		430
Gln Lys Ala Ala Val Ser Gly Glu Ala Asp Leu Gly Gly Thr Met Arg						
		435		440		445
Leu Gly Ala Tyr Pro Ala Thr Leu Glu Glu Gly Ser Leu Val Ala Glu						
		450		455		460
Leu Tyr Gly Thr Thr Glu Val Ser Glu Arg His Arg His Arg Tyr Glu						
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Val Asn Asn Ala Tyr Arg Ala Gln Ile Ala Glu Gly Ser Asp Leu Val  
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Phe Ser Gly Thr Ser Pro Asp Gly His Leu Val Glu Phe Val Glu Tyr  
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Pro Lys Glu Val His Pro Tyr Leu Val Ala Thr Gln Ala His Pro Glu  
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 Met Pro Lys Arg Ser  
 1 5

gat att aac cac gtc ctc gtc atc ggt tcc ggc ccc atc gtc att ggc 163  
 Asp Ile Asn His Val Leu Val Ile Gly Ser Gly Pro Ile Val Ile Gly  
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 Gln Ala Cys Glu Phe Asp Tyr Ser Gly Thr Gln Ala Cys Arg Val Leu  
 25 30 35

aag gaa gag gga ctg cgc gtc acc ctc atc aac tcc aac cca gca acg 259  
 Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn Ser Asn Pro Ala Thr  
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atc atg acc gac cca gaa atg gct gac cac acc tac gtg gag cca atc 307  
 Ile Met Thr Asp Pro Glu Met Ala Asp His Thr Tyr Val Glu Pro Ile  
 55 60 65

gag ccg gaa tac atc gac aag att ttc gct aag gaa atc gag cag ggc 355  
 Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly  
 70 75 80 85

cac cca atc gac gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt 403  
 His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu  
 90 95 100

aac gca gct atc cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc 451  
 Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly  
 105 110 115

gtt gaa ctc atc ggt gca gac atc gat gcc att gag cgc ggc gaa gat 499  
 Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp  
 120 125 130

cgc cag aag ttc aag gat att gtc acc acc atc ggt ggc gaa tcc gcg 547  
 Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala  
 135 140 145

cgt tcc cgc gtc tgc cac aac atg gaa gaa gtc cac gag act gtc gca 595  
 Arg Ser Arg Val Cys His Asn Met Glu Glu Val His Glu Thr Val Ala  
 150 155 160 165

gaa ctc ggc ctt cca gta gtc gtg cgt cca tcc ttc act atg ggt ggc 643  
 Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly  
 170 175 180

ctg ggc tcc ggt ctt gca tac aac acc gaa gac ctt gag cgc atc gct 691  
 Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala  
 185 190 195

ggt ggc gga ctt gct gca tct cct gaa gca aac gtc ttg atc gaa gaa 739  
 Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn Val Leu Ile Glu Glu  
 200 205 210

tcc atc ctt ggt tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc 787  
 Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr  
 215 220 225

gca gac aac gtt gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg 835  
 Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu  
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ggc gtg cac acc ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg 883  
 Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu  
 250 255 260

act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc 931  
 Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile  
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cgc gag gtc ggc gtg gac acc ggt gga tgt aac atc cag ttc gcc atc 979  
 Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile  
 280 285 290

aac cca gtt gat ggc cgc atc atc acc att gag atg aac cca cgt gtg  
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 Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val  
 295 300 305

tct cgt tcc tcc gct ctg gca tcc aag gca acg ggc ttc cca att gcc  
 1075  
 Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala  
 310 315 320 325

aag atg gct gcc aag ctg gct atc gga tac acc ctg gat gag atc acc  
 1123  
 Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr  
 330 335 340

aac gac atc act ggt gaa acc cca gct gcg ttt gag ccc acc atc gac  
1171

Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp  
345 350 355

tac gtc gtg gtc aag gcc cca cgc ttt gct ttc gag aag ttt gtc ggc  
1219

Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly  
360 365 370

gct gat gac act ttg acc acc acc atg aag tcc gtc ggt gag gtc atg  
1267

Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met  
375 380 385

tcc ctg ggc cgc aac tac att gca gca ctg aac aag gca ctg cgt tcc  
1315

Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser  
390 395 400 405

ctg gaa acc aag cag cag ggt ttc tgg acc aag cct gat gag ttc ttc  
1363

Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe  
410 415 420

gca ggg gag cgc gct acc gat aag gca gct gtt ctg gaa gat ctc aag  
1411

Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys  
425 430 435

cgc cca acc gaa ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt  
1459

Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu  
440 445 450

ggc gca agc gtg gaa gaa ctc tac gaa gca tct tct att gat cct tgg  
1507

Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp  
455 460 465

ttc ctc gcc gag ctt gaa gct ctc gtg cag ttc cgc cag aag ctc gtt  
1555

Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val  
470 475 480 485

gac gca cca ttc cta aac gaa gat ctc ctg cgc gaa gca aag ttc atg  
1603

Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met  
490 495 500

ggt ctg tcc gac ctg cag atc gca gcc ctt cgc cca gag ttc gct ggc  
1651

Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg Pro Glu Phe Ala Gly  
505 510 515

gaa gac ggc gta cgc acc ttg cgt ctg tcc cta ggc atc cgc cca gta  
1699

Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val  
520 525 530

ttc aag act gtg gat acc tgt gca gca gag ttt gaa gct aag act ccg  
 1747  
 Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro  
 535 540 545

tac cac tac tcc gca tac gag ctg gat cca gca gct gag tct gag gtc  
 1795  
 Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala Ala Glu Ser Glu Val  
 550 555 560 565

gca cca cag act gag cgt gaa aag gtc ctg atc ttg ggc tcc ggt cca  
 1843  
 Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile Leu Gly Ser Gly Pro  
 570 575 580

aac cgc atc ggc cag ggc atc gag ttc gac tac tcc tgt gtt cac gca  
 1891  
 Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr Ser Cys Val His Ala  
 585 590 595

gct ctt gag ctc tcc cgc gtc ggc tac gaa act gtc atg gtc aac tgc  
 1939  
 Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr Val Met Val Asn Cys  
 600 605 610

aac cca gag acc gtg tcc acc gac tac gac acc gct gac cgc ctg tac  
 1987  
 Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr Ala Asp Arg Leu Tyr  
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ttc gag cca ctg acc ttc gaa gac gtc atg gag gtc tac cac gct gag  
 2035  
 Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu Val Tyr His Ala Glu  
 630 635 640 645

gcg cag tcc ggc acc gtc gca ggt gtt atc gtc cag ctt ggt ggc cag  
 2083  
 Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val Gln Leu Gly Gly Gln  
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act cct ctg ggc ttg gca gat cgt ttg aag aag gct ggc gtc cct gtc  
 2131  
 Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys Ala Gly Val Pro Val  
 665 670 675

att ggt acc tcc cca gag gca atc gac atg gct gag gac cgt ggc gag  
 2179  
 Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala Glu Asp Arg Gly Glu  
 680 685 690

ttc ggt gca ctg ctg aac cgc gag cag ctt cct gct cca gca ttc ggc  
 2227  
 Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro Ala Pro Ala Phe Gly  
 695 700 705

acc gca acc tct ttc gaa gag gct cgc aca gta gcc gat gag atc agc  
 2275  
 Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val Ala Asp Glu Ile Ser  
 710 715 720 725

tac cca gtg ctg gtt cgc cct tcc tac gtc ttg ggt ggc cgt ggc atg  
2323

Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu Gly Gly Arg Gly Met  
730 735 740

gag att gtc tac gat gag gct tcc ctc gag gat tac atc aac cgc gca  
2371

Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp Tyr Ile Asn Arg Ala  
745 750 755

act gag ttg tct tct gac cac cca gtg ctg gtt gac cgc ttc cta gac  
2419

Thr Glu Leu Ser Ser Asp His Pro Val Leu Val Asp Arg Phe Leu Asp  
760 765 770

aac gct att gag atc gac gtc gac gca ctg tgc gac ggc gac gag gtc  
2467

Asn Ala Ile Glu Ile Asp Val Asp Ala Leu Cys Asp Gly Asp Glu Val  
775 780 785

tac ctg gca ggc gtc atg gag cac atc gag gaa gcc ggc att cac tcc  
2515

Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu Ala Gly Ile His Ser  
790 795 800 805

ggt gac tcc gca tgt gca ctt cct cca atg act ttg ggc gca cag gac  
2563

Gly Asp Ser Ala Cys Ala Leu Pro Pro Met Thr Leu Gly Ala Gln Asp  
810 815 820

atc gag aag gtc cgc gaa gca acc aag aag ctg gct ctg ggc atc ggt  
2611

Ile Glu Lys Val Arg Glu Ala Thr Lys Lys Leu Ala Leu Gly Ile Gly  
825 830 835

gta cag ggc ctg atg aac gtc cag tac gca ctc aag gac gac atc ctc  
2659

Val Gln Gly Leu Met Asn Val Gln Tyr Ala Leu Lys Asp Asp Ile Leu  
840 845 850

tac gtc atc gag gca aac cca cgt gca tcc cgc acc gtg ccg ttc gtc  
2707

Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser Arg Thr Val Pro Phe Val  
855 860 865

tcc aag gca acg ggc gtc aac ctg gcc aag gca gca tcc cgt atc gca  
2755

Ser Lys Ala Thr Gly Val Asn Leu Ala Lys Ala Ala Ser Arg Ile Ala  
870 875 880 885

gtg ggc gcc acc atc aag gat ctc caa gat gag ggc atg att cct acc  
2803

Val Gly Ala Thr Ile Lys Asp Leu Gln Asp Glu Gly Met Ile Pro Thr  
890 895 900

gag tac gac ggc ggc tcc ttg cca ctg gac gct cca atc gct gtg aag  
2851

Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp Ala Pro Ile Ala Val Lys  
905 910 915



gaa gca gtg ttg ccg ttc aac cgc ttc cgt cgc cca gat gga aag acc  
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 Glu Ala Val Leu Pro Phe Asn Arg Phe Arg Arg Pro Asp Gly Lys Thr  
 920 925 930

ctg gac acc ctg ctt tcc cca gag atg aag tcc act ggc gag gtc atg  
 2947  
 Leu Asp Thr Leu Leu Ser Pro Glu Met Lys Ser Thr Gly Glu Val Met  
 935 940 945

ggc ttg gcc aac aac ttc ggc gct gca tat gca aag gct gaa gct ggc  
 2995  
 Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr Ala Lys Ala Glu Ala Gly  
 950 955 960 965

gcg ttt ggt gca ttg cca acc gaa ggc acc gtc ttc gtg acc gtg gct  
 3043  
 Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr Val Phe Val Thr Val Ala  
 970 975 980

aac cgc gac aag cgc acc ctg atc ctg cca atc cag cgc ctg gcg ttg  
 3091  
 Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro Ile Gln Arg Leu Ala Leu  
 985 990 995

atg ggc tac aag atc ctc gcc acc gaa ggc acc gca ggc atg ctg cgc  
 3139  
 Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly Thr Ala Gly Met Leu Arg  
 1000 1005 1010

cgc aac ggc att gag tgt gaa gtt gtg ctc aag gct tcc gac atc cgc  
 3187  
 Arg Asn Gly Ile Glu Cys Glu Val Val Leu Lys Ala Ser Asp Ile Arg  
 1015 1020 1025

gaa ggt gta gag ggc aag tcc atc gtg gat cgt atc cgc gaa ggc gaa  
 3235  
 Glu Gly Val Glu Gly Lys Ser Ile Val Asp Arg Ile Arg Glu Gly Glu  
 1030 1035 1040 1045

gtt gac ctc atc ctc aac acc cca gct ggt tct gct ggc gct cgc cac  
 3283  
 Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser Ala Gly Ala Arg His  
 1050 1055 1060

gat ggc tac gat atc cgc gca gca gca gtg acc gtg ggt gtt ccg ctg  
 3331  
 Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val Thr Val Gly Val Pro Leu  
 1065 1070 1075

atc acc act gtt cag ggt gtc acc gca gct gtc cag ggc ata gag gcc  
 3379  
 Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val Gln Gly Ile Glu Ala  
 1080 1085 1090

ctg cgt gag ggc gtt gtc agc gtc cgc gcg ctg cag gaa ctc gac cac  
 3427  
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3462

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1110

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<400> 1000

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35 40 45

Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His Thr  
50 55 60

Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys  
65 70 75 80

Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly  
85 90 95

Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile  
100 105 110

Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile  
115 120 125

Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile  
130 135 140

Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu Val  
145 150 155 160

His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser  
165 170 175

Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp  
180 185 190

Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn  
195 200 205

Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu  
210 215 220

Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu  
225 230 235 240

Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val Ala  
245 250 255

Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln

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Gly	Ile	Ala	Ile	Ile	Arg	Glu	Val	Gly	Val	Asp	Thr	Gly	Gly	Cys	Asn
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Ile	Gln	Phe	Ala	Ile	Asn	Pro	Val	Asp	Gly	Arg	Ile	Ile	Thr	Ile	Glu
	290					295					300				
Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala	Thr
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Gly	Phe	Pro	Ile	Ala	Lys	Met	Ala	Ala	Lys	Leu	Ala	Ile	Gly	Tyr	Thr
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Leu	Asp	Glu	Ile	Thr	Asn	Asp	Ile	Thr	Gly	Glu	Thr	Pro	Ala	Ala	Phe
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Glu	Pro	Thr	Ile	Asp	Tyr	Val	Val	Val	Lys	Ala	Pro	Arg	Phe	Ala	Phe
		355					360					365			
Glu	Lys	Phe	Val	Gly	Ala	Asp	Asp	Thr	Leu	Thr	Thr	Thr	Met	Lys	Ser
	370					375					380				
Val	Gly	Glu	Val	Met	Ser	Leu	Gly	Arg	Asn	Tyr	Ile	Ala	Ala	Leu	Asn
385					390					395					400
Lys	Ala	Leu	Arg	Ser	Leu	Glu	Thr	Lys	Gln	Gln	Gly	Phe	Trp	Thr	Lys
				405					410					415	
Pro	Asp	Glu	Phe	Phe	Ala	Gly	Glu	Arg	Ala	Thr	Asp	Lys	Ala	Ala	Val
			420					425					430		
Leu	Glu	Asp	Leu	Lys	Arg	Pro	Thr	Glu	Gly	Arg	Leu	Tyr	Asp	Val	Glu
		435					440					445			
Leu	Ala	Met	Arg	Leu	Gly	Ala	Ser	Val	Glu	Glu	Leu	Tyr	Glu	Ala	Ser
	450					455					460				
Ser	Ile	Asp	Pro	Trp	Phe	Leu	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gln	Phe
465					470					475					480
Arg	Gln	Lys	Leu	Val	Asp	Ala	Pro	Phe	Leu	Asn	Glu	Asp	Leu	Leu	Arg
				485					490					495	
Glu	Ala	Lys	Phe	Met	Gly	Leu	Ser	Asp	Leu	Gln	Ile	Ala	Ala	Leu	Arg
			500					505					510		
Pro	Glu	Phe	Ala	Gly	Glu	Asp	Gly	Val	Arg	Thr	Leu	Arg	Leu	Ser	Leu
		515					520					525			
Gly	Ile	Arg	Pro	Val	Phe	Lys	Thr	Val	Asp	Thr	Cys	Ala	Ala	Glu	Phe
	530					535					540				
Glu	Ala	Lys	Thr	Pro	Tyr	His	Tyr	Ser	Ala	Tyr	Glu	Leu	Asp	Pro	Ala
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Ala	Glu	Ser	Glu	Val	Ala	Pro	Gln	Thr	Glu	Arg	Glu	Lys	Val	Leu	Ile
				565					570					575	
Leu	Gly	Ser	Gly	Pro	Asn	Arg	Ile	Gly	Gln	Gly	Ile	Glu	Phe	Asp	Tyr
			580					585					590		

Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr  
 595 600 605  
 Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr  
 610 615 620  
 Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu  
 625 630 635 640  
 Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val  
 645 650 655  
 Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys  
 660 665 670  
 Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala  
 675 680 685  
 Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro  
 690 695 700  
 Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val  
 705 710 715 720  
 Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu  
 725 730 735  
 Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp  
 740 745 750  
 Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu Val  
 755 760 765  
 Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu Cys  
 770 775 780  
 Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu  
 785 790 795 800  
 Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met Thr  
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 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg  
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cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355  
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr  
 70 75 80 85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403  
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val  
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 Gly Ala Arg Ile Gly Arg Ile  
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<210> 1004

<211> 108

<212> PRT

<213> Corynebacterium glutamicum

<400> 1004

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg  
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Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val  
 20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr  
 35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu  
 50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg  
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Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys  
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Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile  
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<210> 1005

<211> 418

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(418)

<223> FRXA00450

<400> 1005

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 Val Gly Val Leu Pro  
 1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163  
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu

	10	15	20	
gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc				211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val				
	25	30	35	
att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga				259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg				
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gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga				307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg				
	55	60	65	
cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc				355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr				
	70	75	80	85
gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg				403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val				
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ggt gct cga atc gga				418
Gly Ala Arg Ile Gly				
	105			

&lt;210&gt; 1006

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1006

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
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Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
65 70 75 80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
85 90 95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly
100 105

&lt;210&gt; 1007

&lt;211&gt; 1368

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;



&lt;221&gt; CDS

&lt;222&gt; (101)..(1345)

&lt;223&gt; RXN02272

&lt;400&gt; 1007

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                               Val Arg Ile Thr Asn
                               1 5

gcc cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt 163
Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly
                        10 15 20

gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat 211
Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp
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cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag 259
His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln
                        40 45 50

ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc 307
Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile
                        55 60 65

cct cgc gaa aac tct tcc ggc aca ctt ttt gaa gcc atc gaa atc tgg 355
Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp
70 75 80 85

gcc gac cgc aag acc caa ggc ttc cac atc aaa gaa gac att aaa gcg 403
Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala
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aag gcc ctc cag gca gcc cgt cgg gca gca gaa cac ggc gtt ggt ttc 451
Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe
                        105 110 115

atc cgc act cac gta gat gtc acc gat ccc acg ttt gct gga ttc gaa 499
Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu
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gca att gcg gag ctg cgc gat gaa gtc cgc gag tgg tgc gat atc cag 547
Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln
135 140 145

att gtc gcc ttc ccg caa aat ggc att tac gcc tac gaa ggt ggc cag 595
Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln
150 155 160 165

aag cta atc tca gat gca atg tct gca ggt gca gat gtc gtt ggt ggc 643
Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly
170 175 180

atc cca cac ctt gaa ccc acc cga gac gat ggc gtc gag tcg gtg aaa 691
Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly Val Glu Ser Val Lys
185 190 195

tgg ctg ttc gac ctt gca gag aag cac tca gcc ccc atc gat atc cac 739
Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His

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Thr	Asp	Glu	Ile	Asp	Asp	Pro	His	Ser	Arg	Phe	Val	Glu	Val	Leu	Ala				
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Val	Ala	Pro	Val	Lys	Gln	Leu	Thr	Glu	Trp	Gly	Ile	Pro	Val	Ser	Phe				
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Cys	Gln	Asp	Ser	Leu	Asn	Asp	Pro	Phe	Tyr	Pro	Met	Gly	Asp	Gly	Asp				
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cta	ctc	cgc	att	ctc	gat	tct	gga	tta	cac	gtg	tcc	cac	atg	ctc	aca				
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Leu	Leu	Arg	Ile	Leu	Asp	Ser	Gly	Leu	His	Val	Ser	His	Met	Leu	Thr				
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aac	ctg	ctg	gtt	ctt	gat	gcg	agc	agc	gag	aag	gaa	gct	gta	cag	aga				
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Asn	Leu	Leu	Val	Leu	Asp	Ala	Ser	Ser	Glu	Lys	Glu	Ala	Val	Gln	Arg				
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ctt  
1368

<210> 1008

<211> 415

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1008

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Arg Ser Glu Glu Asp His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg  
35 40 45

Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala  
50 55 60

Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu  
65 70 75 80

Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys  
85 90 95

Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu  
100 105 110

His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr  
115 120 125

Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu  
130 135 140

Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala  
145 150 155 160

Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala  
165 170 175

Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly  
180 185 190

Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala  
195 200 205

Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe  
210 215 220

Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln  
225 230 235 240

Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr  
245 250 255

Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala  
260 265 270

Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly  
 275 280 285

Pro Val Pro Arg Gly Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly  
 290 295 300

Ile Pro Val Ser Phe Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro  
 305 310 315 320

Met Gly Asp Gly Asp Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val  
 325 330 335

Ser His Met Leu Thr Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile  
 340 345 350

Thr Thr Asn Pro Ala Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala  
 355 360 365

Glu Asn Ser Pro Ala Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys  
 370 375 380

Glu Ala Val Gln Arg Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly  
 385 390 395 400

Lys Lys Val Leu Ser Arg Glu Pro Glu Gln Val Asp Trp Asn Ile  
 405 410 415

&lt;210&gt; 1009

&lt;211&gt; 1368

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1345)

&lt;223&gt; FRXA02272

&lt;400&gt; 1009

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 Val Arg Ile Thr Asn  
 1 5

gcc cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt 163  
 Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly  
 10 15 20

gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat 211  
 Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp  
 25 30 35

cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag 259  
 His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln  
 40 45 50

ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc 307  
 Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile  
 55 60 65

cct	cg	gaa	aac	tct	tcc	ggc	aca	ctt	ttt	gaa	gcc	atc	gaa	atc	tgg	355
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Lys	Ala	Leu	Gln	Ala	Ala	Arg	Arg	Ala	Ala	Glu	His	Gly	Val	Gly	Phe	
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Ile	Arg	Thr	His	Val	Asp	Val	Thr	Asp	Pro	Thr	Phe	Ala	Gly	Phe	Glu	
		120					125					130				
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Ala	Ile	Ala	Glu	Leu	Arg	Asp	Glu	Val	Arg	Glu	Trp	Cys	Asp	Ile	Gln	
	135					140					145					
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Ile	Val	Ala	Phe	Pro	Gln	Asn	Gly	Ile	Tyr	Ala	Tyr	Glu	Gly	Gly	Gln	
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Lys	Leu	Ile	Ser	Asp	Ala	Met	Ser	Ala	Gly	Ala	Asp	Val	Val	Gly	Gly	
				170					175					180		
atc	cca	cac	ctt	gaa	ccc	acc	cga	gac	gat	ggc	gtc	gag	tcg	gtg	aaa	691
Ile	Pro	His	Leu	Glu	Pro	Thr	Arg	Asp	Asp	Gly	Val	Glu	Ser	Val	Lys	
			185					190					195			
tgg	ctg	ttc	gac	ctt	gca	gag	aag	cac	tca	gcc	ccc	atc	gat	atc	cac	739
Trp	Leu	Phe	Asp	Leu	Ala	Glu	Lys	His	Ser	Ala	Pro	Ile	Asp	Ile	His	
		200					205					210				
act	gat	gaa	att	gac	gat	cca	cat	tcc	cga	ttt	gtc	gaa	gtc	ctc	gcc	787
Thr	Asp	Glu	Ile	Asp	Asp	Pro	His	Ser	Arg	Phe	Val	Glu	Val	Leu	Ala	
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gca	gaa	gcc	gca	aaa	cgt	gac	atg	ggc	gca	caa	acc	gtg	gtg	tct	cat	835
Ala	Glu	Ala	Ala	Lys	Arg	Asp	Met	Gly	Ala	Gln	Thr	Val	Val	Ser	His	
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Ser	Val	Ala	Met	Ala	Tyr	Tyr	Ser	Pro	Gly	Tyr	Met	Ala	Arg	Leu	Leu	
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ccc	aag	ctc	gca	gca	tca	aag	gtt	cgt	ttt	gca	gta	tgc	ccc	aat	gaa	931
Pro	Lys	Leu	Ala	Ala	Ser	Lys	Val	Arg	Phe	Ala	Val	Cys	Pro	Asn	Glu	
			265					270					275			
aac	ctc	cat	ctg	caa	gga	ctt	ggt	ttc	caa	gga	ccc	gtc	ccc	cga	ggt	979
Asn	Leu	His	Leu	Gln	Gly	Leu	Gly	Phe	Gln	Gly	Pro	Val	Pro	Arg	Gly	
		280					285					290				
gtt	gca	ccg	gta	aag	caa	ctt	acc	gaa	tgg	gga	att	cca	gta	agt	ttt	
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1075

Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro Met Gly Asp Gly Asp  
310 315 320 325

cta ctc cgc att ctc gat tct gga tta cac gtg tcc cac atg ctc aca  
1123

Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val Ser His Met Leu Thr  
330 335 340

gcc agc cac ttg aag aat gca cta tcg ttc atc acc acc aat cca gcc  
1171

Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile Thr Thr Asn Pro Ala  
345 350 355

gga aac cta ggc ctg gac aat tac gac att gca gaa aac tcc ccg gcg  
1219

Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala Glu Asn Ser Pro Ala  
360 365 370

aac ctg ctg gtt ctt gat gcg agc agc gag aag gaa gct gta cag aga  
1267

Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys Glu Ala Val Gln Arg  
375 380 385

aaa gct tcc gta ctt ttg agc atc cac cgc ggc aaa aag gtg ctc tcc  
1315

Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly Lys Lys Val Leu Ser  
390 395 400 405

agg gag ccc gaa cag gtg gac tgg aac atc taacagccca gttgggcctc  
1365

Arg Glu Pro Glu Gln Val Asp Trp Asn Ile  
410 415

ctt  
1368

<210> 1010

<211> 415

<212> PRT

<213> Corynebacterium glutamicum

<400> 1010

Val Arg Ile Thr Asn Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp  
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Ile Thr Ile Glu Gly Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile  
20 25 30

Arg Ser Glu Glu Asp His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg  
35 40 45

Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala  
50 55 60

Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu  
65 70 75 80

Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys  
                             85                            90                            95  
 Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu  
                             100                            105                            110  
 His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr  
                             115                            120                            125  
 Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu  
                             130                            135                            140  
 Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala  
                             145                            150                            155                            160  
 Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala  
                             165                            170                            175  
 Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly  
                             180                            185                            190  
 Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala  
                             195                            200                            205  
 Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe  
                             210                            215                            220  
 Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln  
                             225                            230                            235                            240  
 Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr  
                             245                            250                            255  
 Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala  
                             260                            265                            270  
 Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly  
                             275                            280                            285  
 Pro Val Pro Arg Gly Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly  
                             290                            295                            300  
 Ile Pro Val Ser Phe Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro  
                             305                            310                            315                            320  
 Met Gly Asp Gly Asp Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val  
                             325                            330                            335  
 Ser His Met Leu Thr Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile  
                             340                            345                            350  
 Thr Thr Asn Pro Ala Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala  
                             355                            360                            365  
 Glu Asn Ser Pro Ala Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys  
                             370                            375                            380  
 Glu Ala Val Gln Arg Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly  
                             385                            390                            395                            400  
 Lys Lys Val Leu Ser Arg Glu Pro Glu Gln Val Asp Trp Asn Ile

405	410	415
<p>&lt;210&gt; 1011</p> <p>&lt;211&gt; 580</p> <p>&lt;212&gt; DNA</p> <p>&lt;213&gt; <i>Corynebacterium glutamicum</i></p> <p>&lt;220&gt;</p> <p>&lt;221&gt; CDS</p> <p>&lt;222&gt; (101)..(580)</p> <p>&lt;223&gt; RXN03004</p> <p>&lt;400&gt; 1011</p>		
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<p>cgtggcccaa ccctgaacgc tgaacgctac actggttgac gtg ctt ctt tca gat 115</p> <p>Val Leu Leu Ser Asp 5</p>		
<p>cgt gac att cgt aaa tca att gac gca ggc gac ttg gga att gaa cct 163</p> <p>Arg Asp Ile Arg Lys Ser Ile Asp Ala Gly Asp Leu Gly Ile Glu Pro 20</p>		
<p>ttc gac gct gag ctg att cag ccg tcg agt gtc gat gtc cgc atg gac 211</p> <p>Phe Asp Ala Glu Leu Ile Gln Pro Ser Ser Val Asp Val Arg Met Asp 35</p>		
<p>cgc tac ttc cgg gtt ttc aat aac tct aag tac acc cac att gac cct 259</p> <p>Arg Tyr Phe Arg Val Phe Asn Asn Ser Lys Tyr Thr His Ile Asp Pro 50</p>		
<p>aag ttg aat cag gat gag ctg acc agc ctt gtt gag gtt gag gac ggc 307</p> <p>Lys Leu Asn Gln Asp Glu Leu Thr Ser Leu Val Glu Val Glu Asp Gly 65</p>		
<p>gag ggc ttt gtg ctg cat ccg ggt gag ttt gtg ctg gcg tcc acg ctg 355</p> <p>Glu Gly Phe Val Leu His Pro Gly Glu Phe Val Leu Ala Ser Thr Leu 85</p>		
<p>gaa aag ttc act ttg cct gcg cat ctg gct ggt cgt ttg gag ggt aag 403</p> <p>Glu Lys Phe Thr Leu Pro Ala His Leu Ala Gly Arg Leu Glu Gly Lys 100</p>		
<p>tcg tct ctt ggt cgt ctt ggc ttg ttg acg cac tct act gct ggt ttc 451</p> <p>Ser Ser Leu Gly Arg Leu Gly Leu Leu Thr His Ser Thr Ala Gly Phe 115</p>		
<p>att gat cct ggt ttt agt ggt tac atc acg ttg gag ttg tcc aat gtg 499</p> <p>Ile Asp Pro Gly Phe Ser Gly Tyr Ile Thr Leu Glu Leu Ser Asn Val 130</p>		
<p>gct aat ctg ccg atc acg ttg tgg ccg ggt atg aag gtg ggg cag ctg 547</p> <p>Ala Asn Leu Pro Ile Thr Leu Trp Pro Gly Met Lys Val Gly Gln Leu 145</p>		
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 <213> Corynebacterium glutamicum

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 Asp Val Arg Met Asp Arg Tyr Phe Arg Val Phe Asn Asn Ser Lys Tyr  
             35                    40                    45  
 Thr His Ile Asp Pro Lys Leu Asn Gln Asp Glu Leu Thr Ser Leu Val  
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 Glu Val Glu Asp Gly Glu Gly Phe Val Leu His Pro Gly Glu Phe Val  
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 Leu Ala Ser Thr Leu Glu Lys Phe Thr Leu Pro Ala His Leu Ala Gly  
                     85                    90                    95  
 Arg Leu Glu Gly Lys Ser Ser Leu Gly Arg Leu Gly Leu Leu Thr His  
             100                    105                    110  
 Ser Thr Ala Gly Phe Ile Asp Pro Gly Phe Ser Gly Tyr Ile Thr Leu  
     115                    120                    125  
 Glu Leu Ser Asn Val Ala Asn Leu Pro Ile Thr Leu Trp Pro Gly Met  
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 Lys Val Gly Gln Leu Ala Leu Phe Gln Met Ser Ser Pro Ala Glu Thr  
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   Leu Glu Leu Asn Lys  
   1                    5  
 gca gcg tac atg ttt gag tac agc ttc gat gac atc acc gtg tcc ggc 163  
 Ala Ala Tyr Met Phe Glu Tyr Ser Phe Asp Asp Ile Thr Val Ser Gly  
                     10                    15                    20

tac gat cca cac cca ttg atc cgc ggc aag gtc gcc gta tgatcgggtgc 212  
 Tyr Asp Pro His Pro Leu Ile Arg Gly Lys Val Ala Val  
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 Ala Val

<210> 1015  
 <211> 613  
 <212> DNA  
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 <223> RXN03171

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   Met Asp Ile Thr Ile  
   1                                  5  
 gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163  
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu  
                                   10                                  15                                  20  
 cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211  
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala  
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 atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259  
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp  
                                   40                                  45                                  50  
 acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307  
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro  
                                   55                                  60                                  65  
 ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355  
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro  
   70                                  75                                  80                                  85  
 gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403

Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala  
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451  
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro  
 105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499  
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala  
 120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547  
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly  
 135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595  
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val  
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gac gca ttg gcg gaa tct  
 Asp Ala Leu Ala Glu Ser 613  
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Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu  
 35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr  
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Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu  
 65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly  
 85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr  
 100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val  
 115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu  
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Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser  
 145 150 155 160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser

165

170

<210> 1017  
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 <212> DNA  
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<220>  
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 <223> FRXA02857

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gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
                                   10                               15                               20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
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atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
                                   40                               45                               50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
                                   55                               60                               65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355
Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
                                   70                               75                               80                               85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403
Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
                                   90                               95                               100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451
Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
                                   105                               110                               115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
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acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547
Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
                                   135                               140                               145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val
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gac gca ttg gcg gaa tct

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613

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Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu  
35 40 45  
Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr  
50 55 60  
Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu  
65 70 75 80  
Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly  
85 90 95  
Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr  
100 105 110  
Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val  
115 120 125  
Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu  
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Val Ser Glu Gln Ala  
1 5

cta agc acc ttc gac agg gca cgt gag gcc ctg gac aag aaa acc cga 163  
 Leu Ser Thr Phe Asp Arg Ala Arg Glu Ala Leu Asp Lys Lys Thr Arg  
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tat gtg cag gat ttc cca gaa aaa ggt gtg ctt ttt gaa gac ctc acc 211  
 Tyr Val Gln Asp Phe Pro Glu Lys Gly Val Leu Phe Glu Asp Leu Thr  
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ccg gtg ttg ggc gat gca gaa tca ttt gtg gcc gtg gtg gac gcc atg 259  
 Pro Val Leu Gly Asp Ala Glu Ser Phe Val Ala Val Val Asp Ala Met  
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gct gaa gct gca gaa aaa ctg aat gca gaa atc atc ggt ggc ttg gat 307  
 Ala Glu Ala Ala Glu Lys Leu Asn Ala Glu Ile Ile Gly Gly Leu Asp  
                   55                                  60                                  65

gcg cga gga ttc ctc ctc gga tct gct gtc gct tac aaa ctc ggc cta 355  
 Ala Arg Gly Phe Leu Leu Gly Ser Ala Val Ala Tyr Lys Leu Gly Leu  
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ggt gtg ctg gct atc cgc aag aag gga aag ctc ccc cca cct gtg gtg 403  
 Gly Val Leu Ala Ile Arg Lys Lys Gly Lys Leu Pro Pro Pro Val Val  
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acc cag gag tat gaa ctt gaa tac ggc act gca gca ctc gag ctg ccc 451  
 Thr Gln Glu Tyr Glu Leu Glu Tyr Gly Thr Ala Ala Leu Glu Leu Pro  
                   105                                  110                                  115

agt gaa gga atc gac att gct ggt aaa aac atc gtt ttg atc gac gat 499  
 Ser Glu Gly Ile Asp Ile Ala Gly Lys Asn Ile Val Leu Ile Asp Asp  
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gtg ctg gca acc ggc ggc acc ttg ggc gct gca cgt aaa cta att gaa 547  
 Val Leu Ala Thr Gly Gly Thr Leu Gly Ala Ala Arg Lys Leu Ile Glu  
                   135                                  140                                  145

tcg tgt gac gga cat gtt tcc gga tat gtt ctt gcc att gag gtc cca 595  
 Ser Cys Asp Gly His Val Ser Gly Tyr Val Leu Ala Ile Glu Val Pro  
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ggc ctc ggc ggt agg gat aat ctt ggt gat agg ccc gtc att gtg gtc 643  
 Gly Leu Gly Gly Arg Asp Asn Leu Gly Asp Arg Pro Val Ile Val Val  
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Phe Glu Asp Leu Thr Pro Val Leu Gly Asp Ala Glu Ser Phe Val Ala  
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 Val Val Asp Ala Met Ala Glu Ala Ala Glu Lys Leu Asn Ala Glu Ile  
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 Ile Gly Gly Leu Asp Ala Arg Gly Phe Leu Leu Gly Ser Ala Val Ala  
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 Tyr Lys Leu Gly Leu Gly Val Leu Ala Ile Arg Lys Lys Gly Lys Leu  
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 Pro Pro Pro Val Val Thr Gln Glu Tyr Glu Leu Glu Tyr Gly Thr Ala  
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 Ala Leu Glu Leu Pro Ser Glu Gly Ile Asp Ile Ala Gly Lys Asn Ile  
           115                          120                          125  
 Val Leu Ile Asp Asp Val Leu Ala Thr Gly Gly Thr Leu Gly Ala Ala  
           130                          135                          140  
 Arg Lys Leu Ile Glu Ser Cys Asp Gly His Val Ser Gly Tyr Val Leu  
           145                          150                          155                          160  
 Ala Ile Glu Val Pro Gly Leu Gly Gly Arg Asp Asn Leu Gly Asp Arg  
                           165                          170                          175  
 Pro Val Ile Val Val Arg Asp Pro Gln  
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&lt;210&gt; 1021

&lt;211&gt; 723

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(700)

&lt;223&gt; RXA01512

&lt;400&gt; 1021

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 gaa atg gcc gac cac aaa gat ctc aat gtt cca gcc aac cca tac ggc 163  
 Glu Met Ala Asp His Lys Asp Leu Asn Val Pro Ala Asn Pro Tyr Gly  
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 acc gac att gaa tca gta ttg atc agc gaa gag aag ctc aag cag cgc 211  
 Thr Asp Ile Glu Ser Val Leu Ile Ser Glu Glu Lys Leu Lys Gln Arg  
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 atc gcc gaa atg gcc aag cgc gtc tcc gaa gag ttc aaa gac gcc gaa 259  
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 gaa gac ctc atc ctg gtg tgc gtg ctc aag ggc gcg ttc tac ttc ctg 307

Glu Asp Leu Ile Leu Val Cys Val Leu Lys Gly Ala Phe Tyr Phe Leu  
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 Ala Asp Phe Ser Arg Met Leu Asp Ile Pro Thr Gln Ser Glu Phe Met  
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 gcg gtg tcc tct tac gga aac tcc acc tcc tct tca ggc gtg gtg cgc 403  
 Ala Val Ser Ser Tyr Gly Asn Ser Thr Ser Ser Ser Gly Val Val Arg  
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 atc ctc aag gac ctg gac aag gaa att gaa ggc cgc gac gtt ttg atc 451  
 Ile Leu Lys Asp Leu Asp Lys Glu Ile Glu Gly Arg Asp Val Leu Ile  
 105 110 115  
 gtg gaa gac atc atc gat tcc gga ctg acc ctg tcc tgg ctg atg cgc 499  
 Val Glu Asp Ile Ile Asp Ser Gly Leu Thr Leu Ser Trp Leu Met Arg  
 120 125 130  
 aac ctg aaa aac cgc aac cct aag tcc ctc aac gtg atc acc ttg ctg 547  
 Asn Leu Lys Asn Arg Asn Pro Lys Ser Leu Asn Val Ile Thr Leu Leu  
 135 140 145  
 cgt aag cca gag cgc ctg acc acc aac atc gac atg ttc gac att gga 595  
 Arg Lys Pro Glu Arg Leu Thr Thr Asn Ile Asp Met Phe Asp Ile Gly  
 150 155 160 165  
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 Phe Asp Ile Pro Asn Glu Phe Val Val Gly Tyr Gly Leu Asp Phe Ala  
 170 175 180  
 gaa cgc tac cgc gac ctg cca tat gtg ggc acc ctc gag cct cac gtg 691  
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 185 190 195  
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 Tyr Ser Asp  
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 Lys Leu Lys Gln Arg Ile Ala Glu Met Ala Lys Arg Val Ser Glu Glu  
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 Phe Lys Asp Ala Glu Glu Asp Leu Ile Leu Val Cys Val Leu Lys Gly  
 50 55 60  
 Ala Phe Tyr Phe Leu Ala Asp Phe Ser Arg Met Leu Asp Ile Pro Thr  
 65 70 75 80



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gag	att	ctg	acc	tat	gag	atg	ttc	gga	aca	gca	atg	cg	gag	ctg	gcc	163
Glu	Ile	Leu	Thr	Tyr	Glu	Met	Phe	Gly	Thr	Ala	Met	Arg	Glu	Leu	Ala	
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caa	gaa	att	att	gat	gac	tac	cag	cca	gat	tgc	gtg	ctg	tcc	att	gcg	211
Gln	Glu	Ile	Ile	Asp	Asp	Tyr	Gln	Pro	Asp	Cys	Val	Leu	Ser	Ile	Ala	
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cgt	ggt	ggt	ctt	cta	atc	ggt	ggc	gca	ctt	ggt	tat	gcg	ctg	ggt	atc	259
Arg	Gly	Gly	Leu	Leu	Ile	Gly	Gly	Ala	Leu	Gly	Tyr	Ala	Leu	Gly	Ile	
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Lys	Asn	Val	Ser	Val	Ile	Asn	Val	Glu	Phe	Tyr	Thr	Asp	Ile	Gly	Glu	
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His	Leu	Glu	Glu	Pro	Met	Met	Leu	Pro	Pro	Thr	Pro	Lys	Ala	Val	Asp	
70					75					80					85	

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 90 95 100

aag act ctt gag ttg gtc agg gac ttc ctg ggt gac caa gtt gtc gaa 451  
 Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly Asp Gln Val Val Glu  
 105 110 115

gtg cgc act gca gtg atc tat cac aag cca aac agt gtg ttt aag ccg 499  
 Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn Ser Val Phe Lys Pro  
 120 125 130

gag tat gtg tgg cgt gag act gat aag tgg att aac ttc cca tgg tct 547  
 Glu Tyr Val Trp Arg Glu Thr Asp Lys Trp Ile Asn Phe Pro Trp Ser  
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 Val Leu Ser Ile Ala Arg Gly Gly Leu Leu Ile Gly Gly Ala Leu Gly  
 35 40 45  
 Tyr Ala Leu Gly Ile Lys Asn Val Ser Val Ile Asn Val Glu Phe Tyr  
 50 55 60  
 Thr Asp Ile Gly Glu His Leu Glu Glu Pro Met Met Leu Pro Pro Thr  
 65 70 75 80  
 Pro Lys Ala Val Asp Leu Ser Gly Met Arg Val Leu Val Ala Asp Asp  
 85 90 95  
 Val Ala Asp Thr Gly Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly  
 100 105 110  
 Asp Gln Val Val Glu Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn  
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<220>  
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 <223> RXA00981

<400> 1025

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                                   1          5

cca gcg ccc gag aat ctc ctg gac gcc gag aga att cag atg atc aag      163
Pro Ala Pro Glu Asn Leu Leu Asp Ala Glu Arg Ile Gln Met Ile Lys
                                   10          15          20

aac ttc cgc aac gaa tta acg ggg ttc atg ctc aac tac caa ttt ggc      211
Asn Phe Arg Asn Glu Leu Thr Gly Phe Met Leu Asn Tyr Gln Phe Gly
                                   25          30          35

att gat gag atc ctg acc aag atc aac atc ctg aaa act gaa ttc agc      259
Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu Lys Thr Glu Phe Ser
                                   40          45          50

cag ctg cac gaa tac gca cct atc gag cac gta tct tca cga ttg aag      307
Gln Leu His Glu Tyr Ala Pro Ile Glu His Val Ser Ser Arg Leu Lys
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aca cca gaa agc atc gtc aaa aag gtc atc cga aaa gga gac gag ctc      355
Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg Lys Gly Asp Glu Leu
                                   70          75          80          85

tcc ctc gca gct atc aaa gac aca gtg ttt gat atc gca ggc att cga      403
Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp Ile Ala Gly Ile Arg
                                   90          95          100

atc gtc tgc agt ttc ctc aaa gat gcc tac gca atc gcc gat atg ctg      451
Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala Ile Ala Asp Met Leu
                                   105          110          115

acc aac caa aaa gac gtc acg gtc atc gag gcc aaa gac tac atc gct      499
Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala Lys Asp Tyr Ile Ala
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Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His Leu Ile Leu Gln Val
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cct gtc ttc ctg tct aac tcc gtg gaa aag gtc aat gtt gaa gtc cag      595
Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val Asn Val Glu Val Gln
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atc cgc acc att gcc atg gac ttc tgg gca agc ctc gag cac aaa atc      643
Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser Leu Glu His Lys Ile
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 Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser Ile Leu Asp Glu Leu  
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agt gaa gat gga aag aat cca cgg gga agt gaa gtc act taaacctcca 740  
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<400> 1026

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                   20                                  25                                  30

Asn Tyr Gln Phe Gly Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu  
                   35                                  40                                  45

Lys Thr Glu Phe Ser Gln Leu His Glu Tyr Ala Pro Ile Glu His Val  
                   50                                  55                                  60

Ser Ser Arg Leu Lys Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg  
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Lys Gly Asp Glu Leu Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp  
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Ile Ala Gly Ile Arg Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala  
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Ile Ala Asp Met Leu Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala  
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Lys Asp Tyr Ile Ala Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His  
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Leu Ile Leu Gln Val Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val  
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Asn Val Glu Val Gln Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser  
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Leu Glu His Lys Ile Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser  
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                               1                               5
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Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr Asn Pro Val Leu Asp
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Pro Leu Leu Ser Ile His Arg Gln Phe His Pro Arg Ala Asp Val Gln
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                               55                               60                               65
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Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala
                               70                               75                               80                               85
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Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr Ser Leu Asp Asp Leu
                               105                               110                               115
acc cga gat ttc gga gaa gaa gtt gcc agg ctt gtc gac ggt gtc acc 499
Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu Val Asp Gly Val Thr
                               120                               125                               130
aag ctc gac aaa gtc gca cta ggt gct gcc gcg gag gcc gaa acg att 547
Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala Glu Ala Glu Thr Ile
                               135                               140                               145
cgc aaa atg atc gtc gcc atg agc cag gac ccc cgc gtg ctg gtg att 595
Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro Arg Val Leu Val Ile
                               150                               155                               160                               165
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Lys Val Ala Asp Arg Leu His Asn Met Arg Thr Met Arg Phe Leu Pro
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ccg gaa aag caa gct aaa aaa gca cgc caa acc ctt gaa gtg att gct 691

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 Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys Tyr Glu Glu Ile Val  
 215 220 225  
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 Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp Arg Tyr Leu Lys Glu  
 230 235 240 245  
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 Glu Val Leu Gly Arg Pro Lys His Tyr Trp Ser Ile Tyr Gln Lys Met  
 265 270 275  
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 295 300 305  
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 Phe Ser Pro Ala Leu Arg Cys Leu Pro Ile Pro Ala His His Arg Asp  
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 Ser Leu Asp Asp Leu Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu  
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 Val Asp Gly Val Thr Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala  
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 Glu Ala Glu Thr Ile Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro  
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 Arg Val Leu Val Ile Lys Val Ala Asp Arg Leu His Asn Met Arg Thr  
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 Met Arg Phe Leu Pro Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr  
                                     180                                      185                                      190  
 Leu Glu Val Ile Ala Pro Leu Ala His Arg Leu Gly Met Ala Ser Val  
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 Lys Trp Glu Leu Glu Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys  
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 Tyr Glu Glu Ile Val Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp  
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 Asp Leu Val Gly Ile Arg Ile Leu Val Asp Asn Val Asn Asn Cys Val  
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 Ile Gln Arg Leu Tyr Phe Ser Pro Ala Leu Arg Cys Leu Pro Ile Pro  
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                                   1          5

gcc cgc agc ctc aca gga aac cgc gtt cgc acc aac cct gtg ctg gat      163
Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr Asn Pro Val Leu Asp
                                   10          15          20

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Pro Leu Leu Ser Ile His Arg Gln Phe His Pro Arg Ala Asp Val Gln
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gtg ttg gaa cgt gca tat gac acc gcg gaa cgt ctt cat gat ggt gtg      259
Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg Leu His Asp Gly Val
                                   40          45          50

att cga aaa tcg ggc gat ccg tat att acc cac ccg ttg gct gtc gcc      307
Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala
                                   55          60          65

acc atc gcc gcg gaa atc ggc atg gac acc acc acg ctc gtc gca gcc      355
Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr Thr Leu Val Ala Ala
                                   70          75          80          85

ttg ttg cat gac acg gtg gaa gac acc gac tac tct ttg gac gat ctc      403
Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr Ser Leu Asp Asp Leu
                                   90          95          100

acc cga gat ttc gga gaa gaa gtt gcc agg ctt gtc gac ggt gtc acc      451
Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu Val Asp Gly Val Thr
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aag ctc gac aaa gtc gca cta ggt gct gcc gcg gag gcc gaa acg att      499
Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala Glu Ala Glu Thr Ile
                                   120          125          130

cgc aaa atg atc gtc gcc atg agc cag gac ccc cgc gtg ctg gtg att      547
Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro Arg Val Leu Val Ile
                                   135          140          145

aaa gtg gcc gac cgt ttg cac aat atg cgc acc atg cgg ttc ctg ccg      595
Lys Val Ala Asp Arg Leu His Asn Met Arg Thr Met Arg Phe Leu Pro
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ccg gaa aag caa gct aaa aaa gca cgc caa acc ctt gaa gtg att gct      643
Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr Leu Glu Val Ile Ala
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Pro Leu Ala His Arg Leu Gly Met Ala Ser Val Lys Trp Glu Leu Glu  
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Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys Tyr Glu Glu Ile Val  
200 205 210

cgt ctt gtt gcc gac cgc gcg ccc tct aga gac cgg tac ctc aaa gaa 787  
Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp Arg Tyr Leu Lys Glu  
215 220 225

att att gat caa gtc acc ggt ggc ttg cgc gaa aac aac atc gcg gca 835  
Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu Asn Asn Ile Ala Ala  
230 235 240 245

gaa gtg ctt ggt cgn ccn aag cac tct ggt ctt tct ttc aaa aga 880  
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Leu His Asp Gly Val Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His  
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Pro Leu Ala Val Ala Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr  
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Thr Leu Val Ala Ala Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr  
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Ser Leu Asp Asp Leu Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu  
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Val Asp Gly Val Thr Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala  
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Glu Ala Glu Thr Ile Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro  
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Arg Val Leu Val Ile Lys Val Ala Asp Arg Leu His Asn Met Arg Thr  
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165 170 175

Leu Glu Val Ile Ala Pro Leu Ala His Arg Leu Gly Met Ala Ser Val  
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 Lys Trp Glu Leu Glu Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys  
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 Tyr Glu Glu Ile Val Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp  
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 Met Ile Val Arg Gly  
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                                   25                                  30                                  35  
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 Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp Thr Leu Glu Asp Val  
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 ccc gag gaa tac aat tct gcc caa ctt gaa gct gat ttt ggt ccg cgg 307  
 Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala Asp Phe Gly Pro Arg  
                                   55                                  60                                  65  
 gtg cgc gag ttg gtg gaa gag ctc acc aaa cag ccc tta aaa agc tgg 355  
 Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln Pro Leu Lys Ser Trp  
                                   70                                  75                                  80                                  85  
 aaa gcg cgt gcc gac gct tac ctc ctg cac ctc agc gca ggt gcc agc 403  
 Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu Ser Ala Gly Ala Ser  
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                                   105                                  110                                  115  
 tcc atc ttg gat gac ctt gaa ata cac ggt gaa gat tta tgg caa cgc 499  
 Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu Asp Leu Trp Gln Arg  
                                   120                                  125                                  130  
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Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp Tyr Ser Glu Val Tyr  
 135 140 145  
 cag ata tct ctc cag cgc tta ggg ttc aat gag ttg aat aaa caa ctg 595  
 Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu Leu Asn Lys Gln Leu  
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 ggg ttg tgc gtc gaa aag ctc tta aag caa agc gcc taggcgctcg 641  
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 Thr Leu Glu Asp Val Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala  
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 Asp Phe Gly Pro Arg Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln  
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 Pro Leu Lys Ser Trp Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu  
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Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg Leu Ala Asp Lys Thr
                40                45                50

caa gtg gtt ggc ccc aat gat ggt gat act ccg cgc acc cgg ctg acg 307
Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro Arg Thr Arg Leu Thr
                55                60                65

cac tct ttg gaa gta gct caa att gca cgg gga atc gga gct gga ctg 355
His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly Ile Gly Ala Gly Leu
                70                75                80                85

gat ttg gat cct gat ctg tgc gat ctg gca ggg ctg tgc cat gac att 403
Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly Leu Cys His Asp Ile
                90                95                100

ggg cat ccg ccg tat gga cac aac ggt gaa aac gcg ttg aat gaa gtt 451
Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn Ala Leu Asn Glu Val
                105                110                115

gct gcg gcc tgt gga gga ttt gag ggc aac gcc caa acc ttg cgt att 499
Ala Ala Ala Cys Gly Gly Phe Glu Gly Asn Ala Gln Thr Leu Arg Ile
                120                125                130

ctc acg cgt ctg gag cca aaa att gtc tct gat gag ggg gag agc ttt 547
Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp Glu Gly Glu Ser Phe
                135                140                145

ggg ctg aac ttg tcg cgg gct gct ctt gat gct gca tgt aag tat ccg 595
Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala Ala Cys Lys Tyr Pro
                150                155                160                165

tgg gct aaa aca aat gcg gat ggc agt gtc aat aag aaa tac agt gct 643
Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn Lys Lys Tyr Ser Ala
                170                175                180

tat gac gag gac gca gaa atc ctc gct tgg att aga caa ggc cat gag 691
Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile Arg Gln Gly His Glu
                185                190                195

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gat ctt cgc cca ccg atc gaa gcg cag gtc atg gac ttt tct gat gac 739  
 Asp Leu Arg Pro Pro Ile Glu Ala Gln Val Met Asp Phe Ser Asp Asp  
 200 205 210

att gcc tac tcg gtg cac gat gtg gaa gac ggt att gta tcc ggg cgt 787  
 Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly Ile Val Ser Gly Arg  
 215 220 225

atc gac tta aaa gtg ctg tgg gac ctg gtt gaa tta gca gct ttg gca 835  
 Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu Leu Ala Ala Leu Ala  
 230 235 240 245

gac aaa gga gca gct gct ttc gga ggt tcg cct gca gag ctc atc gag 883  
 Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro Ala Glu Leu Ile Glu  
 250 255 260

ggt gca gca tcg ttg cgg gaa ctt ccg gtg gtg gct gcc gct gcg gat 931  
 Gly Ala Ala Ser Leu Arg Glu Leu Pro Val Val Ala Ala Ala Ala Asp  
 265 270 275

ttt gat ttc tca ctg cgt tcc tac gct gcg ctg aag gcg atg act tca 979  
 Phe Asp Phe Ser Leu Arg Ser Tyr Ala Ala Leu Lys Ala Met Thr Ser  
 280 285 290

gaa cta gtg gga aga tac gtt ggc tct acc atc gag tca aca aag aaa  
 1027  
 Glu Leu Val Gly Arg Tyr Val Gly Ser Thr Ile Glu Ser Thr Lys Lys  
 295 300 305

aca cac gct ggc att gat gtg gga cgc atg cac ggc gat ttg atc att  
 1075  
 Thr His Ala Gly Ile Asp Val Gly Arg Met His Gly Asp Leu Ile Ile  
 310 315 320 325

cca gaa aca gcg gcc agt gaa gta aaa ctg ctc aaa acg tta gcg gtt  
 1123  
 Pro Glu Thr Ala Ala Ser Glu Val Lys Leu Leu Lys Thr Leu Ala Val  
 330 335 340

ctc tac gtg atg gat gac cca ggg cac ctt gcg cgc caa aac agg caa  
 1171  
 Leu Tyr Val Met Asp Asp Pro Gly His Leu Ala Arg Gln Asn Arg Gln  
 345 350 355

cgg gat cgt atc ttc cgg gtt ttt gac tac ctg gtg ctg ggg gct ccg  
 1219  
 Arg Asp Arg Ile Phe Arg Val Phe Asp Tyr Leu Val Leu Gly Ala Pro  
 360 365 370

gga tcg ttg gat ccg atg tat cgc cag tgg ttt att gaa gcg gat tca  
 1267  
 Gly Ser Leu Asp Pro Met Tyr Arg Gln Trp Phe Ile Glu Ala Asp Ser  
 375 380 385

gaa tcg gaa cag atc cgt gtg att gtt gat cag att gcg tcg atg acg  
 1315  
 Glu Ser Glu Gln Ile Arg Val Ile Val Asp Gln Ile Ala Ser Met Thr  
 390 395 400 405

gag tct cgt ctg gaa cgc ctt gcc cgg aat gct gct gac atc tca gga  
 1363

Glu Ser Arg Leu Glu Arg Leu Ala Arg Asn Ala Ala Asp Ile Ser Gly  
 410 415 420

ttt ttg gga taattgggta gagcagcagt aag  
 1395  
 Phe Leu Gly

<210> 1036  
 <211> 424  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1036  
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 Phe Ala Arg Asp Arg Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg  
 35 40 45  
 Leu Ala Asp Lys Thr Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro  
 50 55 60  
 Arg Thr Arg Leu Thr His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly  
 65 70 75 80  
 Ile Gly Ala Gly Leu Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly  
 85 90 95  
 Leu Cys His Asp Ile Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn  
 100 105 110  
 Ala Leu Asn Glu Val Ala Ala Ala Cys Gly Gly Phe Glu Gly Asn Ala  
 115 120 125  
 Gln Thr Leu Arg Ile Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp  
 130 135 140  
 Glu Gly Glu Ser Phe Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala  
 145 150 155 160  
 Ala Cys Lys Tyr Pro Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn  
 165 170 175  
 Lys Lys Tyr Ser Ala Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile  
 180 185 190  
 Arg Gln Gly His Glu Asp Leu Arg Pro Pro Ile Glu Ala Gln Val Met  
 195 200 205  
 Asp Phe Ser Asp Asp Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly  
 210 215 220  
 Ile Val Ser Gly Arg Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu  
 225 230 235 240  
 Leu Ala Ala Leu Ala Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro

245	250	255
Ala Glu Leu Ile Glu Gly Ala Ala Ser Leu Arg Glu Leu Pro Val Val 260 265 270		
Ala Ala Ala Ala Asp Phe Asp Phe Ser Leu Arg Ser Tyr Ala Ala Leu 275 280 285		
Lys Ala Met Thr Ser Glu Leu Val Gly Arg Tyr Val Gly Ser Thr Ile 290 295 300		
Glu Ser Thr Lys Lys Thr His Ala Gly Ile Asp Val Gly Arg Met His 305 310 315 320		
Gly Asp Leu Ile Ile Pro Glu Thr Ala Ala Ser Glu Val Lys Leu Leu 325 330 335		
Lys Thr Leu Ala Val Leu Tyr Val Met Asp Asp Pro Gly His Leu Ala 340 345 350		
Arg Gln Asn Arg Gln Arg Asp Arg Ile Phe Arg Val Phe Asp Tyr Leu 355 360 365		
Val Leu Gly Ala Pro Gly Ser Leu Asp Pro Met Tyr Arg Gln Trp Phe 370 375 380		
Ile Glu Ala Asp Ser Glu Ser Glu Gln Ile Arg Val Ile Val Asp Gln 385 390 395 400		
Ile Ala Ser Met Thr Glu Ser Arg Leu Glu Arg Leu Ala Arg Asn Ala 405 410 415		
Ala Asp Ile Ser Gly Phe Leu Gly 420		

<210> 1037  
 <211> 1131  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1108)  
 <223> RXN01027

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 gaactgtgtg caccacaacg cggaagggtga atcgcaccca atg gca aat aag aac 115  
 Met Ala Asn Lys Asn  
 1 5  
 aat aag cct cat gag gtg gac aaa gac caa gat tca gcc atg ctg atc 163  
 Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp Ser Ala Met Leu Ile  
 10 15 20  
 aac ggt cgc ctg caa cag atc ccg gcg cgt ccc act gag gaa ttc acc 211  
 Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro Thr Glu Glu Phe Thr  
 25 30 35



cgc cca act ctt gca gca ggt gca gta ctg tgg cgc ggc gac atc acc 259  
 Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp Arg Gly Asp Ile Thr  
 40 45 50

aac ccg gac agc atc gag gtc gct gtc atc cac cgc ccg cac tat gat 307  
 Asn Pro Asp Ser Ile Glu Val Ala Val Ile His Arg Pro His Tyr Asp  
 55 60 65

gac tgg tcc ctg gcc aag ggc aaa gtc gat ccc ggc gag tct att ccg 355  
 Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro Gly Glu Ser Ile Pro  
 70 75 80 85

aca acc gcg gcc cgt gaa atc ctt gaa gaa act ggc tac gac atc cgt 403  
 Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr Gly Tyr Asp Ile Arg  
 90 95 100

ctg ggc aag ctg atc ggc aag gtt act tac cct gtg ctc gac cga acc 451  
 Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro Val Leu Asp Arg Thr  
 105 110 115

aaa gtg gtc tac tac tgg act gcc cag gtt ctt ggt gga gag ttt gtc 499  
 Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu Gly Gly Glu Phe Val  
 120 125 130

ccc aac gat gaa gtt gat gaa atc cgt tgg ctg tct gtt gat gaa gca 547  
 Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu Ser Val Asp Glu Ala  
 135 140 145

tgc gag ttg ctc agc tac caa gta gat acc gaa gtt ctg gcc aag gca 595  
 Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu Val Leu Ala Lys Ala  
 150 155 160 165

gca aag cgt ttc cgc act cct tcc acc act cgg gtg ctg tat gtt cgc 643  
 Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg Val Leu Tyr Val Arg  
 170 175 180

cat gct cat gca cat ggt cgc caa acc tgg ggt ggc gac gac aat aag 691  
 His Ala His Ala His Gly Arg Gln Thr Trp Gly Gly Asp Asp Asn Lys  
 185 190 195

cgc cca ttg gac aaa aag ggg cgt cga caa gca gaa atg ctc gta ccc 739  
 Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala Glu Met Leu Val Pro  
 200 205 210

atg ttg ttg ccc ttc aaa ccc acc gca att tac tcg gcg gtg ccc gat 787  
 Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr Ser Ala Val Pro Asp  
 215 220 225

cgc tgc caa gcc acc gcg ctc ccc ctt gcc gat gag ctc ggc ctc gac 835  
 Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp Glu Leu Gly Leu Asp  
 230 235 240 245

gtg tcc gtc aac cga ctg ttc ggc gac gac gcc tgg gaa acc gat ccc 883  
 Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala Trp Glu Thr Asp Pro  
 250 255 260

gag gcc tgc aag aag cgc ttc acc gac gtg gtc gcg caa ggt ggc gtg 931  
 Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln Gly Gly Val  
 265 270 275

ccg atg atc gtt ggg cag ggc gac atc att ccg gaa atg atc aaa tgg 979

Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met Ile Lys Trp  
 280 285 290

ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc aag gcg aaa  
 1027

Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile Lys Ala Lys  
 295 300 305

aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg ttc acc ggc  
 1075

Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val Phe Thr Gly  
 310 315 320 325

gct gat tac ctg gcg agt tcc ctg ccg gtt aaa taggagcgcg tttaaggcct  
 1128

Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys  
 330 335

cca  
 1131

<210> 1038

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 1038

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Ser Ala Met Leu Ile Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro  
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Thr Glu Glu Phe Thr Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp  
 35 40 45

Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His  
 50 55 60

Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro  
 65 70 75 80

Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr  
 85 90 95

Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro  
 100 105 110

Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu  
 115 120 125

Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu  
 130 135 140

Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu  
 145 150 155 160

Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg  
 165 170 175

Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly  
 180 185 190

Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala  
 195 200 205

Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr  
 210 215 220

Ser Ala Val Pro Asp Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp  
 225 230 235 240

Glu Leu Gly Leu Asp Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala  
 245 250 255

Trp Glu Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val  
 260 265 270

Ala Gln Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro  
 275 280 285

Glu Met Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu  
 290 295 300

Lys Ile Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp  
 305 310 315 320

Gly Val Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys  
 325 330 335

<210> 1039  
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(757)  
 <223> FRXA01024

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gaactgtgtg caccacaacg cggaagggtga atcgcaccca atg gca aat aag aac 115  
 Met Ala Asn Lys Asn  
 1 5

aat aag cct cat gag gtg gac aaa gac caa gat tca gcc atg ctg atc 163  
 Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp Ser Ala Met Leu Ile  
 10 15 20

aac ggt cgc ctg caa cag atc ccg gcg cgt ccc act gag gaa ttc acc 211  
 Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro Thr Glu Glu Phe Thr  
 25 30 35

cgc cca act ctt gca gca ggt gca gta ctg tgg cgc ggc gac atc acc 259  
 Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp Arg Gly Asp Ile Thr

40	45	50	
aac ccg gac agc atc gag gtc gct gtc atc cac cgc ccg cac tat gat			307
Asn Pro Asp Ser Ile Glu Val Ala Val Ile His Arg Pro His Tyr Asp			
55	60	65	
gac tgg tcc ctg gcc aag ggc aaa gtc gat ccc ggc gag tct att ccg			355
Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro Gly Glu Ser Ile Pro			
70	75	80	85
aca acc gcg gcc cgt gaa atc ctt gaa gaa act ggc tac gac atc cgt			403
Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr Gly Tyr Asp Ile Arg			
	90	95	100
ctg ggc aag ctg atc ggc aag gtt act tac cct gtg ctc gac cga acc			451
Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro Val Leu Asp Arg Thr			
	105	110	115
aaa gtg gtc tac tac tgg act gcc cag gtt ctt ggt gga gag ttt gtc			499
Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu Gly Gly Glu Phe Val			
	120	125	130
ccc aac gat gaa gtt gat gaa atc cgt tgg ctg tct gtt gat gaa gca			547
Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu Ser Val Asp Glu Ala			
	135	140	145
tgc gag ttg ctc agc tac caa gta gat acc gaa gtt ctg gcc aag gca			595
Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu Val Leu Ala Lys Ala			
150	155	160	165
gca aag cgt ttc cgc act cct tcc acc act cgg gtg ctg tat gtt cgc			643
Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg Val Leu Tyr Val Arg			
	170	175	180
cat gct cat gca cat ggt cgc caa acc tgg ggt ggc gac gac aat aag			691
His Ala His Ala His Gly Arg Gln Thr Trp Gly Gly Asp Asp Asn Lys			
	185	190	195
cgc cca ttg gac aaa aag ggg cgt cga caa gca gaa atg ctc gta ccc			739
Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala Glu Met Leu Val Pro			
	200	205	210
atg ttg ttg ccc ttc aaa			757
Met Leu Leu Pro Phe Lys			
215			
<210> 1040			
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<213> Corynebacterium glutamicum			
<400> 1040			
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1	5	10	15
Ser Ala Met Leu Ile Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro			
	20	25	30
Thr Glu Glu Phe Thr Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp			
	35	40	45

Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His  
50 55 60

Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro  
65 70 75 80

Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr  
85 90 95

Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro  
100 105 110

Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu  
115 120 125

Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu  
130 135 140

Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu  
145 150 155 160

Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg  
165 170 175

Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly  
180 185 190

Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala  
195 200 205

Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys  
210 215

<210> 1041

<211> 257

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(234)

<223> FRXA01027

<400> 1041

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Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln  
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ggt ggc gtg ccg atg atc gtt ggg cag ggc gac atc att ccg gaa atg 96  
Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met  
20 25 30

atc aaa tgg ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc 144  
Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile  
35 40 45

aag gcg aaa aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg 192  
Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val  
50 55 60

ttc acc ggc gct gat tac ctg gcg agt tcc ctg ccg gtt aaa 234  
 Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys  
 65 70 75

taggagcgcg tttaaggcct cca 257

<210> 1042  
 <211> 78  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1042  
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 Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met  
 20 25 30  
 Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile  
 35 40 45  
 Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val  
 50 55 60  
 Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys  
 65 70 75

<210> 1043  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(628)  
 <223> RXA01528

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 Val Asn Gln Ala Trp  
 1 5  
 cag cag tcc cgt ttg gtt act tct gat gag act tcc gca ggt ggt ctc 163  
 Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr Ser Ala Gly Gly Leu  
 10 15 20  
 gtg gtg tca ggt ttg gct gag gcg gtc aac gct aac aat gag gtt gat 211  
 Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala Asn Asn Glu Val Asp  
 25 30 35  
 ctg tcg aag att tat gtt gcg ttg att ggt cgc ctt gat cgt cgt ggt 259  
 Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg Leu Asp Arg Arg Gly  
 40 45 50  
 cgt ttg ttg tgg tcg atg ccg aag ggc cat gtt gag cct ggt gag gat 307  
 Arg Leu Leu Trp Ser Met Pro Lys Gly His Val Glu Pro Gly Glu Asp

55                                      60                                      65  
 aag gct gcg act gct gag cgt gag gtg tgg gag gag acc ggc atc cac 355  
 Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu Glu Thr Gly Ile His  
 70                                      75                                      80                                      85  
 ggt gag gtg ttc act gag ttg ggt gtg att gat tat tgg ttc gtt tcg 403  
 Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp Tyr Trp Phe Val Ser  
 90                                      95                                      100  
 gaa ggg aag cgg atc cat aag acg gtg cat cat cat ttg ttg cgt tat 451  
 Glu Gly Lys Arg Ile His Lys Thr Val His His His Leu Leu Arg Tyr  
 105                                      110                                      115  
 gtt gat ggc gat ttg aat gat gag gat cca gaa gtc act gag gtg gcg 499  
 Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu Val Thr Glu Val Ala  
 120                                      125                                      130  
 tgg att ccg gcg aat cag ttg att gag cat ttg gct ttt gcg gat gag 547  
 Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu Ala Phe Ala Asp Glu  
 135                                      140                                      145  
 cgg aag ttg gct agg cag gcg cat gat ttg ttg cct gag ttt gct ttg 595  
 Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu Pro Glu Phe Ala Leu  
 150                                      155                                      160                                      165  
 aag gaa aag gcg gag gga agg tcc acc cca agg tgattccgaa ccccaacccg 648  
 Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg  
 170                                      175  
 aac 651  
  
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 <211> 176  
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 <213> Corynebacterium glutamicum  
  
 <400> 1044  
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 Ser Ala Gly Gly Leu Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala  
 20                                      25                                      30  
 Asn Asn Glu Val Asp Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg  
 35                                      40                                      45  
 Leu Asp Arg Arg Gly Arg Leu Leu Trp Ser Met Pro Lys Gly His Val  
 50                                      55                                      60  
 Glu Pro Gly Glu Asp Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu  
 65                                      70                                      75                                      80  
 Glu Thr Gly Ile His Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp  
 85                                      90                                      95  
 Tyr Trp Phe Val Ser Glu Gly Lys Arg Ile His Lys Thr Val His His  
 100                                      105                                      110  
 His Leu Leu Arg Tyr Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu

115	120	125
Val Thr Glu Val Ala Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu		
130	135	140
Ala Phe Ala Asp Glu Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu		
145	150	155 160
Pro Glu Phe Ala Leu Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg		
165	170	175

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 <211> 541  
 <212> DNA  
 <213> Corynebacterium glutamicum

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aagaatctct cgaaagacac aaaagaggtg agtcgcaaca atg agc ttt caa cta 115  
 Met Ser Phe Gln Leu  
 1 5

gtt aac gcc ctg aaa aat act ggt tcg gta aaa gat ccc gag atc tca 163  
 Val Asn Ala Leu Lys Asn Thr Gly Ser Val Lys Asp Pro Glu Ile Ser  
 10 15 20

ccc gaa gga cct cgc acg acc aca ccg ttg tca cca gag gta gca aaa 211  
 Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser Pro Glu Val Ala Lys  
 25 30 35

cat aac gag gaa ctc gtc gaa aag cat gct gct gcg ttg tat gac gcc 259  
 His Asn Glu Glu Leu Val Glu Lys His Ala Ala Ala Leu Tyr Asp Ala  
 40 45 50

agc gcg caa gag atc ctg gaa tgg aca gcc gag cac gcg ccg ggc gct 307  
 Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu His Ala Pro Gly Ala  
 55 60 65

att gca gtg acc ttg agc atg gaa aac acc gtg ctg gcg gag ctg gct 355  
 ile Ala Val Thr Leu Ser Met Glu Asn Thr Val Leu Ala Glu Leu Ala  
 70 75 80 85

gcg cgg cac ctg ccg gaa gct gat ttc ctc ttt ttg gac acc ggt tac 403  
 Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe Leu Asp Thr Gly Tyr  
 90 95 100

cac ttc aag gag acc ctt gaa gtt gcc cgt cag gta gat gag cgc tat 451  
 His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln Val Asp Glu Arg Tyr  
 105 110 115

tcc cag aag ctt gtc acc gcg ctg ccg atc ctc aag cgc acg gag cag 499



Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu Lys Arg Thr Glu Gln  
 120 125 130

gat tcc att tat ggt ctc aac ctg tac cgc agc aac cca gcg 541  
 Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser Asn Pro Ala  
 135 140 145

<210> 1046  
 <211> 147  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1046  
 Met Ser Phe Gln Leu Val Asn Ala Leu Lys Asn Thr Gly Ser Val Lys  
 1 5 10 15

Asp Pro Glu Ile Ser Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser  
 20 25 30

Pro Glu Val Ala Lys His Asn Glu Glu Leu Val Glu Lys His Ala Ala  
 35 40 45

Ala Leu Tyr Asp Ala Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu  
 50 55 60

His Ala Pro Gly Ala Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val  
 65 70 75 80

Leu Ala Glu Leu Ala Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe  
 85 90 95

Leu Asp Thr Gly Tyr His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln  
 100 105 110

Val Asp Glu Arg Tyr Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu  
 115 120 125

Lys Arg Thr Glu Gln Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser  
 130 135 140

Asn Pro Ala  
 145

<210> 1047  
 <211> 1002  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(979)  
 <223> RXA01878

<400> 1047  
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 atagtagaaa tctggcatcc aataggtaga ttgggatgct atg gaa gaa ccc tca 115  
 Met Glu Glu Pro Ser  
 1 5

ggt gca cag ctg ctc ggc ccg gta gaa atc cgt gcg ctg gca gaa aag 163  
 Gly Ala Gln Leu Leu Gly Pro Val Glu Ile Arg Ala Leu Ala Glu Lys  
 10 15 20

ctc gac gtc aca cca act aag aag ttg ggg cag aac ttt gtt cac gat 211  
 Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln Asn Phe Val His Asp  
 25 30 35

ccc aac acg gtg cgt cgc att gtt gct gcg gca gag ctc acc cca aac 259  
 Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala Glu Leu Thr Pro Asn  
 40 45 50

gac cac gtg gtg gaa gtt ggc cct ggt ctg ggc tct ctg acc ctt gcc 307  
 Asp His Val Val Glu Val Gly Pro Gly Leu Gly Ser Leu Thr Leu Ala  
 55 60 65

ctg gtg gaa tct gct gct tca gta act gcg gtg gaa att gat ccc cgt 355  
 Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val Glu Ile Asp Pro Arg  
 70 75 80 85

ttg gct gcg gaa ttg ccg gag act ttt cag tgg cgc gcg ccg gcc ctt 403  
 Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp Arg Ala Pro Ala Leu  
 90 95 100

gct cac aag ttg agc atc gtg ctg aaa gac gcc ctg aag gtt caa caa 451  
 Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala Leu Lys Val Gln Gln  
 105 110 115

tcc gat atg gct gtt caa ccc acc gcc ttg gtg gct aac ttg ccg tac 499  
 Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val Ala Asn Leu Pro Tyr  
 120 125 130

aac gtc tct gtc cct gtc ttg ttg cac atg atg gag gag ttt ccc acc 547  
 Asn Val Ser Val Pro Val Leu Leu His Met Met Glu Glu Phe Pro Thr  
 135 140 145

atc aac aag gtg ctt gtc atg gtg cag gca gag gtt gct gat cgt ttg 595  
 Ile Asn Lys Val Leu Val Met Val Gln Ala Glu Val Ala Asp Arg Leu  
 150 155 160 165

gct gcg gat cca gga tcg aag att tat ggt gtg cct agc gtg aag gcg 643  
 Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val Pro Ser Val Lys Ala  
 170 175 180

tcc ttc tac ggt cca gtt act cgc gcc ggg tcg att ggt aag aat gtc 691  
 Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser Ile Gly Lys Asn Val  
 185 190 195

ttt tgg cca gct cca aag atc gaa tcc ggt ttg gtg aag atc gtg cgc 739  
 Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu Val Lys Ile Val Arg  
 200 205 210

gaa gac acc gcg tgg aag cag gac gat gag acg cgt aag aag gtg tgg 787  
 Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr Arg Lys Lys Val Trp  
 215 220 225

ccg atc att gat gct gct ttc ttg cag cgc cgt aaa acc cta aga gct 835  
 Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg Lys Thr Leu Arg Ala  
 230 235 240 245

gcg ctt tct gga cac tac ggt tct ggc cag gca gct gag gaa gct ttg 883  
 Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala Ala Glu Glu Ala Leu  
                   250                                  255                                  260

cgg gcc gct gat att gat cca acg ctt cgt ggc gaa aag ctt gat gtc 931  
 Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly Glu Lys Leu Asp Val  
                   265                                  270                                  275

act gac tat gtg cgc cta gct ggg gtg ttg cag caa aag gat gag aag 979  
 Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln Gln Lys Asp Glu Lys  
                   280                                  285                                  290

tgaaaattac cgctaaggcg tgg  
 1002

<210> 1048

<211> 293

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1048

Met Glu Glu Pro Ser Gly Ala Gln Leu Leu Gly Pro Val Glu Ile Arg  
   1                                  5                                  10                                  15

Ala Leu Ala Glu Lys Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln  
                   20                                  25                                  30

Asn Phe Val His Asp Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala  
                   35                                  40                                  45

Glu Leu Thr Pro Asn Asp His Val Val Glu Val Gly Pro Gly Leu Gly  
                   50                                  55                                  60

Ser Leu Thr Leu Ala Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val  
                   65                                  70                                  75                                  80

Glu Ile Asp Pro Arg Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp  
                   85                                  90                                  95

Arg Ala Pro Ala Leu Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala  
                   100                                  105                                  110

Leu Lys Val Gln Gln Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val  
                   115                                  120                                  125

Ala Asn Leu Pro Tyr Asn Val Ser Val Pro Val Leu Leu His Met Met  
                   130                                  135                                  140

Glu Glu Phe Pro Thr Ile Asn Lys Val Leu Val Met Val Gln Ala Glu  
   145                                  150                                  155                                  160

Val Ala Asp Arg Leu Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val  
                   165                                  170                                  175

Pro Ser Val Lys Ala Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser  
                   180                                  185                                  190

Ile Gly Lys Asn Val Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu  
                   195                                  200                                  205

Val Lys Ile Val Arg Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr  
 210 215 220

Arg Lys Lys Val Trp Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg  
 225 230 235 240

Lys Thr Leu Arg Ala Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala  
 245 250 255

Ala Glu Glu Ala Leu Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly  
 260 265 270

Glu Lys Leu Asp Val Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln  
 275 280 285

Gln Lys Asp Glu Lys  
 290

<210> 1049

<211> 1545

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1531)

<223> RXN02281

<400> 1049

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cctataaaag cacagttttg aatccacagg gcatcagggc gtg cag aaa gat agt 115  
 Val Gln Lys Asp Ser  
 1 5

gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163  
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu  
 10 15 20

att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211  
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn  
 25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259  
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr  
 40 45 50

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307  
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly  
 55 60 65

tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc 355  
 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg  
 70 75 80 85

gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat 403  
 Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn  
 90 95 100

tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg 451

Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro  
 105 110 115  
 gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt 499  
 Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly  
 120 125 130  
 gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac 547  
 Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp  
 135 140 145  
 gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg 595  
 Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro  
 150 155 160 165  
 ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc 643  
 Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile  
 170 175 180  
 gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg 691  
 Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu  
 185 190 195  
 ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg 739  
 Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met  
 200 205 210  
 tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca 787  
 Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro  
 215 220 225  
 aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa 835  
 Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu  
 230 235 240 245  
 acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc 883  
 Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile  
 250 255 260  
 acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca 931  
 Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro  
 265 270 275  
 tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa 979  
 Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu  
 280 285 290  
 gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc  
 1027  
 Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg  
 295 300 305  
 atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att  
 1075  
 Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile  
 310 315 320 325  
 ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa  
 1123  
 Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu  
 330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac  
1171

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp  
345 350 355

aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac  
1219

Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn  
360 365 370

tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc  
1267

Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser  
375 380 385

acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga  
1315

Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly  
390 395 400 405

tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg  
1363

Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu  
410 415 420

cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac  
1411

Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr  
425 430 435

ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa  
1459

Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu  
440 445 450

tac ctg gca gta gat cct gaa cgg ttg cgt acc cgt aaa ctg cgc agg  
1507

Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg  
455 460 465

acc ttg ggt gag gtg ccg ttt cgc taaagtctcg gaga  
1545

Thr Leu Gly Glu Val Pro Phe Arg  
470 475

<210> 1050

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 1050

Val Gln Lys Asp Ser Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp  
1 5 10 15

Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala  
20 25 30

Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val  
35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg  
 50 55 60  
 Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr  
 65 70 75 80  
 Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu  
 85 90 95  
 Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp  
 100 105 110  
 Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu  
 115 120 125  
 Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu  
 130 135 140  
 Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn  
 145 150 155 160  
 Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile  
 165 170 175  
 Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val  
 180 185 190  
 Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe  
 195 200 205  
 Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val  
 210 215 220  
 Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr  
 225 230 235 240  
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro  
 245 250 255  
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn  
 260 265 270  
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala  
 275 280 285  
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met  
 290 295 300  
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln  
 305 310 315 320  
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile  
 325 330 335  
 Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu  
 340 345 350  
 Ile Tyr Gly Ser Asp Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser  
 355 360 365

Thr Asp Asp Arg Asn Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn  
 370 375 380

Trp Leu Lys Gly Ser Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr  
 385 390 395 400

Leu Ala Thr Asn Gly Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu  
 405 410 415

Ser Val Ser Asp Leu Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln  
 420 425 430

Ala Gln Ala Phe Tyr Phe Asn Ser Lys Glu Ala His Val Met Cys Ala  
 435 440 445

Val Arg Ala Met Glu Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr  
 450 455 460

Arg Lys Leu Arg Arg Thr Leu Gly Glu Val Pro Phe Arg  
 465 470 475

<210> 1051

<211> 1191

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1168)

<223> FRXA02281

<400> 1051

aagatcaaca acgccgccga ggtcaacttg gaaattatca cgtgaggatt cttgcatacg 60

cctataaaag cacagttttg aatccacagg gcatcagggc gtg cag aaa gat agt 115  
 Val Gln Lys Asp Ser  
 1 5

gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163  
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Ala Ile Ala Lys Leu  
 10 15 20

att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211  
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn  
 25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259  
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr  
 40 45 50

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307  
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly  
 55 60 65

tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc 355  
 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg  
 70 75 80 85

gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat 403  
 Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn



	90	95	100	
tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg				451
Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro				
	105	110	115	
gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt				499
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly				
	120	125	130	
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac				547
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp				
	135	140	145	
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg				595
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro				
	150	155	160	165
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc				643
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile				
	170	175	180	
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg				691
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu				
	185	190	195	
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg				739
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met				
	200	205	210	
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca				787
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro				
	215	220	225	
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa				835
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu				
	230	235	240	245
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc				883
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile				
	250	255	260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca				931
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro				
	265	270	275	
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa				979
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu				
	280	285	290	
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc				1027
Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg				
	295	300	305	
atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att				1075
Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile				
	310	315	320	325

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa  
1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu  
330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc  
1168

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser  
345 350 355

tagtattcta tagtgtcacc taa  
1191

<210> 1052

<211> 356

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1052

Val Gln Lys Asp Ser Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp  
1 5 10 15

Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala  
20 25 30

Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val  
35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg  
50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr  
65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu  
85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp  
100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu  
115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu  
130 135 140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn  
145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile  
165 170 175

Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val  
180 185 190

Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe  
195 200 205

Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val  
210 215 220

Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr  
 225 230 235 240  
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro  
 245 250 255  
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn  
 260 265 270  
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala  
 275 280 285  
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met  
 290 295 300  
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln  
 305 310 315 320  
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile  
 325 330 335  
 Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu  
 340 345 350  
 Ile Tyr Gly Ser  
 355

<210> 1053  
 <211> 1146  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1123)  
 <223> RXN01240

<400> 1053  
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 ctgcacagga aagtttagcgg cgctactatg aacgatcgat atg tct gac aac act 115  
 Met Ser Asp Asn Thr  
 1 5  
 ctc tcc caa ttt ggc agt tac tac cac gaa ttc cga cgt gcc cat ccc 163  
 Leu Ser Gln Phe Gly Ser Tyr Tyr His Glu Phe Arg Arg Ala His Pro  
 10 15 20  
 atg gcc gac gtc gaa ttc ctc cta gca att gaa gaa tta ctt acg gac 211  
 Met Ala Asp Val Glu Phe Leu Leu Ala Ile Glu Glu Leu Leu Thr Asp  
 25 30 35  
 ggt ggt gtc acc ttc gat cgc gtc acc aca cgc atc aaa gaa tgg tca 259  
 Gly Gly Val Thr Phe Asp Arg Val Thr Thr Arg Ile Lys Glu Trp Ser  
 40 45 50  
 agc ctg aaa gcc aag gct cgc aag cgt cgc aac gat ggc tcg ttg atc 307  
 Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn Asp Gly Ser Leu Ile  
 55 60 65

tac cct gat ccg cgc aaa gac atc cac gac atg atc ggt gtt cgg atc 355  
 Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met Ile Gly Val Arg Ile  
 70 75 80 85

acc acg tac cac tcc acg gaa ata ccc gtg gcc cta aaa gtg ctc caa 403  
 Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala Leu Lys Val Leu Gln  
 90 95 100

gac tcc ttc atc gtc cac aaa tcc gta gac aaa gcc gct gaa act cgc 451  
 Asp Ser Phe Ile Val His Lys Ser Val Asp Lys Ala Ala Glu Thr Arg  
 105 110 115

atc tca ggc ggc ttt ggt tac ggc tcc cac cac ctg att ctg gaa gtc 499  
 Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His Leu Ile Leu Glu Val  
 120 125 130

gat gac acc tcc gat gac ctc cag gac tac aaa ggc ctc gtc ttt gaa 547  
 Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys Gly Leu Val Phe Glu  
 135 140 145

gtt cag gtg cgc acc gtg ctg caa cac gcc tgg gca gag ttc gaa cac 595  
 Val Gln Val Arg Thr Val Leu Gln His Ala Trp Ala Glu Phe Glu His  
 150 155 160 165

gat atc cgc tat aaa cgc gcc gat gtg tcc aac cca gaa gac ttc agc 643  
 Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn Pro Glu Asp Phe Ser  
 170 175 180

gca gaa gta gac cgc atg ttc acc ctc gct gcc gga ctc atc gaa tta 691  
 Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala Gly Leu Ile Glu Leu  
 185 190 195

gcg gac caa caa ttc gac caa atc gcc gca ctc aaa gaa acc agc cga 739  
 Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu Lys Glu Thr Ser Arg  
 200 205 210

gtt gct gat gaa tcc gtc gaa ctc acc gca gag aca ctt ccc ggc gtt 787  
 Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu Thr Leu Pro Gly Val  
 215 220 225

ctt gcc atg ctc att ggc aac cgc ttc ccc cgc cca cgc tcc aca aac 835  
 Leu Ala Met Leu Ile Gly Asn Arg Phe Pro Arg Pro Arg Ser Thr Asn  
 230 235 240 245

tac cgc ttc ctc gaa gac atc ctg gtg gcc aac tcc att acc tct gtg 883  
 Tyr Arg Phe Leu Glu Asp Ile Leu Val Ala Asn Ser Ile Thr Ser Val  
 250 255 260

gtg cag ctg cgc gag ctg ctc aac ccc acc gac att gaa gtg ctg ttg 931  
 Val Gln Leu Arg Glu Leu Leu Asn Pro Thr Asp Ile Glu Val Leu Leu  
 265 270 275

aaa gta atg aac tac cgc ttc cac cca ggc cag atc cgc atc atc gac 979  
 Lys Val Met Asn Tyr Arg Phe His Pro Gly Gln Ile Arg Ile Ile Asp  
 280 285 290

gat tta cta ctc aaa cga ttt ggc caa tca cac atc gat gcc acc gtc  
 1027  
 Asp Leu Leu Leu Lys Arg Phe Gly Gln Ser His Ile Asp Ala Thr Val  
 295 300 305

gcc acc gac tcc caa cca ctc aac gcc aaa cgc cac agg cag cta aaa  
1075

Ala Thr Asp Ser Gln Pro Leu Asn Ala Lys Arg His Arg Gln Leu Lys  
310 315 320 325

cgc aag cta gag ctc atg acc caa gct cat ctt gtg gaa cca cca aac  
1123

Arg Lys Leu Glu Leu Met Thr Gln Ala His Leu Val Glu Pro Pro Asn  
330 335 340

taaagttccc ccaaagtttag ccc  
1146

<210> 1054

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 1054

Met Ser Asp Asn Thr Leu Ser Gln Phe Gly Ser Tyr Tyr His Glu Phe  
1 5 10 15

Arg Arg Ala His Pro Met Ala Asp Val Glu Phe Leu Leu Ala Ile Glu  
20 25 30

Glu Leu Leu Thr Asp Gly Gly Val Thr Phe Asp Arg Val Thr Thr Arg  
35 40 45

Ile Lys Glu Trp Ser Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn  
50 55 60

Asp Gly Ser Leu Ile Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met  
65 70 75 80

Ile Gly Val Arg Ile Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala  
85 90 95

Leu Lys Val Leu Gln Asp Ser Phe Ile Val His Lys Ser Val Asp Lys  
100 105 110

Ala Ala Glu Thr Arg Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His  
115 120 125

Leu Ile Leu Glu Val Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys  
130 135 140

Gly Leu Val Phe Glu Val Gln Val Arg Thr Val Leu Gln His Ala Trp  
145 150 155 160

Ala Glu Phe Glu His Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn  
165 170 175

Pro Glu Asp Phe Ser Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala  
180 185 190

Gly Leu Ile Glu Leu Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu  
195 200 205

Lys Glu Thr Ser Arg Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu

210	215	220
Thr Leu Pro Gly Val	Leu Ala Met Leu Ile	Gly Asn Arg Phe Pro Arg
225	230	235 240
Pro Arg Ser Thr	Asn Tyr Arg Phe Leu Glu	Asp Ile Leu Val Ala Asn
	245	250 255
Ser Ile Thr Ser	Val Val Gln Leu Arg Glu	Leu Leu Asn Pro Thr Asp
	260	265 270
Ile Glu Val Leu	Leu Lys Val Met Asn Tyr	Arg Phe His Pro Gly Gln
	275	280 285
Ile Arg Ile Ile	Asp Asp Leu Leu Leu Lys	Arg Phe Gly Gln Ser His
	290	295 300
Ile Asp Ala Thr	Val Ala Thr Asp Ser Gln	Pro Leu Asn Ala Lys Arg
305	310	315 320
His Arg Gln Leu	Lys Arg Lys Leu Glu Leu	Met Thr Gln Ala His Leu
	325	330 335
Val Glu Pro Pro	Asn	
	340	

<210> 1055  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101) .. (1234)  
 <223> RXN02008

<400> 1055  
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 cttggttgga tccgcacccct ggtagacaac gtgaacaact gtg tac gcc gcc atc 115  
 Val Tyr Ala Ala Ile  
 1 5  
 ggt gtc gtg cac tcc ctg ttc aat gct ctg cct ggc cga ttc aaa gac 163  
 Gly Val Val His Ser Leu Phe Asn Ala Leu Pro Gly Arg Phe Lys Asp  
 10 15 20  
 tat att tca gcc ccg cgc ttc ggt gtc tac caa tcc ctg cac acc acc 211  
 Tyr Ile Ser Ala Pro Arg Phe Gly Val Tyr Gln Ser Leu His Thr Thr  
 25 30 35  
 gtg atg gga cct ggc ggt aag cct ctg gaa gtt cag gca cgt acc cac 259  
 Val Met Gly Pro Gly Gly Lys Pro Leu Glu Val Gln Ala Arg Thr His  
 40 45 50  
 gac atg cac tac aac gcc gaa ttc ggc att gca gcg cac tgg cga tac 307  
 Asp Met His Tyr Asn Ala Glu Phe Gly Ile Ala Ala His Trp Arg Tyr  
 55 60 65  
 aaa gaa acc aaa ggc agc cac agt ggc gag caa gcc gaa gtg gat caa 355

Lys	Glu	Thr	Lys	Gly	Ser	His	Ser	Gly	Glu	Gln	Ala	Glu	Val	Asp	Gln		
70					75					80					85		
atg	gcg	tgg	atg	cgc	caa	ctt	ctg	gac	tgg	caa	aaa	gaa	gca	gcc	gac		403
Met	Ala	Trp	Met	Arg	Gln	Leu	Leu	Asp	Trp	Gln	Lys	Glu	Ala	Ala	Asp		
				90					95					100			
ccc	aac	gag	ttc	ctg	gac	agc	ctg	cgc	tac	gat	ctg	act	tcc	aag	cag		451
Pro	Asn	Glu	Phe	Leu	Asp	Ser	Leu	Arg	Tyr	Asp	Leu	Thr	Ser	Lys	Gln		
			105					110					115				
atc	ttc	gtg	ttc	aca	ccc	aaa	ggg	gat	gtg	gtc	aac	ctg	ccg	gtg	aac		499
Ile	Phe	Val	Phe	Thr	Pro	Lys	Gly	Asp	Val	Val	Asn	Leu	Pro	Val	Asn		
		120					125					130					
tcc	acc	ccg	gtg	gac	ttc	gcc	tac	gcg	gtg	cac	acc	gaa	gtg	ggg	cac		547
Ser	Thr	Pro	Val	Asp	Phe	Ala	Tyr	Ala	Val	His	Thr	Glu	Val	Gly	His		
		135				140					145						
cgc	tgc	atc	ggc	gcc	aaa	atc	aac	ggc	aaa	ctg	gtc	gct	ttg	gaa	acg		595
Arg	Cys	Ile	Gly	Ala	Lys	Ile	Asn	Gly	Lys	Leu	Val	Ala	Leu	Glu	Thr		
150					155					160					165		
aaa	ctc	aaa	tcc	ggc	gat	cgt	gtt	gaa	gtc	ttt	acc	tcc	aag	gac	caa		643
Lys	Leu	Lys	Ser	Gly	Asp	Arg	Val	Glu	Val	Phe	Thr	Ser	Lys	Asp	Gln		
				170					175					180			
aac	gct	ggc	cca	agt	agg	gga	tgg	caa	gaa	ttt	gtt	gtc	tca	cct	cgt		691
Asn	Ala	Gly	Pro	Ser	Arg	Gly	Trp	Gln	Glu	Phe	Val	Val	Ser	Pro	Arg		
			185					190					195				
gca	aag	gcc	aag	att	cgc	cag	tgg	ttt	gcc	aag	gaa	cga	cgc	gaa	gaa		739
Ala	Lys	Ala	Lys	Ile	Arg	Gln	Trp	Phe	Ala	Lys	Glu	Arg	Arg	Glu	Glu		
		200					205					210					
tac	cta	gaa	gcc	gga	cgc	gat	gcg	ctg	gca	gca	gtt	att	cag	cgt	ggc		787
Tyr	Leu	Glu	Ala	Gly	Arg	Asp	Ala	Leu	Ala	Ala	Val	Ile	Gln	Arg	Gly		
		215				220					225						
ggc	ctg	cca	atg	cac	cgc	ttg	ttc	acc	gcg	tcc	tcc	atg	aag	acg	gtg		835
Gly	Leu	Pro	Met	His	Arg	Leu	Phe	Thr	Ala	Ser	Ser	Met	Lys	Thr	Val		
230					235					240					245		
gca	aca	gag	ctg	cac	tac	cca	gat	gta	gat	gcg	ctc	tac	aca	gcc	atc		883
Ala	Thr	Glu	Leu	His	Tyr	Pro	Asp	Val	Asp	Ala	Leu	Tyr	Thr	Ala	Ile		
				250					255					260			
ggc	tcc	ggg	tct	gta	tct	gcg	caa	cac	gta	gtc	aac	cgt	ctc	atg	gct		931
Gly	Ser	Gly	Ser	Val	Ser	Ala	Gln	His	Val	Val	Asn	Arg	Leu	Met	Ala		
			265					270				275					
atc	ttt	ggg	gac	gaa	gaa	gat	gcc	gaa	gac	gca	ttg	gtt	gca	cgc	acc		979
Ile	Phe	Gly	Asp	Glu	Glu	Asp	Ala	Glu	Asp	Ala	Leu	Val	Ala	Arg	Thr		
		280					285					290					
cca	ttc	agc	gag	ctg	gtc	aac	tcc	cgt	gcc	acc	acg	gaa	agc	agc	acc		
1027																	
Pro	Phe	Ser	Glu	Leu	Val	Asn	Ser	Arg	Ala	Thr	Thr	Glu	Ser	Ser	Thr		
		295				300						305					

ggc atc ctg gtc gaa ggc agc cca gat gtc atg gct aag ctc gct aaa  
1075

Gly Ile Leu Val Glu Gly Ser Pro Asp Val Met Ala Lys Leu Ala Lys  
310 315 320 325

tgc tgt atg cca gtg cca gga gat gaa atc ttt gga ttc gtc acc cgt  
1123

Cys Cys Met Pro Val Pro Gly Asp Glu Ile Phe Gly Phe Val Thr Arg  
330 335 340

ggt ggc ggt gtc tcc gta cac cga aca gac tgc acg aat gtg gaa aag  
1171

Gly Gly Gly Val Ser Val His Arg Thr Asp Cys Thr Asn Val Glu Lys  
345 350 355

ctc aaa gaa gag cca gaa cgc att gtc tcc gtc tcc tgg gct tcg gaa  
1219

Leu Lys Glu Glu Pro Glu Arg Ile Val Ser Val Ser Trp Ala Ser Glu  
360 365 370

ggt caa ggt tca gta

1234

Gly Gln Gly Ser Val

375

<210> 1056

<211> 378

<212> PRT

<213> Corynebacterium glutamicum

<400> 1056

Val Tyr Ala Ala Ile Gly Val Val His Ser Leu Phe Asn Ala Leu Pro  
1 5 10 15

Gly Arg Phe Lys Asp Tyr Ile Ser Ala Pro Arg Phe Gly Val Tyr Gln  
20 25 30

Ser Leu His Thr Thr Val Met Gly Pro Gly Gly Lys Pro Leu Glu Val  
35 40 45

Gln Ala Arg Thr His Asp Met His Tyr Asn Ala Glu Phe Gly Ile Ala  
50 55 60

Ala His Trp Arg Tyr Lys Glu Thr Lys Gly Ser His Ser Gly Glu Gln  
65 70 75 80

Ala Glu Val Asp Gln Met Ala Trp Met Arg Gln Leu Leu Asp Trp Gln  
85 90 95

Lys Glu Ala Ala Asp Pro Asn Glu Phe Leu Asp Ser Leu Arg Tyr Asp  
100 105 110

Leu Thr Ser Lys Gln Ile Phe Val Phe Thr Pro Lys Gly Asp Val Val  
115 120 125

Asn Leu Pro Val Asn Ser Thr Pro Val Asp Phe Ala Tyr Ala Val His  
130 135 140

Thr Glu Val Gly His Arg Cys Ile Gly Ala Lys Ile Asn Gly Lys Leu  
145 150 155 160



Val Ala Leu Glu Thr Lys Leu Lys Ser Gly Asp Arg Val Glu Val Phe  
 165 170 175  
 Thr Ser Lys Asp Gln Asn Ala Gly Pro Ser Arg Gly Trp Gln Glu Phe  
 180 185 190  
 Val Val Ser Pro Arg Ala Lys Ala Lys Ile Arg Gln Trp Phe Ala Lys  
 195 200 205  
 Glu Arg Arg Glu Glu Tyr Leu Glu Ala Gly Arg Asp Ala Leu Ala Ala  
 210 215 220  
 Val Ile Gln Arg Gly Gly Leu Pro Met His Arg Leu Phe Thr Ala Ser  
 225 230 235 240  
 Ser Met Lys Thr Val Ala Thr Glu Leu His Tyr Pro Asp Val Asp Ala  
 245 250 255  
 Leu Tyr Thr Ala Ile Gly Ser Gly Ser Val Ser Ala Gln His Val Val  
 260 265 270  
 Asn Arg Leu Met Ala Ile Phe Gly Asp Glu Glu Asp Ala Glu Asp Ala  
 275 280 285  
 Leu Val Ala Arg Thr Pro Phe Ser Glu Leu Val Asn Ser Arg Ala Thr  
 290 295 300  
 Thr Glu Ser Ser Thr Gly Ile Leu Val Glu Gly Ser Pro Asp Val Met  
 305 310 315 320  
 Ala Lys Leu Ala Lys Cys Cys Met Pro Val Pro Gly Asp Glu Ile Phe  
 325 330 335  
 Gly Phe Val Thr Arg Gly Gly Gly Val Ser Val His Arg Thr Asp Cys  
 340 345 350  
 Thr Asn Val Glu Lys Leu Lys Glu Glu Pro Glu Arg Ile Val Ser Val  
 355 360 365  
 Ser Trp Ala Ser Glu Gly Gln Gly Ser Val  
 370 375

<210> 1057  
 <211> 1059  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1036)  
 <223> RXN01940

<400> 1057  
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 gccagctaaa tccacaaact gaactaagga gttttaccct atg acc acc aag atc 115  
 Met Thr Thr Lys Ile  
 1 5

atc ctc gac tgc gat cca gga cac gac gac gct gta gcc atg ctg ctc 163  
 Ile Leu Asp Cys Asp Pro Gly His Asp Asp Ala Val Ala Met Leu Leu  
                   10                                  15                                  20

gca gcc ggc agc cca gaa att gaa ctg ctt gga atc acc acg gtc ggc 211  
 Ala Ala Gly Ser Pro Glu Ile Glu Leu Leu Gly Ile Thr Thr Val Gly  
                   25                                  30                                  35

ggc aac cag acc ttg gac aag gtc acc cac aat acg cag gtc gta gcc 259  
 Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn Thr Gln Val Val Ala  
                   40                                  45                                  50

acc atc gct gat atc aat gcg ccc atc tac cgc ggt gtc acc cga cca 307  
 Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg Gly Val Thr Arg Pro  
                   55                                  60                                  65

ttg gtg cgc ccc gtt gag gta gcc gaa gat atc cac ggc gat acc ggc 355  
 Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile His Gly Asp Thr Gly  
                   70                                  75                                  80                                  85

atg gaa atc cac aag tac gaa ctg cct gaa cca acc aag cag gta gaa 403  
 Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro Thr Lys Gln Val Glu  
                                   90                                  95                                  100

gac acc cac gcg gtg gat ttc atc atc gat acc atc atg aat aac gag 451  
 Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr Ile Met Asn Asn Glu  
                   105                                  110                                  115

ccc ggc agc gta gcg ctg gtt ccc acc gga cca ctg acc aac atc gcg 499  
 Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro Leu Thr Asn Ile Ala  
                   120                                  125                                  130

ctg gca gtc cgg aaa gaa cca cgc atc gcc gag cga gtc aag gaa gtt 547  
 Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val  
                   135                                  140                                  145

gtc ctc atg ggc ggg ggc tac cac gta gga aac tgg acc gcc gta gct 595  
 Val Leu Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala  
                   150                                  155                                  160                                  165

gaa ttc aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac 643  
 Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn  
                                   170                                  175                                  180

gaa aag tgg cca ctg act atg gtc ggc ctc gac ctt acc cac cag gcg 691  
 Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala  
                   185                                  190                                  195

ctc gca aca cct gag atc gaa gcc aag ttc aac gag ctg ggc acc gac 739  
 Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp  
                   200                                  205                                  210

gtc gcc gac ttc gtc gtc gcg ctt ttc gac gct ttc cgc aag aat tac 787  
 Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr  
                   215                                  220                                  225

cag gac gca cag ggt ttt gat aac cca cca gta cac gac cct tgt gct 835  
 Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala  
                   230                                  235                                  240                                  245

gtt gca tac ctt gtt gac cca acc gta ttc acc acc cgc aaa gca cca 883

Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro  
 250 255 260

ctc gat gtg gag ctg tac ggc gca ctc acc aca ggc atg acc gtt gct 931  
 Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala  
 265 270 275

gat ttc cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt 979  
 Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val  
 280 285 290

gac ctg gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag  
 1027  
 Asp Leu Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys  
 295 300 305

cgc atc gga tagacctgtt cacaagggttg tta  
 1059  
 Arg Ile Gly  
 310

<210> 1058  
 <211> 312  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 1058  
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 1 5 10 15  
 Val Ala Met Leu Leu Ala Ala Gly Ser Pro Glu Ile Glu Leu Leu Gly  
 20 25 30  
 Ile Thr Thr Val Gly Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn  
 35 40 45  
 Thr Gln Val Val Ala Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg  
 50 55 60  
 Gly Val Thr Arg Pro Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile  
 65 70 75 80  
 His Gly Asp Thr Gly Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro  
 85 90 95  
 Thr Lys Gln Val Glu Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr  
 100 105 110  
 Ile Met Asn Asn Glu Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro  
 115 120 125  
 Leu Thr Asn Ile Ala Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu  
 130 135 140  
 Arg Val Lys Glu Val Val Leu Met Gly Gly Gly Tyr His Val Gly Asn  
 145 150 155 160  
 Trp Thr Ala Val Ala Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala  
 165 170 175

His Ile Val Phe Asn Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp  
180 185 190

Leu Thr His Gln Ala Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn  
195 200 205

Glu Leu Gly Thr Asp Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala  
210 215 220

Phe Arg Lys Asn Tyr Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val  
225 230 235 240

His Asp Pro Cys Ala Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr  
245 250 255

Thr Arg Lys Ala Pro Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr  
260 265 270

Gly Met Thr Val Ala Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr  
275 280 285

Thr Gln Val Ala Val Asp Leu Asp Phe Asp Lys Phe Trp Asn Met Val  
290 295 300

Ile Asp Ala Val Lys Arg Ile Gly  
305 310

<210> 1059

<211> 602

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(579)

<223> FRXA01940

<400> 1059

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Arg Val Thr Leu Val Ser Thr Gly Pro Leu Thr Asn Ile Ala Leu Ala  
1 5 10 15

gtc cgg aaa gaa cca cgc atc gcc gag cga gtc aag gaa gtt gtc ctc 96  
Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val Val Leu  
20 25 30

atg ggc ggg ggc tac cac gta gga aac tgg acc gcc gta gct gaa ttc 144  
Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala Glu Phe  
35 40 45

aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac gaa aag 192  
Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys  
50 55 60

tgg cca ctg act atg gtc ggc ctc gac ctt acc cac cag gcg ctc gca 240  
Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala  
65 70 75 80

aca cct gag atc gaa gcc aag ttc aac gag ctg ggc acc gac gtc gcc 288  
Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala

85	90	95	
gac ttc gtc gtc gcg ctt ttc gac gct ttc cgc aag aat tac cag gac Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr Gln Asp 100 105 110			336
gca cag ggt ttt gat aac cca cca gta cac gac cct tgt gct gtt gca Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala Val Ala 115 120 125			384
tac ctt gtt gac cca acc gta ttc acc acc cgc aaa gca cca ctc gat Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp 130 135 140			432
gtg gag ctg tac ggc gca ctc acc aca ggc atg acc gtt gct gat ttc Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe 145 150 155 160			480
cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt gac ctg Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu 165 170 175			528
gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag cgc atc Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile 180 185 190			576
gga tagacctgtt cacaagggttg tta Gly			602
 <210> 1060 <211> 193 <212> PRT <213> Corynebacterium glutamicum			
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Arg Val Thr Leu Val Ser Thr Gly Pro Leu Thr Asn Ile Ala Leu Ala 1 5 10 15			
Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val Val Leu 20 25 30			
Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala Glu Phe 35 40 45			
Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys 50 55 60			
Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala 65 70 75 80			
Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala 85 90 95			
Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr Gln Asp 100 105 110			
Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala Val Ala 115 120 125			

Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp  
 130 135 140  
 Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe  
 145 150 155 160  
 Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu  
 165 170 175  
 Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile  
 180 185 190

Gly

<210> 1061  
 <211> 1026  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1003)  
 <223> RXA02559

<400> 1061

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 aacccaaccc caaaaccaga aaacactaag ctcgtgagac atg att cct gtt ctc 115  
 Met Ile Pro Val Leu  
 1 5  
 atc gac tgc gac acc ggc atc gac gac gcc ctc gcc ctg atc tac ctg 163  
 Ile Asp Cys Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ile Tyr Leu  
 10 15 20  
 gtt gct ttg cat aaa cgt ggt gaa atc caa ctt ttt gga gca acg acc 211  
 Val Ala Leu His Lys Arg Gly Glu Ile Gln Leu Phe Gly Ala Thr Thr  
 25 30 35  
 acc gca gga aat gtt gat gtg aaa caa acc gcc atc aat acc agg tgg 259  
 Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala Ile Asn Thr Arg Trp  
 40 45 50  
 gtg ttg gat cag tgt gga tta gcg gac atc ccg gtc ctc gca gga caa 307  
 Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro Val Leu Ala Gly Gln  
 55 60 65  
 cct gaa cca aag cac gtg ccg cta gtg act act cca gaa aca cac ggc 355  
 Pro Glu Pro Lys His Val Pro Leu Val Thr Thr Pro Glu Thr His Gly  
 70 75 80 85  
 gac cat ggc ctt ggt tat ata aac cca ggt cac gtc gaa att cca gaa 403  
 Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His Val Glu Ile Pro Glu  
 90 95 100  
 ggt gac tgg aag cag ctg tgg aaa gaa cac ctc agt aac cca gaa act 451  
 Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu Ser Asn Pro Glu Thr  
 105 110 115

aag ctg att gtc acc ggg ccc gcc acc aac ctt gcg gaa ttc ggg cca 499  
 Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu Ala Glu Phe Gly Pro  
           120                          125                          130

gtg gaa aac gtc acg ctg atg ggt ggc acc tac ctt tat cca ggc aac 547  
 Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr Leu Tyr Pro Gly Asn  
           135                          140                          145

acc act cca acg gca gaa tgg aat acc tgg gtt gat cca cac gga gct 595  
 Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val Asp Pro His Gly Ala  
 150                          155                          160                          165

aaa gaa gca ttc gcg gca gcc caa aag ccc att acg gtg tgt tcc ttg 643  
 Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile Thr Val Cys Ser Leu  
                           170                          175                          180

ggc gtg acc gag cag ttt acg ctg aac ccg gac atc ctt tct aca ctt 691  
 Gly Val Thr Glu Gln Phe Thr Leu Asn Pro Asp Ile Leu Ser Thr Leu  
                           185                          190                          195

atc aac acg ctt ggc agc caa ccc atc gca gag cat tta cct gag atg 739  
 Ile Asn Thr Leu Gly Ser Gln Pro Ile Ala Glu His Leu Pro Glu Met  
           200                          205                          210

ctg cgc ttt tac ttt gaa ttt cac gaa gtg cag ggc gaa ggt tac ctt 787  
 Leu Arg Phe Tyr Phe Glu Phe His Glu Val Gln Gly Glu Gly Tyr Leu  
           215                          220                          225

gct caa att cat gac ctg ctg acc tgc atg att gcc ttg gat aaa atc 835  
 Ala Gln Ile His Asp Leu Leu Thr Cys Met Ile Ala Leu Asp Lys Ile  
 230                          235                          240                          245

cca ttt tca ggc cgt gaa gta acc gtg gac gtg gag gct gat tcg ccc 883  
 Pro Phe Ser Gly Arg Glu Val Thr Val Asp Val Glu Ala Asp Ser Pro  
                           250                          255                          260

ttg atg cgt ggc acc act gtt gca gat att cgc gga cat tgg ggc aag 931  
 Leu Met Arg Gly Thr Thr Val Ala Asp Ile Arg Gly His Trp Gly Lys  
                           265                          270                          275

cca gct aac gca ttt ctt gtg gaa acc gca gac att gag gcc gcc cac 979  
 Pro Ala Asn Ala Phe Leu Val Glu Thr Ala Asp Ile Glu Ala Ala His  
           280                          285                          290

gcg gaa ctt cta aga gca gtg gaa tgaaataatc cggtgctgat gca  
 1026  
 Ala Glu Leu Leu Arg Ala Val Glu  
           295                          300

&lt;210&gt; 1062

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1062

Met Ile Pro Val Leu Ile Asp Cys Asp Thr Gly Ile Asp Asp Ala Leu  
           1                          5                          10                          15

Ala Leu Ile Tyr Leu Val Ala Leu His Lys Arg Gly Glu Il Gln Leu  
                           20                          25                          30

Phe Gly Ala Thr Thr Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala  
 35 40 45  
 Ile Asn Thr Arg Trp Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro  
 50 55 60  
 Val Leu Ala Gly Gln Pro Glu Pro Lys His Val Pro Leu Val Thr Thr  
 65 70 75 80  
 Pro Glu Thr His Gly Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His  
 85 90 95  
 Val Glu Ile Pro Glu Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu  
 100 105 110  
 Ser Asn Pro Glu Thr Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu  
 115 120 125  
 Ala Glu Phe Gly Pro Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr  
 130 135 140  
 Leu Tyr Pro Gly Asn Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val  
 145 150 155 160  
 Asp Pro His Gly Ala Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile  
 165 170 175  
 Thr Val Cys Ser Leu Gly Val Thr Glu Gln Phe Thr Leu Asn Pro Asp  
 180 185 190  
 Ile Leu Ser Thr Leu Ile Asn Thr Leu Gly Ser Gln Pro Ile Ala Glu  
 195 200 205  
 His Leu Pro Glu Met Leu Arg Phe Tyr Phe Glu Phe His Glu Val Gln  
 210 215 220  
 Gly Glu Gly Tyr Leu Ala Gln Ile His Asp Leu Leu Thr Cys Met Ile  
 225 230 235 240  
 Ala Leu Asp Lys Ile Pro Phe Ser Gly Arg Glu Val Thr Val Asp Val  
 245 250 255  
 Glu Ala Asp Ser Pro Leu Met Arg Gly Thr Thr Val Ala Asp Ile Arg  
 260 265 270  
 Gly His Trp Gly Lys Pro Ala Asn Ala Phe Leu Val Glu Thr Ala Asp  
 275 280 285  
 Ile Glu Ala Ala His Ala Glu Leu Leu Arg Ala Val Glu  
 290 295 300

&lt;210&gt; 1063

&lt;211&gt; 1050

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1027)



&lt;223&gt; RXA02497

&lt;400&gt; 1063

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gattcacact ttgccaccct agaccgtcta accttttaggt gtg aga tta ggt gta 115  
 Val Arg Leu Gly Val  
 1 5

tta gat gtg ggc agc aat act gtc cac cta gtt gca gta gac gcg cgt 163  
 Leu Asp Val Gly Ser Asn Thr Val His Leu Val Ala Val Asp Ala Arg  
 10 15 20

ccc ggt gga cac ccc acc ccg atg agc aat tgg cgt acc cca ctg cgc 211  
 Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp Arg Thr Pro Leu Arg  
 25 30 35

ctt gtt gag ctt ctt gat gac tcc ggg gcg atc tcc gaa aag ggc atc 259  
 Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile Ser Glu Lys Gly Ile  
 40 45 50

aac aaa ctc acc tca gca gtc ggg gaa gca gca gac cta gcg aaa acg 307  
 Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala Asp Leu Ala Lys Thr  
 55 60 65

ctc ggc tgc gct gaa ctg atg cca ttt gct aca tcg gca gtc cgc tcc 355  
 Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr Ser Ala Val Arg Ser  
 70 75 80 85

gcc acc aac agc gag gca gtg ctc gac cac gtg gag aag gaa acc ggc 403  
 Ala Thr Asn Ser Glu Ala Val Leu Asp His Val Glu Lys Glu Thr Gly  
 90 95 100

gtc cgc ctg tcc atc ctt tcc ggt gaa gac gaa gca cgc caa act ttc 451  
 Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu Ala Arg Gln Thr Phe  
 105 110 115

ctc gca gtt cga cgt tgg tat gga tgg tcc gca ggg cgc ata act aac 499  
 Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala Gly Arg Ile Thr Asn  
 120 125 130

ctc gac atc ggt ggc ggc tcc ctg gaa cta tcc tcc gga acc gac gaa 547  
 Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser Ser Gly Thr Asp Glu  
 135 140 145

tcc cca gac ctc gcg ttc tca ctg gat ctg ggt gcg ggc cgc ttg acc 595  
 Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly Ala Gly Arg Leu Thr  
 150 155 160 165

cac aac tgg ttc gac acc gat cca ccg gca cgt aag aaa atc aac ctc 643  
 His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg Lys Lys Ile Asn Leu  
 170 175 180

ctg cgc gat tat atc gat gcg gaa ctt gca gaa ccc gcc cgc cag atg 691  
 Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu Pro Ala Arg Gln Met  
 185 190 195

cgc acc cta ggg ccc gcg cgc ctg gca gtg gga aca tcc aaa act ttc 739  
 Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly Thr Ser Lys Thr Phe  
 200 205 210

cgc acc ctg gca cga ctg act ggt gct gcg ccc tca tcc gca gga cca 787  
 Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro Ser Ser Ala Gly Pro  
 215 220 225

cac gtc acc cga acc ctc acc gcg ccg ggt ctg cgc cag ctg atc gca 835  
 His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu Arg Gln Leu Ile Ala  
 230 235 240 245

ttt atc tca cga atg act gcg gcg gac cgc gct gag ctg gaa ggt atc 883  
 Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala Glu Leu Glu Gly Ile  
 250 255 260

agc tcg gat cgg tca cat cag atc gtg gca ggt gcg cta gtt gcg gaa 931  
 Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly Ala Leu Val Ala Glu  
 265 270 275

gct gcg atg cgt gcg ttg gat att gac aag gta gaa att tgt ccg tgg 979  
 Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val Glu Ile Cys Pro Trp  
 280 285 290

gca ctt cgt gaa ggt gtg atc ctc acc agg atc gac aaa gga ctc gag  
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 Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile Asp Lys Gly Leu Glu  
 295 300 305

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 1050

<210> 1064

<211> 309

<212> PRT

<213> Corynebacterium glutamicum

<400> 1064

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Ala Val Asp Ala Arg Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp  
 20 25 30

Arg Thr Pro Leu Arg Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile  
 35 40 45

Ser Glu Lys Gly Ile Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala  
 50 55 60

Asp Leu Ala Lys Thr Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr  
 65 70 75 80

Ser Ala Val Arg Ser Ala Thr Asn Ser Glu Ala Val Leu Asp His Val  
 85 90 95

Glu Lys Glu Thr Gly Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu  
 100 105 110

Ala Arg Gln Thr Phe Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala  
 115 120 125

Gly Arg Ile Thr Asn Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser  
 130 135 140

Ser Gly Thr Asp Glu Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly  
 145 150 155 160  
 Ala Gly Arg Leu Thr His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg  
 165 170 175  
 Lys Lys Ile Asn Leu Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu  
 180 185 190  
 Pro Ala Arg Gln Met Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly  
 195 200 205  
 Thr Ser Lys Thr Phe Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro  
 210 215 220  
 Ser Ser Ala Gly Pro His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu  
 225 230 235 240  
 Arg Gln Leu Ile Ala Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala  
 245 250 255  
 Glu Leu Glu Gly Ile Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly  
 260 265 270  
 Ala Leu Val Ala Glu Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val  
 275 280 285  
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 290 295 300  
 Asp Lys Gly Leu Glu  
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<210> 1065  
 <211> 2226  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2203)  
 <223> RXN01079

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 Met Asp Phe His Ala  
 1 5  
 ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt 163  
 Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe  
 10 15 20  
 gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac 211  
 Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn  
 25 30 35  
 cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg 259

Gln	Asn	Thr	Val	Phe	Phe	His	Asn	Leu	Gln	Glu	Lys	Ile	Asp	Tyr	Leu	
		40					45					50				
ggt	gaa	aac	aag	tac	tat	gac	cca	atc	ggt	ctg	gac	aag	tac	gac	ttc	307
Val	Glu	Asn	Lys	Tyr	Tyr	Asp	Pro	Ile	Val	Leu	Asp	Lys	Tyr	Asp	Phe	
	55					60					65					
cag	ttc	atc	aag	gac	ctc	ttc	aag	cgc	gca	tac	gga	ttc	aag	ttc	cgc	355
Gln	Phe	Ile	Lys	Asp	Leu	Phe	Lys	Arg	Ala	Tyr	Gly	Phe	Lys	Phe	Arg	
70					75					80					85	
ttc	cag	tcc	ttc	ctc	ggt	gca	tac	aag	tac	tac	act	tcc	tac	acc	ctg	403
Phe	Gln	Ser	Phe	Leu	Gly	Ala	Tyr	Lys	Tyr	Tyr	Thr	Ser	Tyr	Thr	Leu	
				90					95					100		
aag	acc	ttc	gac	ggt	cgc	cgc	tac	ctc	gag	cgt	ttc	gaa	gac	cgt	gtc	451
Lys	Thr	Phe	Asp	Gly	Arg	Arg	Tyr	Leu	Glu	Arg	Phe	Glu	Asp	Arg	Val	
			105					110					115			
tgc	atg	gtc	gcc	ctc	acc	ctc	gct	gac	ggc	gac	cgc	gca	ttg	gcc	gag	499
Cys	Met	Val	Ala	Leu	Thr	Leu	Ala	Asp	Gly	Asp	Arg	Ala	Leu	Ala	Glu	
		120					125					130				
aac	ctg	gtc	gat	gag	atc	atg	tct	ggc	cgt	ttc	caa	cca	gca	acc	cca	547
Asn	Leu	Val	Asp	Glu	Ile	Met	Ser	Gly	Arg	Phe	Gln	Pro	Ala	Thr	Pro	
	135					140					145					
acc	ttc	ctg	aac	tcc	ggc	aag	gca	cag	cgc	ggc	gag	cca	gta	tcc	tgc	595
Thr	Phe	Leu	Asn	Ser	Gly	Lys	Ala	Gln	Arg	Gly	Glu	Pro	Val	Ser	Cys	
150					155					160					165	
ttc	ctc	ctg	cgt	atc	gaa	gac	aac	atg	gag	tcc	atc	gga	cgt	tcc	atc	643
Phe	Leu	Leu	Arg	Ile	Glu	Asp	Asn	Met	Glu	Ser	Ile	Gly	Arg	Ser	Ile	
				170					175					180		
aac	tct	gct	ctt	cag	ctg	tcc	aag	cgt	ggc	ggt	ggc	gta	gcg	ttg	ctg	691
Asn	Ser	Ala	Leu	Gln	Leu	Ser	Lys	Arg	Gly	Gly	Gly	Val	Ala	Leu	Leu	
			185					190					195			
ctg	tcc	aac	ctt	cgt	gaa	gcc	ggt	gca	ccg	att	aag	aag	att	gaa	aac	739
Leu	Ser	Asn	Leu	Arg	Glu	Ala	Gly	Ala	Pro	Ile	Lys	Lys	Ile	Glu	Asn	
		200					205					210				
cag	tct	tcc	ggt	gtt	atc	cca	gtg	atg	aaa	ctt	ctg	gaa	gat	gct	ttc	787
Gln	Ser	Ser	Gly	Val	Ile	Pro	Val	Met	Lys	Leu	Leu	Glu	Asp	Ala	Phe	
	215					220					225					
tcc	tac	gct	aac	cag	ctg	ggt	gct	cgt	cag	ggt	gca	ggt	gct	gtg	tac	835
Ser	Tyr	Ala	Asn	Gln	Leu	Gly	Ala	Arg	Gln	Gly	Ala	Gly	Ala	Val	Tyr	
230					235					240					245	
ctc	aac	gct	cac	cac	cca	gat	atc	ctg	tcc	ttc	ctg	gat	acc	aag	cgt	883
Leu	Asn	Ala	His	His	Pro	Asp	Ile	Leu	Ser	Phe	Leu	Asp	Thr	Lys	Arg	
			250					255						260		
gag	aac	gcc	gat	gag	aag	atc	cgc	atc	aag	acc	ctg	tcc	ctg	ggt	gtt	931
Glu	Asn	Ala	Asp	Glu	Lys	Ile	Arg	Ile	Lys	Thr	Leu	Ser	Leu	Gly	Val	
			265					270					275			
gtg	att	ccg	gac	atc	acc	ttc	gag	ctg	gct	aag	cgc	aac	gat	gac	atg	979
Val	Ile	Pro	Asp	Ile	Thr	Phe	Glu	Leu	Ala	Lys	Arg	Asn	Asp	Asp	Met	

280	285	290
tac ctg ttc tcc cca tac gat gtg gag cgc att tac ggc aag cct ttc 1027		
Tyr Leu Phe Ser Pro Tyr Asp Val Glu Arg Ile Tyr Gly Lys Pro Phe 295 300 305		
gca gac gtc tca atc acc gag cac tac gac gag atg gtg gat gat gac 1075		
Ala Asp Val Ser Ile Thr Glu His Tyr Asp Glu Met Val Asp Asp Asp 310 315 320 325		
cgc atc cgc aag acc aag atc aac gcg cgt cag ttc ttc cag acc ctg 1123		
Arg Ile Arg Lys Thr Lys Ile Asn Ala Arg Gln Phe Phe Gln Thr Leu 330 335 340		
gca gaa atc cag ttc gag tcc ggt tac cca tac atc atg tat gaa gac 1171		
Ala Glu Ile Gln Phe Glu Ser Gly Tyr Pro Tyr Ile Met Tyr Glu Asp 345 350 355		
acc gtg aat gca tcc aac cca atc gaa ggt cgc atc acc cac tca aac 1219		
Thr Val Asn Ala Ser Asn Pro Ile Glu Gly Arg Ile Thr His Ser Asn 360 365 370		
ctg tgc tct gag atc ctt cag gtg tcc acc cca tct gaa ttc aac gat 1267		
Leu Cys Ser Glu Ile Leu Gln Val Ser Thr Pro Ser Glu Phe Asn Asp 375 380 385		
gac ctg act tac gca gag gtc ggc gaa gac att tct tgt aac ttg ggt 1315		
Asp Leu Thr Tyr Ala Glu Val Gly Glu Asp Ile Ser Cys Asn Leu Gly 390 395 400 405		
tcc ctc aac gtt gca atg gct atg gat gca cca aac ttt gag aag acc 1363		
Ser Leu Asn Val Ala Met Ala Met Asp Ala Pro Asn Phe Glu Lys Thr 410 415 420		
atc gaa acc gaa atc cgc ggc tta act gca gtg cct gag cag acc agc 1411		
Ile Glu Thr Glu Ile Arg Gly Leu Thr Ala Val Pro Glu Gln Thr Ser 425 430 435		
atc gat tcc gtg cct tcc atc cgt aag ggc aac gaa gca gct cac gcc 1459		
Ile Asp Ser Val Pro Ser Ile Arg Lys Gly Asn Glu Ala Ala His Ala 440 445 450		
atc ggc ctt ggc cag atg aac ctt cac ggc tac ttc ggt cgc gag cac 1507		
Ile Gly Leu Gly Gln Met Asn Leu His Gly Tyr Phe Gly Arg Glu His 455 460 465		
atg cac tac ggc tcc gag gaa gcc ctg gac ttc acc aac gca tac ttt 1555		
Met His Tyr Gly Ser Glu Glu Ala Leu Asp Phe Thr Asn Ala Tyr Phe 470 475 480 485		

gct gcc gtg ctg tac cag tgc ctg cgt gca tcc aac cag atc gct act  
 1603  
 Ala Ala Val Leu Tyr Gln Cys Leu Arg Ala Ser Asn Gln Ile Ala Thr  
 490 495 500

gag cgt gga gag cgt ttc aag aac ttc gaa aac tcc aag tat gca acc  
 1651  
 Glu Arg Gly Glu Arg Phe Lys Asn Phe Glu Asn Ser Lys Tyr Ala Thr  
 505 510 515

ggt gag tac ttc gat gat ttc gat gca aac gac ttc gca cca aag tcc  
 1699  
 Gly Glu Tyr Phe Asp Asp Phe Asp Ala Asn Asp Phe Ala Pro Lys Ser  
 520 525 530

gac aag gtc aag gaa ctc ttt gcc aag tcg aac atc cac acc cca acc  
 1747  
 Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn Ile His Thr Pro Thr  
 535 540 545

gtt gag gac tgg gct gcg ctg aag gcc gac gtg atg gag cac ggt ctg  
 1795  
 Val Glu Asp Trp Ala Ala Leu Lys Ala Asp Val Met Glu His Gly Leu  
 550 555 560 565

ttc aac cgt aac ctg caa gcg gtt cca cca acc ggt tcg atc tcc tac  
 1843  
 Phe Asn Arg Asn Leu Gln Ala Val Pro Pro Thr Gly Ser Ile Ser Tyr  
 570 575 580

atc aac aac tcc acc tcg tcg atc cac cca atc gca tcc aag att gag  
 1891  
 Ile Asn Asn Ser Thr Ser Ser Ile His Pro Ile Ala Ser Lys Ile Glu  
 585 590 595

atc cgc aag gaa ggc aag atc ggc cgc gtt tac tac cca gct cca cac  
 1939  
 Ile Arg Lys Glu Gly Lys Ile Gly Arg Val Tyr Tyr Pro Ala Pro His  
 600 605 610

atg gac aat gac aac ctt gag tac ttc gag gac gcc tac gaa atc ggc  
 1987  
 Met Asp Asn Asp Asn Leu Glu Tyr Phe Glu Asp Ala Tyr Glu Ile Gly  
 615 620 625

tac gag aag atc att gac acc tac gct gtg gca acc aag tac gtt gac  
 2035  
 Tyr Glu Lys Ile Ile Asp Thr Tyr Ala Val Ala Thr Lys Tyr Val Asp  
 630 635 640 645

cag ggc ctg tca ctg acc ttg ttc ttc aag gac act gcc acc acc cgt  
 2083  
 Gln Gly Leu Ser Leu Thr Leu Phe Phe Lys Asp Thr Ala Thr Thr Arg  
 650 655 660

gac atc aac cgt gcg cag atc tac gca tgg cgc aag ggc atc aag acc  
 2131  
 Asp Ile Asn Arg Ala Gln Ile Tyr Ala Trp Arg Lys Gly Ile Lys Thr  
 665 670 675

ttg tac tac att cgc ctg cgc cag gtt gct ctg gaa ggc act gaa gtt  
2179

Leu Tyr Tyr Ile Arg Leu Arg Gln Val Ala Leu Glu Gly Thr Glu Val  
680 685 690

gac ggc tgc gtc agc tgc atg ctg taaaagcact taaaaatatc ccc  
2226

Asp Gly Cys Val Ser Cys Met Leu  
695 700

<210> 1066

<211> 701

<212> PRT

<213> Corynebacterium glutamicum

<400> 1066

Met Asp Phe His Ala Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn  
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Gly Lys Ile Gln Phe Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe  
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Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu  
35 40 45

Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu  
50 55 60

Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr  
65 70 75 80

Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr  
85 90 95

Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg  
100 105 110

Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp  
115 120 125

Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe  
130 135 140

Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly  
145 150 155 160

Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser  
165 170 175

Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly  
180 185 190

Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile  
195 200 205

Lys Lys Ile Glu Asn Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu  
210 215 220

Leu Glu Asp Ala Phe Ser Tyr Ala Asn Gln Leu Gly Ala Arg Gln Gly  
225 230 235 240

Ala Gly Ala Val Tyr Leu Asn Ala His His Pro Asp Ile Leu Ser Phe  
 245 250 255  
 Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile Lys Thr  
 260 265 270  
 Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu Ala Lys  
 275 280 285  
 Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu Arg Ile  
 290 295 300  
 Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr Asp Glu  
 305 310 315 320  
 Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala Arg Gln  
 325 330 335  
 Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr Pro Tyr  
 340 345 350  
 Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu Gly Arg  
 355 360 365  
 Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser Thr Pro  
 370 375 380  
 Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu Asp Ile  
 385 390 395 400  
 Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp Ala Pro  
 405 410 415  
 Asn Phe Glu Lys Thr Ile Glu Thr Glu Ile Arg Gly Leu Thr Ala Val  
 420 425 430  
 Pro Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys Gly Asn  
 435 440 445  
 Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His Gly Tyr  
 450 455 460  
 Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu Asp Phe  
 465 470 475 480  
 Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg Ala Ser  
 485 490 495  
 Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe Glu Asn  
 500 505 510  
 Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala Asn Asp  
 515 520 525  
 Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn  
 530 535 540  
 Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala Asp Val  
 545 550 555 560



Met	Glu	His	Gly	Leu	Phe	Asn	Arg	Asn	Leu	Gln	Ala	Val	Pro	Pro	Thr
				565					570					575	
Gly	Ser	Ile	Ser	Tyr	Ile	Asn	Asn	Ser	Thr	Ser	Ser	Ile	His	Pro	Ile
			580					585					590		
Ala	Ser	Lys	Ile	Glu	Ile	Arg	Lys	Glu	Gly	Lys	Ile	Gly	Arg	Val	Tyr
		595					600					605			
Tyr	Pro	Ala	Pro	His	Met	Asp	Asn	Asp	Asn	Leu	Glu	Tyr	Phe	Glu	Asp
	610					615					620				
Ala	Tyr	Glu	Ile	Gly	Tyr	Glu	Lys	Ile	Ile	Asp	Thr	Tyr	Ala	Val	Ala
625					630					635					640
Thr	Lys	Tyr	Val	Asp	Gln	Gly	Leu	Ser	Leu	Thr	Leu	Phe	Phe	Lys	Asp
				645					650					655	
Thr	Ala	Thr	Thr	Arg	Asp	Ile	Asn	Arg	Ala	Gln	Ile	Tyr	Ala	Trp	Arg
			660					665					670		
Lys	Gly	Ile	Lys	Thr	Leu	Tyr	Tyr	Ile	Arg	Leu	Arg	Gln	Val	Ala	Leu
		675					680					685			
Glu	Gly	Thr	Glu	Val	Asp	Gly	Cys	Val	Ser	Cys	Met	Leu			
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<212> DNA
<213> Corynebacterium glutamicum
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<223> FRXA01079
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Met Asp Phe His Ala  
1 5

ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt 163  
Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe  
10 15 20

gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac 211  
Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn  
25 30 35

cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg 259  
Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu Lys Ile Asp Tyr Leu  
40 45 50

gtt gaa aac aag tac tat gac cca atc gtt ctg gac aag tac gac ttc 307  
Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu Asp Lys Tyr Asp Phe  
55 60 65

cag ttc atc aag gac ctc ttc aag cgc gca tac gga ttc aag ttc cgc 355  
 Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr Gly Phe Lys Phe Arg  
 70 75 80 85  
  
 ttc cag tcc ttc ctc ggt gca tac aag tac tac act tcc tac acc ctg 403  
 Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr Thr Ser Tyr Thr Leu  
 90 95 100  
  
 aag acc ttc gac ggt cgc cgc tac ctc gag cgt ttc gaa gac cgt gtc 451  
 Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg Phe Glu Asp Arg Val  
 105 110 115  
  
 tgc atg gtc gcc ctc acc ctc gct gac ggc gac cgc gca ttg gcc gag 499  
 Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp Arg Ala Leu Ala Glu  
 120 125 130  
  
 aac ctg gtc gat gag atc atg tct ggc cgt ttc caa cca gca acc cca 547  
 Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe Gln Pro Ala Thr Pro  
 135 140 145  
  
 acc ttc ctg aac tcc ggc aag gca cag cgc ggc gag cca gta tcc tgc 595  
 Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly Glu Pro Val Ser Cys  
 150 155 160 165  
  
 ttc ctc ctg cgt atc gaa gac aac atg gag tcc atc gga cgt tcc atc 643  
 Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser Ile Gly Arg Ser Ile  
 170 175 180  
  
 aac tct gct ctt cag ctg tcc aag cgt ggc ggt ggc gta gcg ttg ctg 691  
 Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly Gly Val Ala Leu Leu  
 185 190 195  
  
 ctg tcc aac ctt cgt gaa gcc ggt gca ccg att aag aag att gaa atc 739  
 Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile Lys Lys Ile Glu Ile  
 200 205 210  
  
 cag tct tcc ggt gtt atc cca gtg atg aaa ctt ctg gaa gat gct ttc 787  
 Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu Leu Glu Asp Ala Phe  
 215 220 225  
  
 tcc 790  
 Ser  
 230

&lt;210&gt; 1068

&lt;211&gt; 230

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1068

Met Asp Phe His Ala Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn  
 1 5 10 15  
  
 Gly Lys Ile Gln Phe Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe  
 20 25 30  
  
 Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu  
 35 40 45  
  
 Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu

50                                      55                                      60  
 Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr  
 65                                      70                                      75                                      80  
 Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr  
                                     85                                      90                                      95  
 Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg  
                                     100                                      105                                      110  
 Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp  
                                     115                                      120                                      125  
 Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe  
                                     130                                      135                                      140  
 Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly  
 145                                      150                                      155                                      160  
 Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser  
                                     165                                      170                                      175  
 Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly  
                                     180                                      185                                      190  
 Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile  
                                     195                                      200                                      205  
 Lys Lys Ile Glu Ile Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu  
                                     210                                      215                                      220  
 Leu Glu Asp Ala Phe Ser  
 225                                      230

&lt;210&gt; 1069

&lt;211&gt; 1364

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1341)

&lt;223&gt; FRXA01084

&lt;400&gt; 1069

tcc ttt ctg gat acc aag cgc gag aac gcc gat gag aag atc cgc atc      48  
 Ser Phe Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile  
   1                                      5                                      10                                      15

aag acc ctg tcc ctg ggt gtt gtg att ccg gac atc acc ttc gag ctg      96  
 Lys Thr Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu  
                                     20                                      25                                      30

gct aag cgc aac gat gac atg tac ctg ttc tcc cca tac gat gtg gag      144  
 Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu  
                                     35                                      40                                      45

cgc att tac ggc aag cct ttc gca gac gtc tca atc acc gag cac tac      192  
 Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr

50	55	60	
gac gag atg gtg gat gat gac cgc atc cgc aag acc aag atc aac gcg Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala 65 70 75 80			240
cgt cag ttc ttc cag acc ctg gca gaa atc cag ttc gag tcc ggt tac Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr 85 90 95			288
cca tac atc atg tat gaa gac acc gtg aat gca tcc aac cca atc gaa Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu 100 105 110			336
ggt cgc atc acc cac tca aac ctg tgc tct gag atc ctt cag gtg tcc Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser 115 120 125			384
acc cca tct gaa ttc aac gat gac ctg act tac gca gag gtc ggc gaa Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu 130 135 140			432
gac att tct tgt aac ttg ggt tcc ctc aac gtt gca atg gct atg gat Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp 145 150 155 160			480
gca cca aac ttt gag aag acc atn gaa acc gaa atc cgc ggc tta act Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr 165 170 175			528
gca gtg nct gag cag acc agc atc gat tcc gtg cct tcc atc cgt aag Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys 180 185 190			576
ggc aac gaa gca gct cac gcc atc ggc ctt ggc cag atg aac ctt cac Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His 195 200 205			624
ggc tac ttc ggt cgc gag cac atg cac tac ggc tcc gag gaa gcc ctg Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu 210 215 220			672
gac ttc acc aac gca tac ttt gct gcc gtg ctg tac cag tgc ctg cgt Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg 225 230 235 240			720
gca tcc aac cag atc gct act gag cgt gga gag cgt ttc aag aac ttc Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe 245 250 255			768
gaa aac tcc aag tat gca acc ggt gag tac ttc gat gat ttc gat gca Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala 260 265 270			816
aac gac ttc gca cca aag tcc gac aag gtc aag gaa ctc ttt gcc aag Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys 275 280 285			864
tcg aac atc cac acc cca acc gtt gag gac tgg gct gcg ctg aag gcc Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala 290 295 300			912

gac gtg atg gag cac ggt ctg ttc aac cgt aac ctg caa gcg gtt cca 960  
 Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro  
 305 310 315 320

cca acc ggt tcg atc tcc tac atc aac aac tcc acc tcg tcg atc cac  
 1008  
 Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His  
 325 330 335

cca atc gca tcc aag att gag atc cgc aag gaa ggc aag atc ggc cgc  
 1056  
 Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg  
 340 345 350

gtt tac tac cca gct cca cac atg gac aat gac aac ctt gag tac ttc  
 1104  
 Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe  
 355 360 365

gag gac gcc tac gaa atc ggc tac gag aag atc att gac acc tac gct  
 1152  
 Glu Asp Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala  
 370 375 380

gtg gca acc aag tac gtt gac cag ggc ctg tca ctg acc ttg ttc ttc  
 1200  
 Val Ala Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe  
 385 390 395 400

aag gac act gcc acc acc cgt gac atc aac cgt gcg cag atc tac gca  
 1248  
 Lys Asp Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala  
 405 410 415

tgg cgc aag ggc atc aag acc ttg tac tac att cgc ctg cgc cag gtt  
 1296  
 Trp Arg Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val  
 420 425 430

gct ctg gaa ggc act gaa gtt gac ggc tgc gtc agc tgc atg ctg  
 1341  
 Ala Leu Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu  
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taaaagcact taaaaaatatc ccc  
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<210> 1070

<211> 447

<212> PRT

<213> Corynebacterium glutamicum

<400> 1070

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Lys Thr Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu  
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Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu  
 35 40 45  
 Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr  
 50 55 60  
 Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala  
 65 70 75 80  
 Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr  
 85 90 95  
 Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu  
 100 105 110  
 Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser  
 115 120 125  
 Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu  
 130 135 140  
 Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp  
 145 150 155 160  
 Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr  
 165 170 175  
 Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys  
 180 185 190  
 Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His  
 195 200 205  
 Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu  
 210 215 220  
 Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg  
 225 230 235 240  
 Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe  
 245 250 255  
 Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala  
 260 265 270  
 Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys  
 275 280 285  
 Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala  
 290 295 300  
 Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro  
 305 310 315 320  
 Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His  
 325 330 335  
 Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg  
 340 345 350  
 Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe

355	360	365
Glu Asp Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala 370 375 380		
Val Ala Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe 385 390 395 400		
Lys Asp Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala 405 410 415		
Trp Arg Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val 420 425 430		
Ala Leu Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu 435 440 445		

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 <211> 1125  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1102)  
 <223> RXN01920

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 Met Ala Ala Asp Ser  
 1 5  
 gat ctc agt gtt cac gat gct tac tta aag gag cat gtt gca cct gta 163  
 Asp Leu Ser Val His Asp Ala Tyr Leu Lys Glu His Val Ala Pro Val  
 10 15 20  
 aag gcg atc aac tgg aac tcc atc cca gat tcc aaa gat ctt gaa gtc 211  
 Lys Ala Ile Asn Trp Asn Ser Ile Pro Asp Ser Lys Asp Leu Glu Val  
 25 30 35  
 tgg gat cgt ctg acc ggt aac ttc tgg ctc cca gaa aag gtc cca gta 259  
 Trp Asp Arg Leu Thr Gly Asn Phe Trp Leu Pro Glu Lys Val Pro Val  
 40 45 50  
 tcc aac gac atc aag agc tgg gga acc ctc aac gag gtt gaa aaa gcc 307  
 Ser Asn Asp Ile Lys Ser Trp Gly Thr Leu Asn Glu Val Glu Lys Ala  
 55 60 65  
 gca acc atg cgc gtg ttc acc gga ctt acc ctg ctg gac acc att cag 355  
 Ala Thr Met Arg Val Phe Thr Gly Leu Thr Leu Leu Asp Thr Ile Gln  
 70 75 80 85  
 ggc act gtc ggc gca atc tcc ctg ctt cca gac gca gat tca ctg cac 403  
 Gly Thr Val Gly Ala Ile Ser Leu Leu Pro Asp Ala Asp Ser Leu His  
 90 95 100  
 gaa gaa gcg gtg cta acc aac att gcg ttc atg gaa tcc gtg cac gca 451  
 Glu Glu Ala Val Leu Thr Asn Ile Ala Phe Met Glu Ser Val His Ala

105					110					115						
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Lys	Ser	Tyr	Ser	Asn	Ile	Phe	Met	Thr	Leu	Ala	Ser	Thr	Ala	Glu	Ile	
		120					125					130				
aac	gat	gcg	ttc	cgt	tgg	tct	gag	gaa	aat	gaa	aac	ctg	cag	cgc	aag	547
Asn	Asp	Ala	Phe	Arg	Trp	Ser	Glu	Glu	Asn	Glu	Asn	Leu	Gln	Arg	Lys	
	135					140					145					
gca	aag	atc	atc	ctg	tct	tac	tat	gag	ggc	gat	gat	cca	cta	aag	cgc	595
Ala	Lys	Ile	Ile	Leu	Ser	Tyr	Tyr	Glu	Gly	Asp	Asp	Pro	Leu	Lys	Arg	
150					155				160						165	
aag	atc	gcc	tcc	gtg	atc	ctg	gag	tcc	ttc	ctg	ttc	tac	tcc	ggc	ttc	643
Lys	Ile	Ala	Ser	Val	Ile	Leu	Glu	Ser	Phe	Leu	Phe	Tyr	Ser	Gly	Phe	
				170					175					180		
tac	ctc	cca	atg	tat	tgg	tcc	agc	cac	tcc	aag	ctg	gcc	aac	acc	gcc	691
Tyr	Leu	Pro	Met	Tyr	Trp	Ser	Ser	His	Ser	Lys	Leu	Ala	Asn	Thr	Ala	
			185					190					195			
gac	gtg	atc	cgc	ctg	atc	atc	cgc	gat	gag	gca	gtg	cac	ggc	tac	tac	739
Asp	Val	Ile	Arg	Leu	Ile	Ile	Arg	Asp	Glu	Ala	Val	His	Gly	Tyr	Tyr	
	200						205					210				
att	ggc	tac	aag	tat	caa	aag	gct	gtc	gcg	aag	gag	act	cca	gag	cgt	787
Ile	Gly	Tyr	Lys	Tyr	Gln	Lys	Ala	Val	Ala	Lys	Glu	Thr	Pro	Glu	Arg	
	215					220					225					
cag	gaa	gag	ctg	aag	gag	tac	acc	ttc	gat	ctg	ctc	tac	gat	ctt	tac	835
Gln	Glu	Glu	Leu	Lys	Glu	Tyr	Thr	Phe	Asp	Leu	Leu	Tyr	Asp	Leu	Tyr	
230					235				240						245	
gat	aac	gaa	act	cag	tac	tcc	gaa	gat	ctc	tac	gac	gat	ctt	gga	tgg	883
Asp	Asn	Glu	Thr	Gln	Tyr	Ser	Glu	Asp	Leu	Tyr	Asp	Asp	Leu	Gly	Trp	
				250					255					260		
acc	gag	gat	gtt	aag	cga	ttc	ctt	cgc	tac	aac	gcc	aac	aag	gcc	ctc	931
Thr	Glu	Asp	Val	Lys	Arg	Phe	Leu	Arg	Tyr	Asn	Ala	Asn	Lys	Ala	Leu	
			265					270					275			
aac	aac	ctt	ggc	tac	gaa	gga	ctc	ttc	cca	gcg	gat	gaa	acc	aag	gtg	979
Asn	Asn	Leu	Gly	Tyr	Glu	Gly	Leu	Phe	Pro	Ala	Asp	Glu	Thr	Lys	Val	
		280					285					290				
tcc	cca	aac	atc	ttg	tct	gcg	ctg	tca	cca	aac	gct	gat	gag	aac	cac	
1027																
Ser	Pro	Asn	Ile	Leu	Ser	Ala	Leu	Ser	Pro	Asn	Ala	Asp	Glu	Asn	His	
		295				300					305					
gac	ttc	ttc	tcc	ggc	tcc	ggg	tcc	tct	tac	gtt	att	ggg	aag	gca	gaa	
1075																
Asp	Phe	Phe	Ser	Gly	Ser	Gly	Ser	Ser	Tyr	Val	Ile	Gly	Lys	Ala	Glu	
310					315				320						325	
aac	acc	gag	gat	gat	gac	tgg	gac	ttc	taacttttaa	aaagctgaag						
1122																
Asn	Thr	Glu	Asp	Asp	Asp	Trp	Asp	Phe								
				330												



cgc  
1125

<210> 1072

<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 1072

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Lys	Asp	Leu	Glu	Val	Trp	Asp	Arg	Leu	Thr	Gly	Asn	Phe	Trp	Leu	Pro	35	40	45	
Glu	Lys	Val	Pro	Val	Ser	Asn	Asp	Ile	Lys	Ser	Trp	Gly	Thr	Leu	Asn	50	55	60	
Glu	Val	Glu	Lys	Ala	Ala	Thr	Met	Arg	Val	Phe	Thr	Gly	Leu	Thr	Leu	65	70	75	80
Leu	Asp	Thr	Ile	Gln	Gly	Thr	Val	Gly	Ala	Ile	Ser	Leu	Leu	Pro	Asp	85	90	95	
Ala	Asp	Ser	Leu	His	Glu	Glu	Ala	Val	Leu	Thr	Asn	Ile	Ala	Phe	Met	100	105	110	
Glu	Ser	Val	His	Ala	Lys	Ser	Tyr	Ser	Asn	Ile	Phe	Met	Thr	Leu	Ala	115	120	125	
Ser	Thr	Ala	Glu	Ile	Asn	Asp	Ala	Phe	Arg	Trp	Ser	Glu	Glu	Asn	Glu	130	135	140	
Asn	Leu	Gln	Arg	Lys	Ala	Lys	Ile	Ile	Leu	Ser	Tyr	Tyr	Glu	Gly	Asp	145	150	155	160
Asp	Pro	Leu	Lys	Arg	Lys	Ile	Ala	Ser	Val	Ile	Leu	Glu	Ser	Phe	Leu	165	170	175	
Phe	Tyr	Ser	Gly	Phe	Tyr	Leu	Pro	Met	Tyr	Trp	Ser	Ser	His	Ser	Lys	180	185	190	
Leu	Ala	Asn	Thr	Ala	Asp	Val	Ile	Arg	Leu	Ile	Ile	Arg	Asp	Glu	Ala	195	200	205	
Val	His	Gly	Tyr	Tyr	Ile	Gly	Tyr	Lys	Tyr	Gln	Lys	Ala	Val	Ala	Lys	210	215	220	
Glu	Thr	Pro	Glu	Arg	Gln	Glu	Glu	Leu	Lys	Glu	Tyr	Thr	Phe	Asp	Leu	225	230	235	240
Leu	Tyr	Asp	Leu	Tyr	Asp	Asn	Glu	Thr	Gln	Tyr	Ser	Glu	Asp	Leu	Tyr	245	250	255	
Asp	Asp	Leu	Gly	Trp	Thr	Glu	Asp	Val	Lys	Arg	Phe	Leu	Arg	Tyr	Asn	260	265	270	

Ala Asn Lys Ala Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala  
 275 280 285

Asp Glu Thr Lys Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn  
 290 295 300

Ala Asp Glu Asn His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val  
 305 310 315 320

Ile Gly Lys Ala Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe  
 325 330

<210> 1073

<211> 437

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(414)

<223> FRXA01920

<400> 1073

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 Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr  
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tac att ggc tac aag tat caa aag gct gtc gcg aag gag act cca gag 96  
 Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu  
 20 25 30

cgt cag gaa gag ctg aag gag tac acc ttc gat ctg ctc tac gat ctt 144  
 Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu  
 35 40 45

tac gat aac gaa act cag tac tcc gaa gat ctc tac gac gat ctt gga 192  
 Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly  
 50 55 60

tgg acc gag gat gtt aag cga ttc ctt cgc tac aac gcc aac aag gcc 240  
 Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala  
 65 70 75 80

ctc aac aac ctt ggc tac gaa gga ctc ttc cca gcg gat gaa acc aag 288  
 Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys  
 85 90 95

gtg tcc cca aac atc ttg tct gcg ctg tca cca aac gct gat gag aac 336  
 Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn  
 100 105 110

cac gac ttc ttc tcc ggc tcc ggt tcc tct tac gtt att ggt aag gca 384  
 His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala  
 115 120 125

gaa aac acc gag gat gat gac tgg gac ttc taacttttaa aaagctgaag 434  
 Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe  
 130 135

cgc

437

<400> 1074

Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe  
130 135

<213> Corynebacterium glutamicum

<223> RXA01080

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Leu	Pro	Asn	Val	Arg	Ile	Pro	Leu	Thr	Arg	Val	Glu	Glu	Pro	Leu	Lys	
			25					30					35			

atc aac gag ccc tac gtg cta atc acc ccg acc tat ggt ggt gga gtc 259  
 Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr Tyr Gly Gly Gly Val  
 40 45 50  
 tcc atg act gga gaa aac tcc cgc ccg gtc cca cca caa gtc atc agg 307  
 Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro Pro Gln Val Ile Arg  
 55 60 65  
 ttt tta aat gat gaa cac aac cgc agc ttc atc agg gca gtt gtt gca 355  
 Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile Arg Ala Val Val Ala  
 70 75 80 85  
 ggt gga aac tca aac ttc ggc tcc gat ttt ggg ttg gca ggc gag atc 403  
 Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly Leu Ala Gly Glu Ile  
 90 95 100  
 att tcc aag aaa tgt aaa gtg ccc tat gtc tac cgt ttc gag ctc atg 451  
 Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr Arg Phe Glu Leu Met  
 105 110 115  
 ggc aat gag gaa gat gta agt atc ctt cgt gga ggt ctt act caa aac 499  
 Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly Gly Leu Thr Gln Asn  
 120 125 130  
 gcc caa gct ttg ggg ctg gaa cca caa gaa cca gtt acc tcg cga 544  
 Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro Val Thr Ser Arg  
 135 140 145  
 taaaccttaa aacttaatca atc 567

&lt;210&gt; 1076

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1076

Met Leu Ile Val Tyr Phe Ser Ser Ala Thr Asp Asn Thr His Arg Phe  
 1 5 10 15  
 Val Gln Lys Leu Asp Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val  
 20 25 30  
 Glu Glu Pro Leu Lys Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr  
 35 40 45  
 Tyr Gly Gly Gly Val Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro  
 50 55 60  
 Pro Gln Val Ile Arg Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile  
 65 70 75 80  
 Arg Ala Val Val Ala Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly  
 85 90 95  
 Leu Ala Gly Glu Ile Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr  
 100 105 110  
 Arg Phe Glu Leu Met Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly  
 115 120 125

Gly Leu Thr Gln Asn Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro  
 130 135 140

Val Thr Ser Arg  
 145

<210> 1077

<211> 650

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(627)

<223> RXA00867

<400> 1077

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Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Asp Phe Ile Thr	
1 5 10 15	
gca ctt cag ctg gac acc aag ctg gac ggc att cct tcc aag gtg ctc	96
Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu	
20 25 30	
tcc gat gcg ctt gag cag gca cgc gat gcc cga ctg acc atc ctg aac	144
Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn	
35 40 45	
acc atg gct gat gtc atc aac gga cct gat gag atg agc aag ttc gct	192
Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala	
50 55 60	
cct cgc atc acc acc gtg aag atc cca gtg gca aag atc ggt gag ctg	240
Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu	
65 70 75 80	
atc gga cca aag ggt aag aac atc aac gct ctt acc gaa gag acc ggc	288
Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly	
85 90 95	
gca aac atc tcc atc gaa gat gac ggc acc gtg ttc atc tct gca gct	336
Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala	
100 105 110	
gac ggc gca tct gct gaa gcg gcg atc gaa aag atc aac gct ctg gcg	384
Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala	
115 120 125	
aac cca cag ctg cca aag gtt ggc gag cgc ttc ctc gga acc gtc gtc	432
Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val	
130 135 140	
aag acc acc gca ttc gga gca ttc gtt tcc ttg ctc cca ggc cgc gac	480
Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp	
145 150 155 160	
ggc ctt gtt cac atc tcc aag ctg ggt aac ggc aag cga gta gaa aag	528
Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys	
165 170 175	

gtc gac gat gtg gtg aag gtt ggc gag aag att cag gtc gaa atc gct 576  
 Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala  
                   180                                  185                                  190

gac atc gac aac cgc ggc aag atc tcc ttg gtc cca gtt gtt gaa gag 624  
 Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu  
                   195                                  200                                  205

gac taattagttc tggctagatc ggg 650  
 Asp

<210> 1078

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 1078

Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Asp Phe Ile Thr  
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Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu  
                   20                                  25                                  30

Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn  
           35                                  40                                  45

Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala  
       50                                  55                                  60

Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu  
       65                                  70                                  75                                  80

Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly  
                   85                                  90                                  95

Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala  
                   100                                  105                                  110

Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala  
           115                                  120                                  125

Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val  
       130                                  135                                  140

Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp  
       145                                  150                                  155                                  160

Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys  
                   165                                  170                                  175

Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala  
                   180                                  185                                  190

Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu  
           195                                  200                                  205

Asp

<210> 1079  
 <211> 630  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(630)  
 <223> RXA01416

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 Ala Gly Ala Ser Glu Asn Val Val Asn Arg Val Lys Asp Gly Ala Pro  
 1 5 10 15  
 gca cca acc gaa aag atc gtc tcc gac ggc ctt gaa gca gct aag cca 96  
 Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro  
 20 25 30  
 ttc atc gac atc ctg tgc cgc gca cag gaa ggt ctg gca cag cgc gtt 144  
 Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val  
 35 40 45  
 gga aac gca gcc aag gaa ttc cca ctg ttc cct cca tac acc gac gag 192  
 Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu  
 50 55 60  
 gtg tac tcc gca gtg gag cgc aag gta tcc aag aag cta gct tct ttg 240  
 Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu  
 65 70 75 80  
 ctg acc ctg aag gca aag caa gag cgc gac gac gct acc aac gcc tac 288  
 Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr  
 85 90 95  
 atg gaa gaa atc gaa gcc gaa ctg ctt cca aag ttc gag gct tcc tac 336  
 Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr  
 100 105 110  
 agc tca gca gct gaa gcg tcc aag gaa atc cgt gca gga tac aac gct 384  
 Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala  
 115 120 125  
 gtc atg aag gcc atc gtg cgc cgc atg atc ctc acc gat cac ttc cgc 432  
 Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg  
 130 135 140  
 atc gac ggc cgc gga gtc acc gac atc cgt gac ctg gca gta gaa gtt 480  
 Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val  
 145 150 155 160  
 gag ctc atc cca cgt gcg cac ggt tcc tcc ctc ttc gag cgt ggc gag 528  
 Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu  
 165 170 175  
 acc cag atc ctt ggt gtc acc acc ctg gac atg ctc aag atg gaa cag 576  
 Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln  
 180 185 190

caa atc gac tcc ctg gca cca ggc gat gcg aag cgc tac atg cac cac 624  
 Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His  
           195                          200                          205

tac aac  
 Tyr Asn  
           210 630

<210> 1080  
 <211> 210  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1080  
 Ala Gly Ala Ser Glu Asn Val Val Asn Arg Val Lys Asp Gly Ala Pro  
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 Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro  
                           20                          25                          30  
 Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val  
                           35                          40                          45  
 Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu  
           50                          55                          60  
 Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu  
   65                          70                          75                          80  
 Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr  
                           85                          90                          95  
 Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr  
                           100                          105                          110  
 Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala  
           115                          120                          125  
 Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg  
   130                          135                          140  
 Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val  
 145                          150                          155                          160  
 Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu  
                           165                          170                          175  
 Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln  
                           180                          185                          190  
 Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His  
           195                          200                          205  
 Tyr Asn  
           210

<210> 1081  
 <211> 757  
 <212> DNA



&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(757)

&lt;223&gt; RXA01486

&lt;400&gt; 1081

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agagaactgg taagggttttt accgttctag accgcagaaa tcttcgcggc gacaccgatg 60

atcgccgagc agaactaaac atgaggagac ctactcgcac atg agc gat gta aag 115
Met Ser Asp Val Lys
1 5

gac ttc gaa gac acc gaa ttt ggc ctg atc gag gcc gtc gca acc atc 163
Asp Phe Glu Asp Thr Glu Phe Gly Leu Ile Glu Ala Val Ala Thr Ile
10 15 20

gac aac ggt gac ttc gga acc cgc acc atc cgt ttt gaa acc ggc caa 211
Asp Asn Gly Asp Phe Gly Thr Arg Thr Ile Arg Phe Glu Thr Gly Gln
25 30 35

ctt gcc cgc cag gca gat ggt gca gtg acc acc tac ctc gac gat gac 259
Leu Ala Arg Gln Ala Asp Gly Ala Val Thr Thr Tyr Leu Asp Asp Asp
40 45 50

acg atg ctg ctg gca acc acc acc gca tcc aac cag cca cgc gag ggc 307
Thr Met Leu Leu Ala Thr Thr Thr Ala Ser Asn Gln Pro Arg Glu Gly
55 60 65

ttt gac ttc ttc cca ctg acc gtg gac gtt gaa gag cgt atg tac gca 355
Phe Asp Phe Phe Pro Leu Thr Val Asp Val Glu Glu Arg Met Tyr Ala
70 75 80 85

gct ggt cgc atc cct ggc tct ttc ttc cgt cgg gag ggt cgc cca tcc 403
Ala Gly Arg Ile Pro Gly Ser Phe Phe Arg Arg Glu Gly Arg Pro Ser
90 95 100

acc gaa gct atc ctg gct tgc cgt ctc atc gac cgc cca ctg cgc cca 451
Thr Glu Ala Ile Leu Ala Cys Arg Leu Ile Asp Arg Pro Leu Arg Pro
105 110 115

acc ttt gtt aag ggc ctg cgc aat gag gtt cag atc gtt gtc acc gtc 499
Thr Phe Val Lys Gly Leu Arg Asn Glu Val Gln Ile Val Val Thr Val
120 125 130

atg tcc atg aac cct gag gat tac tac gat gtc gta gca atc aac gga 547
Met Ser Met Asn Pro Glu Asp Tyr Tyr Asp Val Val Ala Ile Asn Gly
135 140 145

gct tcc gca gca acc cgc atc tcc gga ctt cct gtc tcc ggc gct gtc 595
Ala Ser Ala Ala Thr Arg Ile Ser Gly Leu Pro Val Ser Gly Ala Val
150 155 160 165

ggt ggc gtt cgc atg gca ctg gtt ggt gat gaa aag cac cca gaa ggc 643
Gly Gly Val Arg Met Ala Leu Val Gly Asp Glu Lys His Pro Glu Gly
170 175 180

caa tgg gtt gca ttc cca acc cac gct caa cat gag cag tcc gta ttt 691
Gln Trp Val Ala Phe Pro Thr His Ala Gln His Glu Gln Ser Val Phe
185 190 195

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gaa atc gtt gtg gct ggt cgc ctc gtc gag cgc aag cgc ggc aac aag 739  
 Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg Lys Arg Gly Asn Lys  
           200                                  205                                  210

acc ttc tcc gac gtc gca 757  
 Thr Phe Ser Asp Val Ala  
           215

<210> 1082  
 <211> 219  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1082  
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 Ala Val Ala Thr Ile Asp Asn Gly Asp Phe Gly Thr Arg Thr Ile Arg  
                                   20                                  25                                  30  
 Phe Glu Thr Gly Gln Leu Ala Arg Gln Ala Asp Gly Ala Val Thr Thr  
                                   35                                  40                                  45  
 Tyr Leu Asp Asp Asp Thr Met Leu Leu Ala Thr Thr Thr Ala Ser Asn  
           50                                  55                                  60  
 Gln Pro Arg Glu Gly Phe Asp Phe Phe Pro Leu Thr Val Asp Val Glu  
   65                                  70                                  75                                  80  
 Glu Arg Met Tyr Ala Ala Gly Arg Ile Pro Gly Ser Phe Phe Arg Arg  
                                   85                                  90                                  95  
 Glu Gly Arg Pro Ser Thr Glu Ala Ile Leu Ala Cys Arg Leu Ile Asp  
                                   100                                  105                                  110  
 Arg Pro Leu Arg Pro Thr Phe Val Lys Gly Leu Arg Asn Glu Val Gln  
                                   115                                  120                                  125  
 Ile Val Val Thr Val Met Ser Met Asn Pro Glu Asp Tyr Tyr Asp Val  
           130                                  135                                  140  
 Val Ala Ile Asn Gly Ala Ser Ala Ala Thr Arg Ile Ser Gly Leu Pro  
   145                                  150                                  155                                  160  
 Val Ser Gly Ala Val Gly Gly Val Arg Met Ala Leu Val Gly Asp Glu  
                                   165                                  170                                  175  
 Lys His Pro Glu Gly Gln Trp Val Ala Phe Pro Thr His Ala Gln His  
                                   180                                  185                                  190  
 Glu Gln Ser Val Phe Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg  
                                   195                                  200                                  205  
 Lys Arg Gly Asn Lys Thr Phe Ser Asp Val Ala  
           210                                  215

<210> 1083  
 <211> 651

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(628)

&lt;223&gt; RXA01678

&lt;400&gt; 1083

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tattgtccag gcgcaggaaa atatctcata gttcaacatc gcaaatatca ccgacttcca 60
cggctatatc tctgcaactg cagctcaccc cggtgcagca atg ctg aaa tgt gca 115
                                         Met Leu Lys Cys Ala
                                         1                               5

gtc gat gaa gcc gct ggc gga cgc gcc caa gct ttc gta tcc tca ggc 163
Val Asp Glu Ala Ala Gly Gly Arg Ala Gln Ala Phe Val Ser Ser Gly
              10                      15                      20

gat aac att ggt ggc agc ccg ttc caa tcc tcc att ctt ggt gat gaa 211
Asp Asn Ile Gly Gly Ser Pro Phe Gln Ser Ser Ile Leu Gly Asp Glu
              25                      30                      35

ccc acc ttg gaa gca ctc aac caa atg ggt ctt gat tac tca gca gtg 259
Pro Thr Leu Glu Ala Leu Asn Gln Met Gly Leu Asp Tyr Ser Ala Val
              40                      45                      50

ggc aac cac gaa ttt gat aaa ggc tac gca gac tta agc agt cga gtc 307
Gly Asn His Glu Phe Asp Lys Gly Tyr Ala Asp Leu Ser Ser Arg Val
              55                      60                      65

gct gac ctt gct gat ttt gat tat ctc ggc gca aac gtt gag ggc gaa 355
Ala Asp Leu Ala Asp Phe Asp Tyr Leu Gly Ala Asn Val Glu Gly Glu
              70                      75                      80                      85

aac cca gat ctt gca cca tat gga att tct cac ctt gat ggt gtg aag 403
Asn Pro Asp Leu Ala Pro Tyr Gly Ile Ser His Leu Asp Gly Val Lys
              90                      95                      100

gtt gct ttc gta ggc acc gta tcc caa gaa act ccg atg ttg gtc aat 451
Val Ala Phe Val Gly Thr Val Ser Gln Glu Thr Pro Met Leu Val Asn
              105                      110                      115

tct gaa ggc att gag gga atc acg ttt act gac cca ctt gaa gca acc 499
Ser Glu Gly Ile Glu Gly Ile Thr Phe Thr Asp Pro Leu Glu Ala Thr
              120                      125                      130

aac cgt gta gct gat gaa ctc gtg gga agt ggc gca gca gat gtt gtc 547
Asn Arg Val Ala Asp Glu Leu Val Gly Ser Gly Ala Ala Asp Val Val
              135                      140                      145

gtt gcg ctt tac cac gaa ggc att acc ggc acc gaa gca tgg tca gaa 595
Val Ala Leu Tyr His Glu Gly Ile Thr Gly Thr Glu Ala Trp Ser Glu
              150                      155                      160                      165

aat atc gac gtt gtt ttc gca ggt cac acc cac taagtctcgtg atctaggaac 648
Asn Ile Asp Val Val Phe Ala Gly His Thr His
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cga 651

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<210> 1084  
 <211> 176  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1084  
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           20                  25                  30  
 Ile Leu Gly Asp Glu Pro Thr Leu Glu Ala Leu Asn Gln Met Gly Leu  
       35                  40                  45  
 Asp Tyr Ser Ala Val Gly Asn His Glu Phe Asp Lys Gly Tyr Ala Asp  
       50                  55                  60  
 Leu Ser Ser Arg Val Ala Asp Leu Ala Asp Phe Asp Tyr Leu Gly Ala  
   65                  70                  75                  80  
 Asn Val Glu Gly Glu Asn Pro Asp Leu Ala Pro Tyr Gly Ile Ser His  
           85                  90                  95  
 Leu Asp Gly Val Lys Val Ala Phe Val Gly Thr Val Ser Gln Glu Thr  
       100                  105                  110  
 Pro Met Leu Val Asn Ser Glu Gly Ile Glu Gly Ile Thr Phe Thr Asp  
       115                  120                  125  
 Pro Leu Glu Ala Thr Asn Arg Val Ala Asp Glu Leu Val Gly Ser Gly  
       130                  135                  140  
 Ala Ala Asp Val Val Val Ala Leu Tyr His Glu Gly Ile Thr Gly Thr  
   145                  150                  155                  160  
 Glu Ala Trp Ser Glu Asn Ile Asp Val Val Phe Ala Gly His Thr His  
           165                  170                  175

<210> 1085  
 <211> 1359  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1336)  
 <223> RXA01679

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   Met Gln Ser Gly Asn  
   1                  5

tac ggg cac gca ctt gcc gat gta gat ttc agc ttc aac cac gac acc	163
Tyr Gly His Ala Leu Ala Asp Val Asp Phe Ser Phe Asn His Asp Thr	
10 15 20	
ggt gag ctc acc gta gat gat gcc cgc atg ctc gga gtc gac gat atc	211
Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu Gly Val Asp Asp Ile	
25 30 35	
aac gcg tgt gaa aac cca gat gac acc att gca gat att gtt gct cag	259
Asn Ala Cys Glu Asn Pro Asp Asp Thr Ile Ala Asp Ile Val Ala Gln	
40 45 50	
gcg gaa ctt gat gct ggt gaa gcc ggc aaa gaa gta gta gcg acc atc	307
Ala Glu Leu Asp Ala Gly Glu Ala Gly Lys Glu Val Val Ala Thr Ile	
55 60 65	
gat ggc gat ttt ctc cgc gcc agc gac gaa gga gca gaa tct ggc tcc	355
Asp Gly Asp Phe Leu Arg Ala Ser Asp Glu Gly Ala Glu Ser Gly Ser	
70 75 80 85	
aac tac ggc gct gaa tcc cag ctc gtc aac atg att gcc agt gct gtg	403
Asn Tyr Gly Ala Glu Ser Gln Leu Val Asn Met Ile Ala Ser Ala Val	
90 95 100	
cgt tgg tcc atg tcc acc aat acc gcc acc acc gca gac att ggg ctt	451
Arg Trp Ser Met Ser Thr Asn Thr Ala Thr Thr Ala Asp Ile Gly Leu	
105 110 115	
atg aac gcc gga gga ctc cac act gac cta ttc agc ggc gat gtt acc	499
Met Asn Ala Gly Gly Leu His Thr Asp Leu Phe Ser Gly Asp Val Thr	
120 125 130	
tac gcc gaa gct ttt gaa atc cag cct ttc tcc ggt gaa gat tca ttt	547
Tyr Ala Glu Ala Phe Glu Ile Gln Pro Phe Ser Gly Glu Asp Ser Phe	
135 140 145	
gtc acc ctc aag gga tca gtc ttc aaa gat gcc ctt gac cag cag tgg	595
Val Thr Leu Lys Gly Ser Val Phe Lys Asp Ala Leu Asp Gln Gln Trp	
150 155 160 165	
gaa gaa ggt tct gca cga cca gtg gca gca ctt ggc gta tcc gac aac	643
Glu Glu Gly Ser Ala Arg Pro Val Ala Ala Leu Gly Val Ser Asp Asn	
170 175 180	
gtt tcc tac acc tac gac atc aac cgt cca atc ggt gac cgc gtc act	691
Val Ser Tyr Thr Tyr Asp Ile Asn Arg Pro Ile Gly Asp Arg Val Thr	
185 190 195	
tcc gtg acc att gat gat acc cca ctt gat ccg gaa cgc gac tac gtt	739
Ser Val Thr Ile Asp Asp Thr Pro Leu Asp Pro Glu Arg Asp Tyr Val	
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gtt gca gct tcc ctg tac ctc cag tcc ggc aac gaa ggt atg acc gca	787
Val Ala Ala Ser Leu Tyr Leu Gln Ser Gly Asn Glu Gly Met Thr Ala	
215 220 225	
ctg acc cgc gga acc gca cct gca caa acc ggc atc gtg gat gta cag	835
Leu Thr Arg Gly Thr Ala Pro Ala Gln Thr Gly Ile Val Asp Val Gln	
230 235 240 245	
tcc acc atc gga tac ttg tcc aac aac aat gtc acc cca cgt act ggt	883

Ser Thr Ile Gly Tyr Leu Ser Asn Asn Asn Val Thr Pro Arg Thr Gly  
 250 255 260  
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 Gln Ala Gln Ile Ser Ile Thr Pro Ser Gly Glu Phe Asn Ala Gly Glu  
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 acc atc acc ctt gac atg gca gga ctc cgc tac acc caa ggc gac act 979  
 Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr Thr Gln Gly Asp Thr  
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 gcc acg gaa gta act gtc agc ctt cga gaa gaa att gtt tca gca cca  
 1027  
 Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu Ile Val Ser Ala Pro  
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 Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly Glu Ala Gly Thr Ala  
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 Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro Ser Phe Ile Gln Gln  
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 Ile Gln Gln Gln Ile Phe Ala  
 410

&lt;210&gt; 1086

&lt;211&gt; 412

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1086

Met Gln Ser Gly Asn Tyr Gly His Ala Leu Ala Asp Val Asp Phe Ser  
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Phe Asn His Asp Thr Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu  
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 Gly Val Asp Asp Ile Asn Ala Cys Glu Asn Pro Asp Asp Thr Ile Ala  
                     35                                    40                                    45  
 Asp Ile Val Ala Gln Ala Glu Leu Asp Ala Gly Glu Ala Gly Lys Glu  
                     50                                    55                                    60  
 Val Val Ala Thr Ile Asp Gly Asp Phe Leu Arg Ala Ser Asp Glu Gly  
                     65                                    70                                    75                                    80  
 Ala Glu Ser Gly Ser Asn Tyr Gly Ala Glu Ser Gln Leu Val Asn Met  
                                     85                                    90                                    95  
 Ile Ala Ser Ala Val Arg Trp Ser Met Ser Thr Asn Thr Ala Thr Thr  
                                     100                                    105                                    110  
 Ala Asp Ile Gly Leu Met Asn Ala Gly Gly Leu His Thr Asp Leu Phe  
                     115                                    120                                    125  
 Ser Gly Asp Val Thr Tyr Ala Glu Ala Phe Glu Ile Gln Pro Phe Ser  
                     130                                    135                                    140  
 Gly Glu Asp Ser Phe Val Thr Leu Lys Gly Ser Val Phe Lys Asp Ala  
                     145                                    150                                    155                                    160  
 Leu Asp Gln Gln Trp Glu Glu Gly Ser Ala Arg Pro Val Ala Ala Leu  
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 Gly Val Ser Asp Asn Val Ser Tyr Thr Tyr Asp Ile Asn Arg Pro Ile  
                     180                                    185                                    190  
 Gly Asp Arg Val Thr Ser Val Thr Ile Asp Asp Thr Pro Leu Asp Pro  
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 Glu Arg Asp Tyr Val Val Ala Ala Ser Leu Tyr Leu Gln Ser Gly Asn  
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 Glu Gly Met Thr Ala Leu Thr Arg Gly Thr Ala Pro Ala Gln Thr Gly  
                     225                                    230                                    235                                    240  
 Ile Val Asp Val Gln Ser Thr Ile Gly Tyr Leu Ser Asn Asn Asn Val  
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 Thr Pro Arg Thr Gly Gln Ala Gln Ile Ser Ile Thr Pro Ser Gly Glu  
                                     260                                    265                                    270  
 Phe Asn Ala Gly Glu Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr  
                     275                                    280                                    285  
 Thr Gln Gly Asp Thr Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu  
                     290                                    295                                    300  
 Ile Val Ser Ala Pro Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly  
                     305                                    310                                    315                                    320  
 Glu Ala Gly Thr Ala Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser  
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 Gly Thr Gln Asn Leu Val Val Thr Thr Asp Thr Gly Thr Arg Ile Ser

340	345	350
Met Pro Val Glu Ile Val Gly Ala Glu Gln Pro Ala Pro Gln Pro Ala		
355	360	365
Gly Ser Ser Val Leu Gly Thr Gly Val Leu Ser Gly Leu Leu Gly Ile		
370	375	380
Val Val Gly Ile Leu Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro		
385	390	395
400		
Ser Phe Ile Gln Gln Ile Gln Gln Gln Ile Phe Ala		
405	410	

&lt;210&gt; 1087

&lt;211&gt; 1071

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1048)

&lt;223&gt; RXN01488

&lt;400&gt; 1087

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gcccgacctt aaaaataaaa acctgaaagg ttaaaaacgc atg agc aaa aaa gcc 115
                                         Met Ser Lys Lys Ala
                                         1                               5

atc ctt gat atc gac acc ggc atc gat gat gcc ctc gca ctt gcc tac 163
Ile Leu Asp Ile Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ala Tyr
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gca ctg ggc tca cct gaa cta gag ctc att ggt gtc acc acc acc tac 211
Ala Leu Gly Ser Pro Glu Leu Glu Leu Ile Gly Val Thr Thr Thr Tyr
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ggt aac gtg cta ctc gaa acc ggt gca gtc aat gac ctg gca ctg ctt 259
Gly Asn Val Leu Leu Glu Thr Gly Ala Val Asn Asp Leu Ala Leu Leu
                               40                               45                               50

gat ctg ttc ggt gca cca gaa gta cct gtg tac ttg ggt gag cca cac 307
Asp Leu Phe Gly Ala Pro Glu Val Pro Val Tyr Leu Gly Glu Pro His
                               55                               60                               65

gca cag acc aag gat ggc ttt gaa gtt ctt gag atc tcc gcg ttc att 355
Ala Gln Thr Lys Asp Gly Phe Glu Val Leu Glu Ile Ser Ala Phe Ile
                               70                               75                               80                               85

cac gga caa aac ggc atc ggc gaa gtc gag ctg cca gca agc gag tca 403
His Gly Gln Asn Gly Ile Gly Glu Val Glu Leu Pro Ala Ser Glu Ser
                               90                               95                               100

aag gca ctc ccc ggc gca gtg gat ttc ctc att gat tcc gtc aac acc 451
Lys Ala Leu Pro Gly Ala Val Asp Phe Leu Ile Asp Ser Val Asn Thr
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cac ggc gat gac ctg gtg atc atc gca act ggt ccc atg acc aac ctg 499

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His	Gly	Asp	Asp	Leu	Val	Ile	Ile	Ala	Thr	Gly	Pro	Met	Thr	Asn	Leu		
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Ser	Ala	Ala	Ile	Ala	Lys	Asp	Pro	Ser	Phe	Ala	Ser	Lys	Ala	His	Val		
	135					140					145						
gtc	atc	atg	ggg	ggc	gcc	ttg	act	gtc	cca	ggc	aac	gtc	agc	aca	tgg	595	
Val	Ile	Met	Gly	Gly	Ala	Leu	Thr	Val	Pro	Gly	Asn	Val	Ser	Thr	Trp		
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gca	gaa	gca	aac	atc	aac	cag	gac	cca	gat	gca	gca	aac	gat	ctg	ttc	643	
Ala	Glu	Ala	Asn	Ile	Asn	Gln	Asp	Pro	Asp	Ala	Ala	Asn	Asp	Leu	Phe		
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cgt	tcc	ggg	gca	gat	gtc	acc	atg	atc	ggg	ctt	gat	gtc	acc	ctg	cag	691	
Arg	Ser	Gly	Ala	Asp	Val	Thr	Met	Ile	Gly	Leu	Asp	Val	Thr	Leu	Gln		
			185				190						195				
acc	ctt	ctt	acc	aag	aag	cac	act	gcg	cag	tgg	cgc	gaa	ctg	ggc	act	739	
Thr	Leu	Leu	Thr	Lys	Lys	His	Thr	Ala	Gln	Trp	Arg	Glu	Leu	Gly	Thr		
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cca	gct	gct	atc	gca	ctg	gcc	gac	atg	act	gat	tac	tac	atc	aag	gca	787	
Pro	Ala	Ala	Ile	Ala	Leu	Ala	Asp	Met	Thr	Asp	Tyr	Tyr	Ile	Lys	Ala		
	215					220					225						
tat	gag	acc	acc	gca	cca	cac	ctg	ggc	ggg	tgc	ggc	ctg	cac	gac	cca	835	
Tyr	Glu	Thr	Thr	Ala	Pro	His	Leu	Gly	Gly	Cys	Gly	Leu	His	Asp	Pro		
230					235					240					245		
ctg	gca	gta	ggc	gtt	gca	gtg	gac	cca	agc	ctg	gtc	act	ttg	ctc	ccc	883	
Leu	Ala	Val	Gly	Val	Ala	Val	Asp	Pro	Ser	Leu	Val	Thr	Leu	Leu	Pro		
			250						255					260			
atc	aac	ctc	aag	gta	gac	att	gag	ggc	gag	acc	cgt	gga	cgc	acc	att	931	
Ile	Asn	Leu	Lys	Val	Asp	Ile	Glu	Gly	Glu	Thr	Arg	Gly	Arg	Thr	Ile		
			265				270						275				
ggc	gat	gaa	gtc	cgc	ctc	aac	gat	cca	gtg	cgc	acc	tcc	cgc	gca	gct	979	
Gly	Asp	Glu	Val	Arg	Leu	Asn	Asp	Pro	Val	Arg	Thr	Ser	Arg	Ala	Ala		
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gtc	gcc	gta	gac	gtg	gat	cgt	ttc	ctt	tct	gaa	ttc	atg	acc	cgc	atc		
1027																	
Val	Ala	Val	Asp	Val	Asp	Arg	Phe	Leu	Ser	Glu	Phe	Met	Thr	Arg	Ile		
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ggc	cga	gtc	gca	gca	cag	cag	taaaagcagc	tctgggtgaag	gtt								
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Val Thr Thr Thr Tyr Gly Asn Val Leu Leu Glu Thr Gly Ala Val Asn	35	40	45
Asp Leu Ala Leu Leu Asp Leu Phe Gly Ala Pro Glu Val Pro Val Tyr	50	55	60
Leu Gly Glu Pro His Ala Gln Thr Lys Asp Gly Phe Glu Val Leu Glu	65	70	75
Ile Ser Ala Phe Ile His Gly Gln Asn Gly Ile Gly Glu Val Glu Leu	85	90	95
Pro Ala Ser Glu Ser Lys Ala Leu Pro Gly Ala Val Asp Phe Leu Ile	100	105	110
Asp Ser Val Asn Thr His Gly Asp Asp Leu Val Ile Ile Ala Thr Gly	115	120	125
Pro Met Thr Asn Leu Ser Ala Ala Ile Ala Lys Asp Pro Ser Phe Ala	130	135	140
Ser Lys Ala His Val Val Ile Met Gly Gly Ala Leu Thr Val Pro Gly	145	150	155
Asn Val Ser Thr Trp Ala Glu Ala Asn Ile Asn Gln Asp Pro Asp Ala	165	170	175
Ala Asn Asp Leu Phe Arg Ser Gly Ala Asp Val Thr Met Ile Gly Leu	180	185	190
Asp Val Thr Leu Gln Thr Leu Leu Thr Lys Lys His Thr Ala Gln Trp	195	200	205
Arg Glu Leu Gly Thr Pro Ala Ala Ile Ala Leu Ala Asp Met Thr Asp	210	215	220
Tyr Tyr Ile Lys Ala Tyr Glu Thr Thr Ala Pro His Leu Gly Gly Cys	225	230	235
Gly Leu His Asp Pro Leu Ala Val Gly Val Ala Val Asp Pro Ser Leu	245	250	255
Val Thr Leu Leu Pro Ile Asn Leu Lys Val Asp Ile Glu Gly Glu Thr	260	265	270
Arg Gly Arg Thr Ile Gly Asp Glu Val Arg Leu Asn Asp Pro Val Arg	275	280	285
Thr Ser Arg Ala Ala Val Ala Val Asp Val Asp Arg Phe Leu Ser Glu	290	295	300
Phe Met Thr Arg Ile Gly Arg Val Ala Ala Gln Gln	305	310	315

&lt;210&gt; 1089

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 <213> Corynebacterium glutamicum

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 Val Ala Arg Val Val  
 1 5  
 gtc aat gtc atg cct aag gct gag att ctg gat ccc cag ggg cag gcg 163  
 Val Asn Val Met Pro Lys Ala Glu Ile Leu Asp Pro Gln Gly Gln Ala  
 10 15 20  
 gta cac cgc gcc ctc gga cgt atc gga gtt tct ggc gtt tcc gat gtc 211  
 Val His Arg Ala Leu Gly Arg Ile Gly Val Ser Gly Val Ser Asp Val  
 25 30 35  
 cgt cag gga aag cgc ttc gag ctt gag gta gat gat tcc gtc acc gaa 259  
 Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp Asp Ser Val Thr Glu  
 40 45 50  
 gct gac cta aag aaa att gct gaa acc ctc ctc gca aac acc gtc atc 307  
 Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu Ala Asn Thr Val Ile  
 55 60 65  
 gaa gac ttc gat gtg gtg gga gtt gag gtc gcg aag tgagcgccaa 353  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Gly Val Ser Asp Val Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp  
 35 40 45  
 Asp Ser Val Thr Glu Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu  
 50 55 60  
 Ala Asn Thr Val Ile Glu Asp Phe Asp Val Val Gly Val Glu Val Ala  
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 Lys

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							Met	Arg	Ile	Asp	Pro						
							1				5						
ctg	gaa	acc	cgg	caa	gcc	gta	ttg	gcc	gtc	aaa	gac	tgg	att	gaa	ggg	163	
Leu	Glu	Thr	Arg	Gln	Ala	Val	Leu	Ala	Val	Lys	Asp	Trp	Ile	Glu	Gly		
				10					15					20			
gag	gga	gac	gtc	aaa	aag	cct	ggt	cgt	gcg	gca	ctt	gcc	gcc	gca	act	211	
Glu	Gly	Asp	Val	Lys	Lys	Pro	Gly	Arg	Ala	Ala	Leu	Ala	Ala	Ala	Thr		
				25					30					35			
cgc	ctg	agc	gtc	cga	ctg	ctc	gcg	caa	cac	gcg	ccg	gga	aac	agc	gtg	259	
Arg	Leu	Ser	Val	Arg	Leu	Leu	Ala	Gln	His	Ala	Pro	Gly	Asn	Ser	Val		
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gag	gtg	cgg	gta	ccc	cca	ttt	gtt	gcg	gtg	caa	tgc	ata	gag	ggg	cca	307	
Glu	Val	Arg	Val	Pro	Pro	Phe	Val	Ala	Val	Gln	Cys	Ile	Glu	Gly	Pro		
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aaa	cat	aca	cgc	ggc	aca	cca	ccc	aac	gtg	gtg	gag	acc	gac	gcc	aag	355	
Lys	His	Thr	Arg	Gly	Thr	Pro	Pro	Asn	Val	Val	Glu	Thr	Asp	Ala	Lys		
				70					75					80			85
acc	tgg	tta	cgc	tta	gca	cct	ggg	caa	acc	aca	ttt	gat	gca	gaa	ttt	403	
Thr	Trp	Leu	Arg	Leu	Ala	Pro	Gly	Gln	Thr	Thr	Phe	Asp	Ala	Glu	Phe		
				90					95					100			
gaa	agc	gga	aaa	att	agc	gca	tca	ggt	acc	cga	gcc	aaa	gag	att	gcg	451	
Glu	Ser	Gly	Lys	Ile	Ser	Ala	Ser	Gly	Thr	Arg	Ala	Lys	Glu	Ile	Ala		
				105					110					115			
gac	tgg	tta	cca	gtg	gtc	aaa	ctt	tagatttcct				aatgctcatt				agt	498
Asp	Trp	Leu	Pro	Val	Val	Lys	Leu										
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<212> PRT
<213> Corynebacterium glutamicum
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 Pro Gly Asn Ser Val Glu Val Arg Val Pro Pro Phe Val Ala Val Gln  
                   50                                  55                                  60  
 Cys Ile Glu Gly Pro Lys His Thr Arg Gly Thr Pro Pro Asn Val Val  
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 Glu Thr Asp Ala Lys Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr  
                                   85                                  90                                  95  
 Phe Asp Ala Glu Phe Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg  
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 Ala Lys Glu Ile Ala Asp Trp Leu Pro Val Val Lys Leu  
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   Met Gly Leu Trp Ile  
   1                                  5  
 gat gca acc gct ggc gtt gca ggg gat atg ttg ctg gga gca ctc att 163  
 Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu Leu Gly Ala Leu Ile  
                                   10                                  15                                  20  
 gat gca ggt gca gaa cta gaa aaa atc caa cag gtt gtg gaa gca gtc 211  
 Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln Val Val Glu Ala Val  
                                   25                                  30                                  35  
 atc ccc ggt gac gtg ctc ttg cgc acc gaa gag gta gtg cgc caa ggc 259  
 Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu Val Val Arg Gln Gly  
                                   40                                  45                                  50  
 caa cga ggc atc aag ctg cat gtg gac gca caa cat gaa cac cat cat 307  
 Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln His Glu His His His  
                                   55                                  60                                  65  
 cac cgc cac tta agc acc att aaa gaa ctg ctt gtc aat gct gac atc 355  
 His Arg His Leu Ser Thr Ile Lys Glu Leu Leu Val Asn Ala Asp Ile  
                                   70                                  75                                  80                                  85  
 cct gaa caa acc aag cag gat gcc tta ggc gtt ttt gaa ctc atc gct 403

3

Pro	Glu	Gln	Thr	Lys	Gln	Asp	Ala	Leu	Gly	Val	Phe	Glu	Leu	Ile	Ala		
				90					95					100			
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Ile	Ala	Glu	Gly	Lys	Val	His	Gly	Ile	Glu	Pro	Glu	Lys	Ile	His	Phe		
			105					110					115				
cat	gag	gta	gga	gct	tgg	gat	tcc	atc	gca	gac	att	gtg	ggt	gtg	tgc	499	
His	Glu	Val	Gly	Ala	Trp	Asp	Ser	Ile	Ala	Asp	Ile	Val	Gly	Val	Cys		
		120					125					130					
gaa	gcg	atc	agg	cag	ctt	aac	cca	ggt	ttg	att	gct	gca	tct	ccg	att	547	
Glu	Ala	Ile	Arg	Gln	Leu	Asn	Pro	Gly	Leu	Ile	Ala	Ala	Ser	Pro	Ile		
	135					140					145						
gct	tta	gga	ttc	gga	cgc	atc	aag	gca	gct	cac	gga	gat	att	cca	gtg	595	
Ala	Leu	Gly	Phe	Gly	Arg	Ile	Lys	Ala	Ala	His	Gly	Asp	Ile	Pro	Val		
150					155					160					165		
cca	gtt	cca	gcc	gtg	gca	gag	ctg	gtg	aaa	ggc	tgg	ccc	acc	caa	acc	643	
Pro	Val	Pro	Ala	Val	Ala	Glu	Leu	Val	Lys	Gly	Trp	Pro	Thr	Gln	Thr		
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gga	gct	ctt	atg	gag	agc	acc	gaa	cct	gtt	ggt	gaa	tta	gcc	acc	cca	691	
Gly	Ala	Leu	Met	Glu	Ser	Thr	Glu	Pro	Val	Gly	Glu	Leu	Ala	Thr	Pro		
		185						190					195				
act	ggt	gtt	gcg	ttg	atc	cgt	cac	ttt	gcc	acc	caa	gat	ggc	cct	ttc	739	
Thr	Gly	Val	Ala	Leu	Ile	Arg	His	Phe	Ala	Thr	Gln	Asp	Gly	Pro	Phe		
		200					205					210					
cca	ggt	ggc	atc	atc	aat	gaa	gtt	ggc	att	ggt	gca	gga	aca	aaa	gat	787	
Pro	Gly	Gly	Ile	Ile	Asn	Glu	Val	Gly	Ile	Gly	Ala	Gly	Thr	Lys	Asp		
	215					220					225						
aca	gaa	ggc	cgt	cca	aat	ata	gtg	cgc	gca	att	ttg	ttc	aac	acc	tct	835	
Thr	Glu	Gly	Arg	Pro	Asn	Ile	Val	Arg	Ala	Ile	Leu	Phe	Asn	Thr	Ser		
230					235					240					245		
agg	agt	aac	cca	gat	acc	cgc	aca	ctg	gtg	caa	tta	gaa	gcc	aat	gtt	883	
Arg	Ser	Asn	Pro	Asp	Thr	Arg	Thr	Leu	Val	Gln	Leu	Glu	Ala	Asn	Val		
				250					255					260			
gat	gat	caa	gac	cca	cgg	ctg	tgg	cca	gga	gta	ata	gag	atc	ctc	ttt	931	
Asp	Asp	Gln	Asp	Pro	Arg	Leu	Trp	Pro	Gly	Val	Ile	Glu	Ile	Leu	Phe		
			265					270					275				
gcc	gct	ggc	gca	gta	gat	gca	tgg	ctg	act	cca	att	ttg	atg	aag	aag	979	
Ala	Ala	Gly	Ala	Val	Asp	Ala	Trp	Leu	Thr	Pro	Ile	Leu	Met	Lys	Lys		
		280					285					290					
ggc	cgt	cct	gca	cat	agg	gtg	tca	gca	ttg	gtg	gat	agc	tcc	gag	gtg		
1027																	
Gly	Arg	Pro	Ala	His	Arg	Val	Ser	Ala	Leu	Val	Asp	Ser	Ser	Glu	Val		
	295					300					305						
gaa	gca	gtg	aaa	acc	gca	tta	ttt	gca	gcc	acc	acg	act	ttt	ggg	atc		
1075																	
Glu	Ala	Val	Lys	Thr	Ala	Leu	Phe	Ala	Ala	Thr	Thr	Thr	Phe	Gly	Ile		
310					315					320					325		

aga tca tgg gaa gtc gaa cga gaa ggc ttg gac cgt cgt ttc gaa caa  
1123

Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp Arg Arg Phe Glu Gln  
330 335 340

gtc gag gtg gac gga cac acc atc aac atc aaa atc ggt tcc cgt gat  
1171

Val Glu Val Asp Gly His Thr Ile Asn Ile Lys Ile Gly Ser Arg Asp  
345 350 355

gat caa gta atc agt gca cag tcc gag ttt gaa gat att cgg tct gca  
1219

Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu Asp Ile Arg Ser Ala  
360 365 370

gcg gtg gcc ttg gga att tca gag cgg gaa gtt gtg gca aga att ccg  
1267

Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val Val Ala Arg Ile Pro  
375 380 385

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1305

Gln Gly Thr Thr Glu  
390

<210> 1094

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 1094

Met Gly Leu Trp Ile Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu  
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Leu Gly Ala Leu Ile Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln  
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Val Val Glu Ala Val Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu  
35 40 45

Val Val Arg Gln Gly Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln  
50 55 60

His Glu His His His His Arg His Leu Ser Thr Ile Lys Glu Leu Leu  
65 70 75 80

Val Asn Ala Asp Ile Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val  
85 90 95

Phe Glu Leu Ile Ala Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro  
100 105 110

Glu Lys Ile His Phe His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp  
115 120 125

Ile Val Gly Val Cys Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile  
130 135 140

Ala Ala Ser Pro Ile Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His  
145 150 155 160

Gly Asp Ile Pro Val Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly  
 165 170 175  
 Trp Pro Thr Gln Thr Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly  
 180 185 190  
 Glu Leu Ala Thr Pro Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr  
 195 200 205  
 Gln Asp Gly Pro Phe Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly  
 210 215 220  
 Ala Gly Thr Lys Asp Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile  
 225 230 235 240  
 Leu Phe Asn Thr Ser Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln  
 245 250 255  
 Leu Glu Ala Asn Val Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val  
 260 265 270  
 Ile Glu Ile Leu Phe Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro  
 275 280 285  
 Ile Leu Met Lys Lys Gly Arg Pro Ala His Arg Val Ser Ala Leu Val  
 290 295 300  
 Asp Ser Ser Glu Val Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr  
 305 310 315 320  
 Thr Thr Phe Gly Ile Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp  
 325 330 335  
 Arg Arg Phe Glu Gln Val Glu Val Asp Gly His Thr Ile Asn Ile Lys  
 340 345 350  
 Ile Gly Ser Arg Asp Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu  
 355 360 365  
 Asp Ile Arg Ser Ala Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val  
 370 375 380  
 Val Ala Arg Ile Pro Gln Gly Thr Thr Glu  
 385 390  
  
 <210> 1095  
 <211> 1419  
 <212> DNA  
 <213> Corynebacterium glutamicum  
  
 <220>  
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 <222> (101)..(1396)  
 <223> RXC02624  
  
 <400> 1095  
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											Val	Leu	Ile	Pro	His	
											1				5	
ggc	gtg	gcg	gtg	ctt	ttg	gtt	att	att	ctc	gcc	gta	gcc	tcc	cta	atg	163
Gly	Val	Ala	Val	Leu	Leu	Val	Ile	Ile	Leu	Ala	Val	Ala	Ser	Leu	Met	
				10					15					20		
ttc	acc	aat	tct	tca	atg	gtg	aat	ctt	tcg	gca	acg	att	gca	cag	ctg	211
Phe	Thr	Asn	Ser	Ser	Met	Val	Asn	Leu	Ser	Ala	Thr	Ile	Ala	Gln	Leu	
			25					30					35			
tgg	ctt	tcc	cta	aat	ctc	ggc	gcg	gtg	gac	ggc	agt	ggg	gaa	gtg	atc	259
Trp	Leu	Ser	Leu	Asn	Leu	Gly	Ala	Val	Asp	Gly	Ser	Gly	Glu	Val	Ile	
		40					45					50				
tca	gta	ctg	ccc	acg	ctt	ccc	ggc	ttt	ata	ttc	ctc	tgg	gcc	atc	gcc	307
Ser	Val	Leu	Pro	Thr	Leu	Pro	Gly	Phe	Ile	Phe	Leu	Trp	Ala	Ile	Ala	
	55					60					65					
gcg	cgc	atc	cac	cgc	gca	gtc	aaa	gat	cgt	gtc	agc	atc	gcc	gac	tta	355
Ala	Arg	Ile	His	Arg	Ala	Val	Lys	Asp	Arg	Val	Ser	Ile	Ala	Asp	Leu	
70					75					80					85	
ggc	gtc	ctc	gca	gca	ctc	gtc	ctc	ggc	atc	ccg	ctt	gcg	ctc	acc	gcc	403
Gly	Val	Leu	Ala	Ala	Leu	Val	Leu	Gly	Ile	Pro	Leu	Ala	Leu	Thr	Ala	
				90					95					100		
atc	gca	gcg	ttc	atg	ctt	ttc	gac	gcc	tcc	agc	gtc	ctc	aac	gtc	gag	451
Ile	Ala	Ala	Phe	Met	Leu	Phe	Asp	Ala	Ser	Ser	Val	Leu	Asn	Val	Glu	
			105					110					115			
gtc	ccg	cca	atc	acg	cgc	ctc	cta	cgc	gtg	atg	ttg	ttc	cac	ctc	agc	499
Val	Pro	Pro	Ile	Thr	Arg	Leu	Leu	Arg	Val	Met	Leu	Phe	His	Leu	Ser	
		120					125					130				
gcc	ctc	ttc	ctc	ggc	atg	ggg	cca	cgc	ctg	tgg	cag	gcg	ttg	gcg	cgc	547
Ala	Leu	Phe	Leu	Gly	Met	Gly	Pro	Arg	Leu	Trp	Gln	Ala	Leu	Ala	Arg	
	135					140					145					
cgc	tac	ggt	gct	cca	gaa	tgg	ctt	atc	gac	gcc	atc	acc	caa	gct	ttc	595
Arg	Tyr	Gly	Ala	Pro	Glu	Trp	Leu	Ile	Asp	Ala	Ile	Thr	Gln	Ala	Phe	
150					155					160					165	
cgc	ttc	ctc	atc	gca	ttt	gga	aca	gtc	tcc	ttg	gtt	tcc	gtg	ctc	gtg	643
Arg	Phe	Leu	Ile	Ala	Phe	Gly	Thr	Val	Ser	Leu	Val	Ser	Val	Leu	Val	
				170					175					180		
atg	acc	gcg	atc	aac	cac	agt	gca	ttc	acc	gcg	acc	atg	cag	ggt	tac	691
Met	Thr	Ala	Ile	Asn	His	Ser	Ala	Phe	Thr	Ala	Thr	Met	Gln	Gly	Tyr	
			185					190					195			
gac	gac	tcc	gcc	tct	gtt	gtg	gcc	ttg	atc	gtc	ctg	agc	att	ctg	tat	739
Asp	Asp	Ser	Ala	Ser	Val	Val	Ala	Leu	Ile	Val	Leu	Ser	Ile	Leu	Tyr	
		200					205					210				
ctg	ccc	aac	atg	atg	atc	ttt	gcg	atg	ggc	aat	ctg	atc	ggc	tca	ccc	787
Leu	Pro	Asn	Met	Met	Ile	Phe	Ala	Met	Gly	Asn	Leu	Ile	Gly	Ser	Pro	
	215					220					225					
ctt	tac	ttc	ggt	gac	gcc	tcc	atc	agc	gtc	ttc	agc	gtg	cat	tcc	gtt	835
Leu	Tyr	Phe	Gly	Asp	Ala	Ser	Ile	Ser	Val	Phe	Ser	Val	His	Ser	Val	

230	235	240	245	
cca ttg cca ccg ctt ccc atc ctc gca gct ctc ccc agc gaa gcc ctc				883
Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu Pro Ser Glu Ala Leu	250	255	260	
tca tgg gca gtg gcc tta ctg gtc atc cct gca att att gcc acc tgg				931
Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile Ala Thr Trp	265	270	275	
gtc tgc gtg aga aac ccc atg cgc ctt gcc gtg aac aca aca gca gca				979
Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr Thr Ala Ala	280	285	290	
gtc att tca gca ctg tgt ttc ctc gtc ctg gca gtt ttc gcc ggc gga				
1027 Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe Ala Gly Gly	295	300	305	
acc ttg ggc gta tac aac tac gtc gga ctc aac ctc ctg gcg tca gtt				
1075 Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu Ala Ser Val	310	315	320	325
ggc cta gtt ttc gtc tat ttc gcc ctc gtt gga ctc ctc atc gcc gga				
1123 Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu Ile Ala Gly	330	335	340	
atc gac aag ctg cgc aac cct gta gaa gtt aag tct gtt aag gct gtg				
1171 Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val Lys Ala Val	345	350	355	
gct gtt gtg gag ccc gag cct gaa gaa gtt gaa gag gac gaa gag gag				
1219 Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp Glu Glu Glu	360	365	370	
cat gtt gaa gaa gaa gta gat gag gag gaa gag gaa gtt gag gaa ggg				
1267 His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Glu Val Glu Glu Gly	375	380	385	
gta gaa gag gtc gaa gaa gac gac gca gag gat cct gaa gag aat cct				
1315 Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu Glu Asn Pro	390	395	400	405
gaa gag gaa gaa tcc gac gaa gaa att gag aca gaa act gag gct gaa				
1363 Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr Glu Ala Glu	410	415	420	
gaa acc aat gat ggt tcc gag gcc gaa gac cgt taacatatct gttgtgaatt				
1416 Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg	425	430		
ctg				
1419				

&lt;210&gt; 1096

&lt;211&gt; 432

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1096

Val Leu Ile Pro His Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala  
 1 5 10 15

Val Ala Ser Leu Met Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala  
 20 25 30

Thr Ile Ala Gln Leu Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly  
 35 40 45

Ser Gly Glu Val Ile Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe  
 50 55 60

Leu Trp Ala Ile Ala Ala Arg Ile His Arg Ala Val Lys Asp Arg Val  
 65 70 75 80

Ser Ile Ala Asp Leu Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro  
 85 90 95

Leu Ala Leu Thr Ala Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser  
 100 105 110

Val Leu Asn Val Glu Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met  
 115 120 125

Leu Phe His Leu Ser Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp  
 130 135 140

Gln Ala Leu Ala Arg Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala  
 145 150 155 160

Ile Thr Gln Ala Phe Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu  
 165 170 175

Val Ser Val Leu Val Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala  
 180 185 190

Thr Met Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val  
 195 200 205

Leu Ser Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn  
 210 215 220

Leu Ile Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe  
 225 230 235 240

Ser Val His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu  
 245 250 255

Pro Ser Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala  
 260 265 270

Ile Ile Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val  
 275 280 285

Asn Thr Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala  
 290 295 300  
 Val Phe Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn  
 305 310 315 320  
 Leu Leu Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly  
 325 330 335  
 Leu Leu Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys  
 340 345 350  
 Ser Val Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu  
 355 360 365  
 Glu Asp Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu  
 370 375 380  
 Glu Val Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp  
 385 390 395 400  
 Pro Glu Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr  
 405 410 415  
 Glu Thr Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg  
 420 425 430

<210> 1097  
 <211> 603  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(580)  
 <223> RXC02665

<400> 1097  
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 Val Thr Asn Pro Ile  
 1 5  
 atc ccc cgc gta gga atc gcc aca gac gcc cac caa atc gaa gcg gga 163  
 Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His Gln Ile Glu Ala Gly  
 10 15 20  
 aaa ccc tgc tgg atc gcc tgc ctc ctc ttt gaa ggc gtc gac ggc tgc 211  
 Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu Gly Val Asp Gly Cys  
 25 30 35  
 gaa ggc cac tcc gac ggt gat gtt gta gct cat gca att gtg gat gct 259  
 Glu Gly His Ser Asp Gly Asp Val Val Ala His Ala Ile Val Asp Ala  
 40 45 50

ctc ctt tct gcc tct ggt ctg ggg gat ttg ggc tct ttc gtt ggt gtg 307  
 Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly Ser Phe Val Gly Val  
 55 60 65

ggg aga cct gaa tac gat ggt gtt tct ggt aca cag ttg ttg aag gaa 355  
 Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr Gln Leu Leu Lys Glu  
 70 75 80 85

gtt cgg gag ctg ctt tcg gca cac ggg tac gtc att gga aat gtc gcc 403  
 Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val Ile Gly Asn Val Ala  
 90 95 100

gcc caa ctg gtt ggc caa acc ccc aaa ttt gga ccc cgc cgc gaa gaa 451  
 Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly Pro Arg Arg Glu Glu  
 105 110 115

gca caa caa gtc atc tcc gaa atc atc ggc gca cca tgc tca ctg tct 499  
 Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala Pro Cys Ser Leu Ser  
 120 125 130

gcc acc acc act gat cac atg gga ttc act ggt cgc agc gag ggt cgt 547  
 Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly Arg Ser Glu Gly Arg  
 135 140 145

gca tcg gta gca acg gca gtg gtg tgg aag gct taagttttct gtagggattg 600  
 Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala  
 150 155 160

ggc 603

&lt;210&gt; 1098

&lt;211&gt; 160

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1098

Val Thr Asn Pro Ile Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His  
 1 5 10 15

Gln Ile Glu Ala Gly Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu  
 20 25 30

Gly Val Asp Gly Cys Glu Gly His Ser Asp Gly Asp Val Val Ala His  
 35 40 45

Ala Ile Val Asp Ala Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly  
 50 55 60

Ser Phe Val Gly Val Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr  
 65 70 75 80

Gln Leu Leu Lys Glu Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val  
 85 90 95

Ile Gly Asn Val Ala Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly  
 100 105 110

Pro Arg Arg Glu Glu Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala  
 115 120 125

Pro Cys Ser Leu Ser Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly  
 130 135 140

Arg Ser Glu Gly Arg Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala  
 145 150 155 160

<210> 1099

<211> 1689

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1666)

<223> RXC02770

<400> 1099

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 Met Leu Val Ala Ala  
 1 5

tta gtg atg aca agc tgt ggt gat ggg gaa ccg gaa cca acc agc cac 163  
 Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro Glu Pro Thr Ser His  
 10 15 20

caa aca agc ctt ttc ggc tac gca gtt aac tct tcg ctg gct aca acc 211  
 Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser Ser Leu Ala Thr Thr  
 25 30 35

aac gcg gcg tcg ctg ttg gga gtg gct aat gat gct ggt ctt ttg gct 259  
 Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp Ala Gly Leu Leu Ala  
 40 45 50

gcc aga gtg tat ccg ggt gtg tat gtt cag ggt cct tct ggg cag atg 307  
 Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly Pro Ser Gly Gln Met  
 55 60 65

att ccc aac act gat ctt gct tcc acg cag gta ttg ccg ggt att aac 355  
 Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val Leu Pro Gly Ile Asn  
 70 75 80 85

cgc cag gtg att tac act atc aat gaa gat gcc acc tac tca gat ggt 403  
 Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala Thr Tyr Ser Asp Gly  
 90 95 100

cag cct gtg gtg tgt gat gat ttt ctg ctc tct gcg aca gct ggg cag 451  
 Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr Ala Gly Gln  
 105 110 115

atg ccg gaa ctg ttc cag tcc cat gtg cca ttg acc tcg cag att gag 499  
 Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser Gln Ile Glu  
 120 125 130

cga gtg gac tgt gta tct ggt tct aaa gta gcc acc gtg gtg ttc aag 547  
 Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val Val Phe Lys

135	140	145	
gaa gac ctc ggt gag cgt tgg cgt tat ctt ttt gag cag ggc gat ttg Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln Gly Asp Leu 150 155 160 165			595
ttg cca gcc cat gcc gtt gct tcc aaa gca ggt atg acc ttg gag gag Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr Leu Glu Glu 170 175 180			643
ctt aat cag gcg ttg aag gat aag gat cct gaa gcg ttg act gaa cct Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu Thr Glu Pro 185 190 195			691
gct cgt gtg tgg agc gaa ggt ttc cag ctg tcc cag ttt gat cca gag Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe Asp Pro Glu 200 205 210			739
ctg cag acg gct ttt ggc ccg tac aag gtg gat tct gtg ggt gaa ttc Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val Gly Glu Phe 215 220 225			787
ggc gaa gtc aag ctg gta cgc aat gag ttt tac agt ggc gac cag gcg Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly Asp Gln Ala 230 235 240 245			835
gtt gaa gca gaa atc acg atg tgg cct aaa ggc tcg gat ctc agc gcc Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp Leu Ser Ala 250 255 260			883
att gcg gat aat gga aac ctt cag atc gca cat gtt gtg gcg tgg gag Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val Ala Trp Glu 265 270 275			931
agc gag ccg tgg gta aat cgc gat gac cca ttg aat cct tat gac att Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro Tyr Asp Ile 280 285 290			979
aag gaa gag gtc ggt gtt ttg act gag cag ctc acc ttg gcc agt gcc 1027 Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu Ala Ser Ala 295 300 305			
ggt gtg ttt tac gct gcg gag gcc cgg cag gcg ttt gcg gcc tgc gtt 1075 Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala Ala Cys Val 310 315 320 325			
gac cag gaa gcg gtg gct gcg gcg tcg tca agc atc tct gga atc gat 1123 Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser Ile Ser Gly Ile Asp 330 335 340			
gtg cct gcc gta ggt gtg cac tcg gtg cgt cac caa aat ccg gtc gtg 1171 Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn Pro Val Val 345 350 355			
cac caa atc ggt gat ctg cca gca cag cac atg gcg gtg gat att aat 1219 His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val Asp Ile Asn			

360 365 370  
 gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc tac gac gga  
 1267  
 Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly Tyr Asp Gly  
 375 380 385  
 ccc gat gag cgc aag gct gca atg gtg gag gcg att cgc caa agt tgt  
 1315  
 Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg Gln Ser Cys  
 390 395 400 405  
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 1363  
 Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu Ala Val Ser  
 410 415 420  
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 1411  
 Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly Tyr Glu Gln  
 425 430 435  
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 1459  
 Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val Asp Pro His  
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 Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala Glu Ser Thr  
 455 460 465  
 agg cgc act gaa gaa caa ttg tgg gct gaa gtc cca tca att cca cta  
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 Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser Ile Pro Leu  
 470 475 480 485  
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 1603  
 Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val Gly Asn Val  
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 Ser Leu Ala Thr Thr Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp  
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 Ala Gly Leu Leu Ala Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly  
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 Pro Ser Gly Gln Met Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val  
                   65                                  70                                  75                                  80  
 Leu Pro Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala  
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 Thr Tyr Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser  
                   100                                  105                                  110  
 Ala Thr Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu  
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 Thr Ser Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala  
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 Thr Val Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe  
                   145                                  150                                  155                                  160  
 Glu Gln Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly  
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 Met Thr Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu  
                                   180                                  185                                  190  
 Ala Leu Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser  
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 Gln Phe Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp  
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 Ser Val Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr  
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 Ser Gly Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly  
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 Ser Asp Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His  
                                   260                                  265                                  270  
 Val Val Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu  
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 Asn Pro Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu  
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 Thr Leu Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala  
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 Phe Ala Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser  
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 Ile Gly Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala  
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 Thr Val Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr  
 450 455 460  
 Asp Ala Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val  
 465 470 475 480  
 Pro Ser Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg  
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 Val Thr Asn Val Ser 1 5  
 aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163  
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile 10 15 20  
 acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211  
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr 25 30 35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259  
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe  
           40                          45                          50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307  
 Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val  
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act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355  
 Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile  
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aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405  
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cac 408

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           20                          25                          30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg  
           35                          40                          45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe  
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Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile  
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Tyr	Glu	Ala	Asp	Ala	Glu	Ala	Ala	Gln	Ile	Cys	Asp	Asn	Leu	Gly	Leu	
			20					25					30			
gag	gca	cgc	atc	ctc	gac	cag	cag	ctt	aaa	acc	ctg	tcc	ggc	ggc	cag	144
Glu	Ala	Arg	Ile	Leu	Asp	Gln	Gln	Leu	Lys	Thr	Leu	Ser	Gly	Gly	Gln	
		35				40					45					
cgc	cgc	cgc	gtc	gag	ttg	gcg	cag	atc	ctc	ttc	gcc	gcc	acc	aac	ggc	192
Arg	Arg	Arg	Val	Glu	Leu	Ala	Gln	Ile	Leu	Phe	Ala	Ala	Thr	Asn	Gly	
		50				55					60					
tcc	ggc	aaa	tca	aaa	acc	aca	ttg	ctt	ctc	gac	gag	ccc	acc	aac	cac	240
Ser	Gly	Lys	Ser	Lys	Thr	Thr	Leu	Leu	Leu	Asp	Glu	Pro	Thr	Asn	His	
		65			70					75					80	
ttg	gac	gca	gac	tcg	atc	acc	tgg	ctc	cgt	gac	ttc	ctg	gcg	aag	cac	288
Leu	Asp	Ala	Asp	Ser	Ile	Thr	Trp	Leu	Arg	Asp	Phe	Leu	Ala	Lys	His	
				85					90					95		
gaa	ggt	gga	ctg	atc	atg	att	tcg	cac	gac	gtc	gaa	ctg	ctt	ggc	gcc	336
Glu	Gly	Gly	Leu	Ile	Met	Ile	Ser	His	Asp	Val	Glu	Leu	Leu	Gly	Ala	
			100					105					110			
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Val	Cys	Asn	Lys	Ile	Trp	Tyr	Leu	Asp	Ala	Val	Arg	Ser	Glu	Ala	Asp	
		115					120					125				
gtc	tac	aac	atg	ggc	ttt	agc	aaa	tac	gtc	gat	gca	cgt	gca	ctc	gat	432
Val	Tyr	Asn	Met	Gly	Phe	Ser	Lys	Tyr	Val	Asp	Ala	Arg	Ala	Leu	Asp	
		130				135					140					
gaa	gca	cgc	cga	cgc	cgt	gag	cgc	gca	aac	gcc	gaa	aag	aag	gcc	gga	480
Glu	Ala	Arg	Arg	Arg	Arg	Glu	Arg	Ala	Asn	Ala	Glu	Lys	Lys	Ala	Gly	
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gcc	ctc	aag	gac	cag	gct	gca	cgc	ctc	ggc	gcg	aaa	gca	acc	aag	gct	528
Ala	Leu	Lys	Asp	Gln	Ala	Ala	Arg	Leu	Gly	Ala	Lys	Ala	Thr	Lys	Ala	
				165					170					175		
gcc	gca	gct	aag	cag	atg	atc	gcc	cgt	gcg	gaa	cga	atg	atc	gac	aac	576
Ala	Ala	Ala	Lys	Gln	Met	Ile	Ala	Arg	Ala	Glu	Arg	Met	Ile	Asp	Asn	
			180					185					190			
ctc	gac	gaa	atc	cgc	gta	gct	gac	cgc	gcc	gcc	aac	atc	gtt	ttc	cca	624
Leu	Asp	Glu	Ile	Arg	Val	Ala	Asp	Arg	Ala	Ala	Asn	Ile	Val	Phe	Pro	
		195					200					205				
gaa	cca	gca	ccc	tgt	gga	aaa	acc	cca	ctc	aac	gcc	aag	ggc	ctg	acc	672
Glu	Pro	Ala	Pro	Cys	Gly	Lys	Thr	Pro	Leu	Asn	Ala	Lys	Gly	Leu	Thr	
		210				215					220					
aag	atg	tac	ggc	tcc	ctc	gaa	gtc	ttc	gcc	ggc	gtc	gac	cta	gcc	atc	720
Lys	Met	Tyr	Gly	Ser	Leu	Glu	Val	Phe	Ala	Gly	Val	Asp	Leu	Ala	Ile	
					230					235					240	
gac	aaa	ggc	tcc	cgc	gta	gtc	gtc	ctc	gga	ttc	aac	ggc	gca	ggc	aaa	768
Asp	Lys	Gly	Ser	Arg	Val	Val	Val	Leu	Gly	Phe	Asn	Gly	Ala	Gly	Lys	
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acc	acc	ctg	ctc	aaa	ctc	ctc	gcc	ggc	gtg	gaa	cgc	acc	gac	ggc	gaa	816
Thr	Thr	Leu	Leu	Lys	Leu	Leu	Ala	Gly	Val	Glu	Arg	Thr	Asp	Gly	Glu	

260	265	270	
ggc ggc atc gtc acc gga tac	ggc ctc aaa atc ggc tac	ttc gcc cag	864
Gly Gly Ile Val Thr Gly Tyr	Gly Leu Lys Ile Gly Tyr	Phe Ala Gln	
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gaa cac gac acc atc gac ccc	gac aaa tcc gtc tgg caa aac acc atc		912
Glu His Asp Thr Ile Asp Pro	Asp Lys Ser Val Trp Gln Asn Thr Ile		
290	295	300	
gaa gcc tgc gcc gac gcc gac	caa caa agc ctc cgc agc ctc ctc gga		960
Glu Ala Cys Ala Asp Ala Asp	Gln Gln Ser Leu Arg Ser Leu Leu Gly		
305	310	315	320
tcc ttc atg ttc tcc ggc gaa	caa ctc gac caa cca gca gga aca ctc		
1008			
Ser Phe Met Phe Ser Gly Glu	Gln Leu Asp Gln Pro Ala Gly Thr Leu		
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Ser Gly Gly Glu Lys Thr Arg	Leu Ala Leu Ala Thr Leu Val Ser Ser		
340	345	350	
cgc gca aac gtc ctg ctt ctc	gac gag ccc acc aac aac ctt gac ccg		
1104			
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355	360	365	
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1152			
Ile Ser Arg Glu Gln Val Leu	Asp Ala Leu Arg Thr Tyr Thr Gly Ala		
370	375	380	
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1200			
Val Val Leu Val Thr His Asp	Pro Gly Ala Val Lys Ala Leu Glu Pro		
385	390	395	400
gaa cgc gtc atc gtg ctt cct	gat ggc acc gag gat ctt tgg aat gat		
1248			
Glu Arg Val Ile Val Leu Pro	Asp Gly Thr Glu Asp Leu Trp Asn Asp		
405	410	415	
cag tac atg gaa atc gtg gaa	ttg gcg taggttctaa ggctgtttat		
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gct			
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 Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln  
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 Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly  
 50 55 60  
 Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His  
 65 70 75 80  
 Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His  
 85 90 95  
 Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Leu Gly Ala  
 100 105 110  
 Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp  
 115 120 125  
 Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp  
 130 135 140  
 Glu Ala Arg Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly  
 145 150 155 160  
 Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala  
 165 170 175  
 Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn  
 180 185 190  
 Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro  
 195 200 205  
 Glu Pro Ala Pro Cys Gly Lys Thr Pro Leu Asn Ala Lys Gly Leu Thr  
 210 215 220  
 Lys Met Tyr Gly Ser Leu Glu Val Phe Ala Gly Val Asp Leu Ala Ile  
 225 230 235 240  
 Asp Lys Gly Ser Arg Val Val Val Leu Gly Phe Asn Gly Ala Gly Lys  
 245 250 255  
 Thr Thr Leu Leu Lys Leu Leu Ala Gly Val Glu Arg Thr Asp Gly Glu  
 260 265 270  
 Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln  
 275 280 285  
 Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile  
 290 295 300  
 Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly  
 305 310 315 320  
 Ser Phe Met Phe Ser Gly Glu Gln Leu Asp Gln Pro Ala Gly Thr Leu  
 325 330 335

Ser Gly Gly Glu Lys Thr Arg Leu Ala Leu Ala Thr Leu Val Ser Ser  
340 345 350

Arg Ala Asn Val Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Pro  
355 360 365

Ile Ser Arg Glu Gln Val Leu Asp Ala Leu Arg Thr Tyr Thr Gly Ala  
370 375 380

Val Val Leu Val Thr His Asp Pro Gly Ala Val Lys Ala Leu Glu Pro  
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Glu Arg Val Ile Val Leu Pro Asp Gly Thr Glu Asp Leu Trp Asn Asp  
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Gln Tyr Met Glu Ile Val Glu Leu Ala  
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<211> 613

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXN03171

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Met Asp Ile Thr Ile  
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gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163  
Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu  
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cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211  
Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala  
25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259  
Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp  
40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307  
Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro  
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ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355  
Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro  
70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403  
Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala  
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cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451

Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro  
 105 110 115

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 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala  
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 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly  
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gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595  
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gac gca ttg gcg gaa tct 613  
 Asp Ala Leu Ala Glu Ser  
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Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu  
 35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr  
 50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu  
 65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly  
 85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr  
 100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val  
 115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu  
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 Met Asp Ile Thr Ile  
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 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu  
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 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala  
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 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp  
 40 45 50  
 acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307  
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro  
 55 60 65  
 ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355  
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro  
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 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala  
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 cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451  
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro  
 105 110 115  
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 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala  
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 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly  
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Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
          35           40           45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
          50           55           60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
 65           70           75           80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
          85           90           95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
          100          105          110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
          115          120          125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
          130          135          140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
          145          150          155          160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
          165          170

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<210> 1109  
 <211> 424  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(424)  
 <223> RXN00450

<400> 1109

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tttgcgatga catggatttg gatccttccg aacaattgct gcgcacgcgc gaagaactcg 60

gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115
                               Val Gly Val Leu Pro
                               1           5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
          10           15           20

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```

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
      25              30              35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
      40              45              50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
      55              60              65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
      70              75              80              85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
      90              95              100

ggt gct cga atc gga cgc atc 424
Gly Ala Arg Ile Gly Arg Ile
      105

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<210> 1110  
 <211> 108  
 <212> PRT  
 <213> Corynebacterium glutamicum

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<400> 1110
Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
  1              5              10              15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
      20              25              30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
      35              40              45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
      50              55              60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
      65              70              75              80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
      85              90              95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile
      100              105

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<210> 1111  
 <211> 418  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101) .. (418)

&lt;223&gt; FRXA00450

&lt;400&gt; 1111

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gttttgataa tgatctggct cgggtgggtgg gattcgacta gtg ggc gtt tta cct 115  
 Val Gly Val Leu Pro  
 1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163  
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu  
 10 15 20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211  
 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val  
 25 30 35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259  
 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg  
 40 45 50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307  
 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg  
 55 60 65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355  
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr  
 70 75 80 85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403  
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val  
 90 95 100

ggt gct cga atc gga 418  
 Gly Ala Arg Ile Gly  
 105

&lt;210&gt; 1112

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1112

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg  
 1 5 10 15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val  
 20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr  
 35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu  
 50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg  
 65 70 75 80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys  
 85 90 95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly  
 100 105

<210> 1113

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(592)

<223> RXA00465

<400> 1113

tccccaacgc gcaccgaact tagccggatc gcagacttca cctggatgtc caccgcagcc 60  
 caagcgctac cagcgttgat gcgaggtttg agcgcctaac atg act gaa gat gac 115  
 Met Thr Glu Asp Asp  
 1 5  
 tta gat ctg ctg cac cgc aca gta gaa cta gcc acc cag gca ctc aag 163  
 Leu Asp Leu Leu His Arg Thr Val Glu Leu Ala Thr Gln Ala Leu Lys  
 10 15 20  
 cag gga aac agt cct tat gga tcc ctg ctg gtt gat ccc ttc ggc gcg 211  
 Gln Gly Asn Ser Pro Tyr Gly Ser Leu Leu Val Asp Pro Phe Gly Ala  
 25 30 35  
 gtc gtt ttt gaa gac cac aac cga gat gcc gat ggg gat ctg acc aag 259  
 Val Val Phe Glu Asp His Asn Arg Asp Ala Asp Gly Asp Leu Thr Lys  
 40 45 50  
 cac ccg gaa ttc gcc atc gcc aaa tat gcg atc gaa aat tac agt gca 307  
 His Pro Glu Phe Ala Ile Ala Lys Tyr Ala Ile Glu Asn Tyr Ser Ala  
 55 60 65  
 tca gaa cgt gct gcg tgc act gtt tat acc tcg acg gaa cat tgc gcg 355  
 Ser Glu Arg Ala Ala Cys Thr Val Tyr Thr Ser Thr Glu His Cys Ala  
 70 75 80 85  
 atg tgc gcc ggt gcc cat gcg tgg gct gga ctg ggc aaa att tac tgc 403  
 Met Cys Ala Gly Ala His Ala Trp Ala Gly Leu Gly Lys Ile Tyr Cys  
 90 95 100  
 gcc acc aca ggt ggg caa aca gcc gct tgg tac gca aag tgg ggt gca 451  
 Ala Thr Thr Gly Gly Gln Thr Ala Ala Trp Tyr Ala Lys Trp Gly Ala  
 105 110 115  
 gaa tct ggg cct ttg aac ccg att tca gcg gac aaa att agc ccg aac 499  
 Glu Ser Gly Pro Leu Asn Pro Ile Ser Ala Asp Lys Ile Ser Pro Asn  
 120 125 130  
 ata tcc atc gaa gga cct gct tcc aga ttt gag gaa gtc ctg tat gaa 547  
 Ile Ser Ile Glu Gly Pro Ala Ser Arg Phe Glu Glu Val Leu Tyr Glu  
 135 140 145  
 ctg cat cga tgg ttt tat tta ggg cag tct ccg aat aag gct ctt 592  
 Leu His Arg Trp Phe Tyr Leu Gly Gln Ser Pro Asn Lys Ala Leu  
 150 155 160

tagcgctggg catgtgactt taa

615

&lt;210&gt; 1114

&lt;211&gt; 164

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1114

Met	Thr	Glu	Asp	Asp	Leu	Asp	Leu	Leu	His	Arg	Thr	Val	Glu	Leu	Ala
1				5					10					15	

Thr	Gln	Ala	Leu	Lys	Gln	Gly	Asn	Ser	Pro	Tyr	Gly	Ser	Leu	Leu	Val
			20					25					30		

Asp	Pro	Phe	Gly	Ala	Val	Val	Phe	Glu	Asp	His	Asn	Arg	Asp	Ala	Asp
		35					40					45			

Gly	Asp	Leu	Thr	Lys	His	Pro	Glu	Phe	Ala	Ile	Ala	Lys	Tyr	Ala	Ile
	50					55						60			

Glu	Asn	Tyr	Ser	Ala	Ser	Glu	Arg	Ala	Ala	Cys	Thr	Val	Tyr	Thr	Ser
65					70					75					80

Thr	Glu	His	Cys	Ala	Met	Cys	Ala	Gly	Ala	His	Ala	Trp	Ala	Gly	Leu
			85						90					95	

Gly	Lys	Ile	Tyr	Cys	Ala	Thr	Thr	Gly	Gly	Gln	Thr	Ala	Ala	Trp	Tyr
		100						105					110		

Ala	Lys	Trp	Gly	Ala	Glu	Ser	Gly	Pro	Leu	Asn	Pro	Ile	Ser	Ala	Asp
		115					120					125			

Lys	Ile	Ser	Pro	Asn	Ile	Ser	Ile	Glu	Gly	Pro	Ala	Ser	Arg	Phe	Glu
	130					135					140				

Glu	Val	Leu	Tyr	Glu	Leu	His	Arg	Trp	Phe	Tyr	Leu	Gly	Gln	Ser	Pro
145					150					155					160

Asn Lys Ala Leu

&lt;210&gt; 1115

&lt;211&gt; 1083

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1060)

&lt;223&gt; RXA00717

&lt;400&gt; 1115

aagcatcagt taaagccccg actattaaaa tctcctaaaa taggctagaa ttcacgggat 60

tcaatttcat	acgttttctc	tcaagattaa	ggacacttac	gtg	acc	cca	ccc	gct	115
				Val	Thr	Pro	Pro	Ala	
				1				5	

cgc cga gat ggc aca ccg gac aag aag cag agc aat cgc tct ggc gga	163
Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser Asn Arg Ser Gly Gly	
10 15 20	
tac cgg tct tca gtt cgt ggc tac aag cca gga tca tcc cgc cca aac	211
Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly Ser Ser Arg Pro Asn	
25 30 35	
aca cgc cag cag cct cag aag aag gat gag att ctt ctc tcc aac gct	259
Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile Leu Leu Ser Asn Ala	
40 45 50	
aag cct gcc aag aag caa aac gta aaa tcc gac gac gat tgg tcg atg	307
Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp Asp Asp Trp Ser Met	
55 60 65	
ggt ttc tta aac cgc aat gac tct gac gga gtt cgc ctg cag aag gtg	355
Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val Arg Leu Gln Lys Val	
70 75 80 85	
ctt gcc caa gca ggt gtg gca tca cgt cga cac gca gaa atc ctg att	403
Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His Ala Glu Ile Leu Ile	
90 95 100	
gat cag ggc cgt gtg gag gtc aac gat cgt atc gtg acc acc cag ggc	451
Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile Val Thr Thr Gln Gly	
105 110 115	
gtg cgc gtg gat cca aac aac gat gtc atc cgt gtt gac ggc gtc cgc	499
Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg Val Asp Gly Val Arg	
120 125 130	
atc cac atc aac gag gac ctc gag tac ttc gtg ctc aac aag cct cgt	547
Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val Leu Asn Lys Pro Arg	
135 140 145	
ggc atg cac tcc acc atg agc gat gaa ctt ggt cgc cca tgc gtg ggt	595
Gly Met His Ser Thr Met Ser Asp Glu Leu Gly Arg Pro Cys Val Gly	
150 155 160 165	
gat ctg gtc agt gag aag act gca tct gga cag cgt ctg ttc cac gtc	643
Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln Arg Leu Phe His Val	
170 175 180	
ggt cgc ctc gac gcg gac acc gaa ggt ttg ctg ctg ctc acc aac gat	691
Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu Leu Leu Thr Asn Asp	
185 190 195	
ggt gag ttg gct aac cgc ctc atg cac cct aag tac gaa gtg tcc aag	739
Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys Tyr Glu Val Ser Lys	
200 205 210	
act tac ctt gct acc gtt cgc ggt gaa gca acc aat aag cta gtc agc	787
Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr Asn Lys Leu Val Ser	
215 220 225	
gct ctt cgt gat ggc gtg gag ttg gaa gat ggc cct gcc aag gct gac	835
Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly Pro Ala Lys Ala Asp	
230 235 240 245	
ttt gcg cag att atc gac gta ttc cag ggc aag tcc ttg ttg cgc atc	883

1518



Arg Pro Cys Val Gly Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln  
 165 170 175  
 Arg Leu Phe His Val Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu  
 180 185 190  
 Leu Leu Thr Asn Asp Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys  
 195 200 205  
 Tyr Glu Val Ser Lys Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr  
 210 215 220  
 Asn Lys Leu Val Ser Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly  
 225 230 235 240  
 Pro Ala Lys Ala Asp Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys  
 245 250 255  
 Ser Leu Leu Arg Ile Glu Ile His Glu Gly Arg Lys His Ile Val Arg  
 260 265 270  
 Arg Leu Phe Asp Glu Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr  
 275 280 285  
 Lys Leu His Thr Val Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg  
 290 295 300  
 Ala Leu Asn Ser Ser Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu  
 305 310 315 320

&lt;210&gt; 1117

&lt;211&gt; 978

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(955)

&lt;223&gt; RXA01894

&lt;400&gt; 1117

agaatttttt cgaaaatgct ggcaccatca acagtgcacat tgtagaaac ttcaaggaga 60  
 acccatgaat gaaccggagc aacatcaccg gtccatgagg atg ccc aaa ccc aaa 115  
 Met Pro Lys Pro Lys  
 1 5  
 aat aat gcg ggt cga gat ctc aaa gct gcc att gct gtg ggg atc gga 163  
 Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile Ala Val Gly Ile Gly  
 10 15 20  
 ctg ggg gtc ctg gtt ctt ttg ggg att gtc cta agc cca tgg ggt tgg 211  
 Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu Ser Pro Trp Gly Trp  
 25 30 35  
 tac atc ctc gtt gca ggt ttt atg gct gca gca aca tgg gaa gtt ggt 259  
 Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala Thr Trp Glu Val Gly

40	45	50	
agc aga ctt aaa gaa ggc ggc tat cat ttg cca ctg ccg att atg atc Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro Leu Pro Ile Met Ile 55 60 65			307
atc ggc ggt cag gca atc atc tgg ctg tca tgg cca ttt ggc acg atg Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp Pro Phe Gly Thr Met 70 75 80 85			355
ggc att ttg gcg tct ttt gtg gcc act gtg ttg gtg ctg atg tat ttc Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu Val Leu Met Tyr Phe 90 95 100			403
cga att ttc tac aat ggc acg gaa aaa gaa gcc cgc aac tat ttg agg Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala Arg Asn Tyr Leu Arg 105 110 115			451
gac acc tct gtg ggc atc ttc gtg ctc acc tgg att cca ttg ttc gga Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp Ile Pro Leu Phe Gly 120 125 130			499
agc ttc gct gcg atg ctg tcg ctg atg caa aac aat tcc atc ccg ggt Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn Asn Ser Ile Pro Gly 135 140 145			547
aca tat ttc att ttg acg ttc atg ctg tgt gtg atc gca tcg gat gtg Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val Ile Ala Ser Asp Val 150 155 160 165			595
ggc ggg tat atc gcg ggt gtg ttc ttt gga tcg cac cca atg gcg ccg Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser His Pro Met Ala Pro 170 175 180			643
ttg gtg agt ccg aag aag tct tgg gaa ggc ttt gcc ggc tcc att gtc Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe Ala Gly Ser Ile Val 185 190 195			691
tta gga tcg gtc act ggt gca ctc agt gtt cac ttc ctg ctc gat cac Leu Gly Ser Val Thr Gly Ala Leu Ser Val His Phe Leu Leu Asp His 200 205 210			739
cac tgg tgg atg ggt gtg atc ttg ggt tgt gcc cta gtt gtg tgc gcc His Trp Trp Met Gly Val Ile Leu Gly Cys Ala Leu Val Val Cys Ala 215 220 225			787
acg ttg ggt gac ttg gtt gag tcg cag ttc aaa cgc gat ttg ggc atc Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys Arg Asp Leu Gly Ile 230 235 240 245			835
aag gat atg tcg aac ctt ctt cca ggc cac ggc gga ttg atg gac cgt Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly Gly Leu Met Asp Arg 250 255 260			883
ttg gat ggc atg ctc ccg gcc gcg atg gtg acg tgg ttg atc ctg agt Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr Trp Leu Ile Leu Ser 265 270 275			931
gtg atc agc agc tcg tat ccg tcg taaagcttgg gccagcttta agt Val Ile Ser Ser Ser Tyr Pro Ser 280 285			978

&lt;210&gt; 1118

&lt;211&gt; 285

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1118

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Met Pro Lys Pro Lys Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile
  1              5              10              15

Ala Val Gly Ile Gly Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu
      20              25              30

Ser Pro Trp Gly Trp Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala
      35              40              45

Thr Trp Glu Val Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro
      50              55              60

Leu Pro Ile Met Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp
      65              70              75              80

Pro Phe Gly Thr Met Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu
      85              90              95

Val Leu Met Tyr Phe Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala
      100             105             110

Arg Asn Tyr Leu Arg Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp
      115             120             125

Ile Pro Leu Phe Gly Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn
      130             135             140

Asn Ser Ile Pro Gly Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val
      145             150             155             160

Ile Ala Ser Asp Val Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser
      165             170             175

His Pro Met Ala Pro Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe
      180             185             190

Ala Gly Ser Ile Val Leu Gly Ser Val Thr Gly Ala Leu Ser Val His
      195             200             205

Phe Leu Leu Asp His His Trp Trp Met Gly Val Ile Leu Gly Cys Ala
      210             215             220

Leu Val Val Cys Ala Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys
      225             230             235             240

Arg Asp Leu Gly Ile Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly
      245             250             255

Gly Leu Met Asp Arg Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr
      260             265             270

Trp Leu Ile Leu Ser Val Ile Ser Ser Ser Tyr Pro Ser
      275             280             285

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<210> 1119  
 <211> 879  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(856)  
 <223> RXA02536

<400> 1119

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gcgtattgcc ttgcttcaga tctcgacgaa ttccgataag atg gac aac ttc gcc 115
                                         Met Asp Asn Phe Ala
                                         1                               5

ctg ctg cgt gat gct gct gaa aaa gct gcg gaa cag ggg gct cgg gtg 163
Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu Gln Gly Ala Arg Val
                        10                        15                        20

ttg gtg ttt ccg gag gcg act tcg caa agc ttt ggt acg gga agg ctt 211
Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe Gly Thr Gly Arg Leu
                        25                        30                        35

gat act cag gcg gag gag ctc gat ggc gaa ttc tcc acc gcg gta cga 259
Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe Ser Thr Ala Val Arg
                        40                        45                        50

aaa tta gcc gat gag ctg gac gtt gtc atc gtt gcg ggc atg ttc acc 307
Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val Ala Gly Met Phe Thr
                        55                        60                        65

cct gct gac acc gtg cag cgc ggt gaa aaa acg atc tcg cgc gtc aac 355
Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr Ile Ser Arg Val Asn
70                        75                        80                        85

aac acc gtg ctg att agt ggc gct gga ttg cat cag gga tac aac aaa 403
Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His Gln Gly Tyr Asn Lys
                        90                        95                        100

att cac aca tat gac gcg ttc ggt tat agg gaa tcc gac act gtg aaa 451
Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu Ser Asp Thr Val Lys
                        105                        110                        115

ccg ggc gat gag ctg gtt gta ttc gag gtc gac gat att aaa ttt ggt 499
Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp Asp Ile Lys Phe Gly
                        120                        125                        130

gtg gcg aca tgc tac gat att cga ttc cca gaa cag ttc aaa gac ctc 547
Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu Gln Phe Lys Asp Leu
                        135                        140                        145

gcc cgc aac ggt gca cag ata att gtg gtt ccc acg tcg tgg caa gac 595
Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro Thr Ser Trp Gln Asp
150                        155                        160                        165

ggt cct gga aaa tta gaa caa tgg gaa gtc ctc cct cgc gcg cgt gca 643
Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu Pro Arg Ala Arg Ala

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	170	175	180	
ctg gat tcc acc tgc tgg atc gta gcg tgt ggg caa gcg cga ctt cca				691
Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly Gln Ala Arg Leu Pro				
	185	190	195	
gaa gaa tta cgc gat gaa cga aaa ggc cct acg ggg att ggt cat tcc				739
Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr Gly Ile Gly His Ser				
	200	205	210	
atg gtg aca aac cca cac ggt gaa gta att gct agc gcg ggt tat gag				787
Met Val Thr Asn Pro His Gly Glu Val Ile Ala Ser Ala Gly Tyr Glu				
	215	220	225	
cca gaa atg ttg atc gcg gat att gat gtc agc ggt ttg gcc aaa att				835
Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser Gly Leu Ala Lys Ile				
	230	235	240	245
cgg gag gca ttg cct gtt ctt taaccactgt ctaaggaatc act				879
Arg Glu Ala Leu Pro Val Leu				
	250			

&lt;210&gt; 1120

&lt;211&gt; 252

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1120

Met Asp Asn Phe Ala Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu	
1 5 10 15	

Gln Gly Ala Arg Val Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe	
20 25 30	

Gly Thr Gly Arg Leu Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe	
35 40 45	

Ser Thr Ala Val Arg Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val	
50 55 60	

Ala Gly Met Phe Thr Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr	
65 70 75 80	

Ile Ser Arg Val Asn Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His	
85 90 95	

Gln Gly Tyr Asn Lys Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu	
100 105 110	

Ser Asp Thr Val Lys Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp	
115 120 125	

Asp Ile Lys Phe Gly Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu	
130 135 140	

Gln Phe Lys Asp Leu Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro	
145 150 155 160	

Thr Ser Trp Gln Asp Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu	
165 170 175	

Pro Arg Ala Arg Ala Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly  
 180 185 190

Gln Ala Arg Leu Pro Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr  
 195 200 205

Gly Ile Gly His Ser Met Val Thr Asn Pro His Gly Glu Val Ile Ala  
 210 215 220

Ser Ala Gly Tyr Glu Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser  
 225 230 235 240

Gly Leu Ala Lys Ile Arg Glu Ala Leu Pro Val Leu  
 245 250

<210> 1121  
 <211> 1528  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1528)  
 <223> RXN01209

<400> 1121  
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 Met Cys Glu Arg Pro  
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gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163  
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val  
 10 15 20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211  
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile  
 25 30 35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259  
 Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val  
 40 45 50

gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct 307  
 Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala  
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cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag 355  
 Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu  
 70 75 80 85

ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa 403  
 Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln  
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gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa 451  
 Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu  
 105 110 115

aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt 499  
 Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly  
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gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg 547  
 Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala  
 135 140 145

acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag 595  
 Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu  
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atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga 643  
 Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly  
 170 175 180

ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac 691  
 Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp  
 185 190 195

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 215 220 225

act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat 835  
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 230 235 240 245

tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca 883  
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 250 255 260

ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc 931  
 Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly  
 265 270 275

ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979  
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His  
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag  
 1027  
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln  
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc  
 1075  
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly  
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt  
 1123  
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 330 335 340

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1171

Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
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1219

Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc  
1267

Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct  
1315

Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
1363

Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
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1411

Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac  
1459

Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc  
1507

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<210> 1122

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<212> PRT

<213> Corynebacterium glutamicum

<400> 1122

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35 40 45



Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys  
 50 55 60  
 Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
 65 70 75 80  
 Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
 85 90 95  
 Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
 100 105 110  
 Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
 115 120 125  
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
 130 135 140  
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
 145 150 155 160  
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
 165 170 175  
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
 180 185 190  
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
 195 200 205  
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
 210 215 220  
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
 225 230 235 240  
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
 245 250 255  
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
 260 265 270  
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val  
 275 280 285  
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
 290 295 300  
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
 305 310 315 320  
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
 325 330 335  
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350  
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu  
 355 360 365  
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn

370	375	380
Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met		
385	390	395 400
Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr		
	405	410 415
Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn		
	420	425 430
Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg		
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Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser		
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Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu		
465	470	475

&lt;210&gt; 1123

&lt;211&gt; 1528

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1528)

&lt;223&gt; FRXA01209

&lt;400&gt; 1123

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                                         1 5
gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
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Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
                        25 30 35
tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val
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gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct 307
Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala
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cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag 355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu
                        70 75 80 85
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa 403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln
                        90 95 100

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gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa 451  
 Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu  
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aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt 499  
 Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly  
 120 125 130

gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg 547  
 Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala  
 135 140 145

acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag 595  
 Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu  
 150 155 160 165

atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga 643  
 Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly  
 170 175 180

ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac 691  
 Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp  
 185 190 195

ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct 739  
 Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala  
 200 205 210

gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa 787  
 Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu  
 215 220 225

act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat 835  
 Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn  
 230 235 240 245

tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca 883  
 Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr  
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ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc 931  
 Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly  
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ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979  
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His  
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag  
 1027  
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln  
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc  
 1075  
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly  
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt  
 1123

Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly  
 330 335 340  
 tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc  
 1171  
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
 345 350 355  
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 1219  
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
 360 365 370  
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 1267  
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
 375 380 385  
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 1315  
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
 390 395 400 405  
 cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
 1363  
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 410 415 420  
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 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
 425 430 435  
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 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
 440 445 450  
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 1507  
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 35 40 45  
 Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys  
 50 55 60  
 Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
 65 70 75 80  
 Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
 85 90 95  
 Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
 100 105 110  
 Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
 115 120 125  
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
 130 135 140  
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
 145 150 155 160  
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
 165 170 175  
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
 180 185 190  
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
 195 200 205  
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
 210 215 220  
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
 225 230 235 240  
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 245 250 255  
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
 260 265 270  
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 275 280 285  
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
 290 295 300  
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
 305 310 315 320  
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
 325 330 335  
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350  
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu

1532

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gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg 451  
 Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu  
                     105                                    110                                    115

aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt 499  
 Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val  
                     120                                    125                                    130

gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt 547  
 Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu  
                     135                                    140                                    145

ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac 595  
 Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp  
 150                                    155                                    160                                    165

gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca 643  
 Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala  
                     170                                    175                                    180

gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag 691  
 Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys  
                     185                                    190                                    195

cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg 739  
 Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro  
                     200                                    205                                    210

ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc 792  
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cct 795

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<212> PRT

<213> Corynebacterium glutamicum

<400> 1126

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                     20                                    25                                    30

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr  
                     35                                    40                                    45

Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp  
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Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr  
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Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr

85					90					95					
Pro	Asn	Asn	Phe	Glu	Ala	Thr	Thr	Leu	Ser	Gly	Leu	Asp	Lys	Leu	Glu
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Thr	Ile	Asp	Asp	Leu	Lys	Glu	Ala	Ala	Arg	Leu	Ile	His	Glu	Gln	Gly
		115					120					125			
Pro	Gln	Tyr	Val	Val	Val	Lys	Gly	Gly	Ile	Asp	Phe	Pro	Gly	Asp	Asn
	130					135					140				
Ala	Val	Asp	Val	Leu	Phe	Asp	Gly	Thr	Asp	Tyr	His	Val	Phe	Ser	Glu
145					150					155					160
Pro	Lys	Ile	Gly	Asp	Glu	Arg	Val	Ser	Gly	Ala	Gly	Cys	Thr	Phe	Ala
				165					170					175	
Ala	Val	Ile	Thr	Ala	Glu	Leu	Ala	Lys	Gly	Asn	Ser	Ala	Val	Asp	Ala
			180					185						190	
Val	Thr	Thr	Ala	Lys	Arg	Val	Val	Thr	Arg	Ala	Val	Lys	Asp	Ala	Val
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 <223> FRXA01617

<400> 1127																
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1				5				10						15		
aag	atc	ggt	atg	ttg	ggt	act	cct	gca	acg	atc	gat	act	gtg	gca	acc	96
Lys	Ile	Gly	Met	Leu	Gly	Thr	Pro	Ala	Thr	Ile	Asp	Thr	Val	Ala	Thr	
			20					25					30			
gct	ttg	gag	gaa	aac	agc	ttc	aag	cac	gtt	gtc	cta	gac	ccg	gta	ctg	144
Ala	Leu	Glu	Glu	Asn	Ser	Phe	Lys	His	Val	Val	Leu	Asp	Pro	Val	Leu	
		35					40					45				
atc	tgc	aag	ggc	cag	gag	ccc	ggc	gcg	gca	ctt	gat	act	gac	act	gcc	192
Ile	Cys	Lys	Gly	Gln	Glu	Pro	Gly	Ala	Ala	Leu	Asp	Thr	Asp	Thr	Ala	
	50					55					60					
ctt	cgc	gcg	aag	gtg	ctg	cca	cag	gca	acc	gtg	gtt	act	cca	aac	aac	240
Leu	Arg	Ala	Lys	Val	Leu	Pro	Gln	Ala	Thr	Val	Val	Thr	Pro	Asn	Asn	
65					70					75					80	



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 Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp  
                             85                            90                            95

gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac 336  
 Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr  
                             100                            105                            110

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 Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp  
                             115                            120                            125

gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc 432  
 Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile  
                             130                            135                            140

ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc 480  
 Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile  
                             145                            150                            155                            160

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 Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr  
                             165                            170                            175

gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac 576  
 Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn  
                             180                            185                            190

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 Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
                             195                            200                            205

aaacaagctc cct 638

<210> 1128  
 <211> 205  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1128  
 Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val  
   1                            5                            10                            15  
 Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr  
                             20                            25                            30  
 Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu  
                             35                            40                            45  
 Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala  
                             50                            55                            60  
 Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn  
                             65                            70                            75                            80  
 Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp  
                             85                            90                            95  
 Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr  
                             100                            105                            110

Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp  
115 120 125

Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Il  
130 135 140

Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile  
145 150 155 160

Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr  
165 170 175

Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn  
180 185 190

Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
195 200 205

<210> 1129

<211> 792

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(769)

<223> RXC01600

<400> 1129

tgagtacaaa tctcgtccaa cccatgctca tccactgttt tacggcctgg tgaagaccgc 60

tttggagctg cgtgtccacc cttagatcta caatgtgatc atg gtt tcg aag atg 115  
Met Val Ser Lys Met  
1 5

cac att ccc ggt acc cat gag ttc acg gtg aca gat act gaa ctg ttg 163  
His Ile Pro Gly Thr His Glu Phe Thr Val Thr Asp Thr Glu Leu Leu  
10 15 20

tta gag tcc cca att ttg ggc gtt cgt cga gat tca ttg atc atg ccg 211  
Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp Ser Leu Ile Met Pro  
25 30 35

ggt ggt tcc act gcc cgc cgt gaa gtg gtt gaa cac ttt ggg gcg gtc 259  
Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu His Phe Gly Ala Val  
40 45 50

gca gtg gtt gcc ttt gat ggt gaa aac att gcg atg gtc aag cag tac 307  
Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala Met Val Lys Gln Tyr  
55 60 65

cgt cgc agc gtg ggg gat tcc ttg tgg gag ctg cct gca ggt ttg ttg 355  
Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu Pro Ala Gly Leu Leu  
70 75 80 85

gat att gct gat gag gat gaa ctc acg ggc gcg cag cgc gag ctc atg 403  
Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala Gln Arg Glu Leu Met  
90 95 100

gag gag gct ggt ttg gag gcc agt gag tgg tcc gtg ctc act gat ttg 451  
 Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser Val Leu Thr Asp Leu  
                   105                                  110                                  115

att acc tcg cct ggt ttc tgc gat gaa gcg gtg cgt gtc ttt cta gcc 499  
 Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val Arg Val Phe Leu Ala  
                   120                                  125                                  130

cga ggc ctc aca aag gtt gag cgc ccg aag gtt atg ggc gat gaa gaa 547  
 Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val Met Gly Asp Glu Glu  
                   135                                  140                                  145

gcg gac atg att aac cag tgg gtt ccg cta cat gag gca gtg gga atg 595  
 Ala Asp Met Ile Asn Gln Trp Val Pro Leu His Glu Ala Val Gly Met  
 150                                  155                                  160                                  165

gtg ttt agt ggc cag ttg gtt aac tcc att gcc att gcg ggt gtc atg 643  
 Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala Ile Ala Gly Val Met  
                   170                                  175                                  180

gct gct gat gct gtg att gcg ggt cgt gcg tct gcg cgt gcc gtc acc 691  
 Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser Ala Arg Ala Val Thr  
                   185                                  190                                  195

gcg ccg ttt acc tat cgc cct acg gcg ttg gcg cag cgt cga aaa gcg 739  
 Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala Gln Arg Arg Lys Ala  
                   200                                  205                                  210

cac ggc att gtt cct gac atg aaa aaa cta tgaaggctcg cgtttttagcg 789  
 His Gly Ile Val Pro Asp Met Lys Lys Leu  
                   215                                  220

aaa 792

<210> 1130

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 1130

Met Val Ser Lys Met His Ile Pro Gly Thr His Glu Phe Thr Val Thr  
           1                                  5                                  10                                  15

Asp Thr Glu Leu Leu Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp  
                   20                                  25                                  30

Ser Leu Ile Met Pro Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu  
           35                                  40                                  45

His Phe Gly Ala Val Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala  
           50                                  55                                  60

Met Val Lys Gln Tyr Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu  
           65                                  70                                  75                                  80

Pro Ala Gly Leu Leu Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala  
                   85                                  90                                  95

Gln Arg Glu Leu Met Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser  
           100                                  105                                  110

Val Leu Thr Asp Leu Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val  
115 120 125

Arg Val Phe Leu Ala Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val  
130 135 140

Met Gly Asp Glu Glu Ala Asp Met Ile Asn Gln Trp Val Pro Leu His  
145 150 155 160

Glu Ala Val Gly Met Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala  
165 170 175

Ile Ala Gly Val Met Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser  
180 185 190

Ala Arg Ala Val Thr Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala  
195 200 205

Gln Arg Arg Lys Ala His Gly Ile Val Pro Asp Met Lys Lys Leu  
210 215 220

<210> 1131

<211> 726

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(703)

<223> RXC01622

<400> 1131

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gccatcgcag agctgaagag ctggtgggaa ggagaaaaca atg agt gat ttt tat 115  
Met Ser Asp Phe Tyr  
1 5

gcc gac agg ttg ttt aac gcg atg gag cgc aat gag gta gct cca ggc 163  
Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn Glu Val Ala Pro Gly  
10 15 20

atg ttg ttg gtg gct gcg ccc gat atg gcg tcg gag gat ttt gag cgc 211  
Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser Glu Asp Phe Glu Arg  
25 30 35

agc atc gtg ttg atc atc gag cat tct cct gcc acc act ttt ggt gtg 259  
Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala Thr Thr Phe Gly Val  
40 45 50

aac att tct tca cgt tcc gat gtt gct gtg gcc aat gtg ttg ccc gag 307  
Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala Asn Val Leu Pro Glu  
55 60 65

tgg gtg gac ctc acc tcg aag cca cag gca ctg tac atc ggt ggg ccg 355  
Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu Tyr Ile Gly Gly Pro  
70 75 80 85

ttg agc cag cag gct gtg gtt ggt ttg ggc gtg acc aag ccg ggc gtg 403

Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val Thr Lys Pro Gly Val  
                             90                            95                            100  
 gat att gaa aat tcc acc agc ttc aac aag ctc gcc aac cgc ctg gtg 451  
 Asp Ile Glu Asn S r Thr Ser Phe Asn Lys Leu Ala Asn Arg Leu Val  
                             105                            110                            115  
 cac gtg gat ctg cgt tct gca cct gaa gat gtg gct gat gat ctt gag 499  
 His Val Asp Leu Arg Ser Ala Pro Glu Asp Val Ala Asp Asp Leu Glu  
                             120                            125                            130  
 ggc atg cgc ttt ttt gcg ggc tac gcg gag tgg gct ccg ggc cag ctc 547  
 Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp Ala Pro Gly Gln Leu  
                             135                            140                            145  
 aac gag gaa att gag cag ggt gat tgg ttc gtc aca cct gcg ttg ccg 595  
 Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val Thr Pro Ala Leu Pro  
                             150                            155                            160                            165  
 tcg gac att atc gcg ccg ggc cgc gtc gat att tgg ggc gac gtg atg 643  
 Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile Trp Gly Asp Val Met  
                             170                            175                            180  
 cgt cga caa gca atg cct ttg ccg ttg tat tcc acg ttt ccg tcg gac 691  
 Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser Thr Phe Pro Ser Asp  
                             185                            190                            195  
 cct tca gat aat tagatgagtt ccgaaaattt aaa 726  
 Pro Ser Asp Asn  
                             200

&lt;210&gt; 1132

&lt;211&gt; 201

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1132

Met Ser Asp Phe Tyr Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn  
   1                            5                            10                            15  
 Glu Val Ala Pro Gly Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser  
                             20                            25                            30  
 Glu Asp Phe Glu Arg Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala  
                             35                            40                            45  
 Thr Thr Phe Gly Val Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala  
                             50                            55                            60  
 Asn Val Leu Pro Glu Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu  
                             65                            70                            75                            80  
 Tyr Ile Gly Gly Pro Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val  
                             85                            90                            95  
 Thr Lys Pro Gly Val Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu  
                             100                            105                            110  
 Ala Asn Arg Leu Val His Val Asp Leu Arg Ser Ala Pro Glu Asp Val  
                             115                            120                            125

Ala Asp Asp Leu Glu Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp  
 130 135 140

Ala Pro Gly Gln Leu Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val  
 145 150 155 160

Thr Pro Ala Leu Pro Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile  
 165 170 175

Trp Gly Asp Val Met Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser  
 180 185 190

Thr Phe Pro Ser Asp Pro Ser Asp Asn  
 195 200

<210> 1133

<211> 1827

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1804)

<223> RXC00128

<400> 1133

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 cggtgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115  
 Val Ser Lys Ile Ser  
 1 5  
 acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163  
 Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val  
 10 15 20  
 gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211  
 Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg  
 25 30 35  
 tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259  
 Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro  
 40 45 50  
 aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307  
 Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala  
 55 60 65  
 tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355  
 Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly  
 70 75 80 85  
 acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc 403  
 Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg  
 90 95 100  
 att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att 451  
 Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile  
 105 110 115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat	499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr	
120 125 130	
cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa	547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu	
135 140 145	
gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag	595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu	
150 155 160 165	
aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt	643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe	
170 175 180	
gat cct tct ggc cag gtg ttg gtg ggg gat ccg cgt tgg ttg ttc aat	691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn	
185 190 195	
gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt	739
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly	
200 205 210	
cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat	787
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp	
215 220 225	
gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg	835
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu	
230 235 240 245	
gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg	883
Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val	
250 255 260	
tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct	931
Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala	
265 270 275	
gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac	979
Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp	
280 285 290	
ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg	
1027	
Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu	
295 300 305	
ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg	
1075	
Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val	
310 315 320 325	
agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg	
1123	
Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala	
330 335 340	

att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac  
 1171  
 Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn  
 345 350 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg  
 1219  
 Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala  
 360 365 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt  
 1267  
 Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser  
 375 380 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga  
 1315  
 Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg  
 390 395 400 405

tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg  
 1363  
 Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu  
 410 415 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act  
 1411  
 Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr  
 425 430 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc  
 1459  
 Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val  
 440 445 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag  
 1507  
 Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu  
 455 460 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca  
 1555  
 Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro  
 470 475 480 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg  
 1603  
 Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp  
 490 495 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat  
 1651  
 Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn  
 505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac  
 1699  
 Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr  
 520 525 530



gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat  
1747

Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp  
535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg  
1795

Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val  
550 555 560 565

gtt gcg tac tgatggagct gttcttcccg cgc  
1827

Val Ala Tyr

<210> 1134

<211> 568

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1134

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser  
1 5 10 15

Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp  
20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile  
35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe  
50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala  
65 70 75 80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr  
85 90 95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn  
100 105 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu  
115 120 125

Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile  
130 135 140

Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp  
145 150 155 160

Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His  
165 170 175

Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg  
180 185 190

Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala  
195 200 205

Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn  
 210 215 220  
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr  
 225 230 235 240  
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Ala Arg Leu Arg Phe  
 245 250 255  
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro  
 260 265 270  
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr  
 275 280 285  
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn  
 290 295 300  
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val  
 305 310 315 320  
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp  
 325 330 335  
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val  
 340 345 350  
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly  
 355 360 365  
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe  
 370 375 380  
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro  
 385 390 395 400  
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu  
 405 410 415  
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe  
 420 425 430  
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys  
 435 440 445  
 Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val  
 450 455 460  
 Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser  
 465 470 475 480  
 Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro  
 485 490 495  
 Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser  
 500 505 510  
 Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser  
 515 520 525  
 Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro



gat

555

&lt;210&gt; 1136

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1136

Val Phe Glu Gln Ala Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly  
 1 5 10 15

Ala Gly Ala Ala Gly Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser  
 20 25 30

Ala Gly Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly  
 35 40 45

Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg  
 50 55 60

Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys  
 65 70 75 80

Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser  
 85 90 95

Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser  
 100 105 110

Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu  
 115 120 125

Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser  
 130 135 140

&lt;210&gt; 1137

&lt;211&gt; 898

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(898)

&lt;223&gt; RXC02207

&lt;400&gt; 1137

gaatcgggtga ctttgccaac accaatcaca caagcccttg atgatgtctc cctgtgactt 60

ggtccaatta cattcactgg taatctgaaa ccttgtgaat atg cgc cgt cga tcc 115  
 Met Arg Arg Arg Ser  
 1 5

cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca 163  
 Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu Leu Ala Ser Thr Ala  
 10 15 20

ctt ctt tta agt gca tgt acg caa ggg gta acg gac tcc ccg gat atg	211
Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr Asp Ser Pro Asp Met	
25 30 35	
ggc aag gca act ccc gct gtc tcc ccc gca gca agc aac ccg gat ggc	259
Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala Ser Asn Pro Asp Gly	
40 45 50	
caa gta att gag ttc ggc aac atc act gac atg gaa gtc act gat ggt	307
Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met Glu Val Thr Asp Gly	
55 60 65	
gac atc ctc ggt gta cgc acc gaa gac gca ctc gct att ggt aca gtc	355
Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu Ala Ile Gly Thr Val	
70 75 80 85	
tcc gac ttc gaa gcg ggt agc cag gtg gaa ctg gac gtc gat aag caa	403
Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu Asp Val Asp Lys Gln	
90 95 100	
tgc ggc gac ctg acc gca acc ggc ggc act ttc gtg ctc ccc tgc gcc	451
Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe Val Leu Pro Cys Ala	
105 110 115	
gat ggc gtt tat ttg att gat gcc aag gac ccg gat ctg gat gag ttg	499
Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro Asp Leu Asp Glu Leu	
120 125 130	
cgt gca act gac aag cca gtc acg gtg gca gcc ttg acc agc gat gat	547
Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala Leu Thr Ser Asp Asp	
135 140 145	
cag ctt ctg gtg ggc aat ggt gaa gat gaa gaa ctc acc atc tac cgc	595
Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu Leu Thr Ile Tyr Arg	
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gag ggc gaa gag cca gaa acc ttc acc gtc gcg ggt ccc aat acc cag	643
Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala Gly Pro Asn Thr Gln	
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ctc atc gcc gtt cct gtc att gat cgc cac gac gcc gtt gtg cgc acc	691
Leu Ile Ala Val Pro Val Ile Asp Arg His Asp Ala Val Val Arg Thr	
185 190 195	
tgg aac gaa aac acc acg att caa gat gtg gac tac ccc aac gac cgt	739
Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp Tyr Pro Asn Asp Arg	
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Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val Gly Gln Met Ala Gly	
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Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu Met Gly Gly Gln Ile	
230 235 240 245	
gcc atc tac aac gct gat gat gtc atc cga ctt caa aat gac cgc ccc	883
Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu Gln Asn Asp Arg Pro	
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His Arg Arg Gly Thr  
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898

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<213> Corynebacterium glutamicum

<400> 1138

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Asp Ser Pro Asp Met Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala  
35 40 45  
Ser Asn Pro Asp Gly Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met  
50 55 60  
Glu Val Thr Asp Gly Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu  
65 70 75 80  
Ala Ile Gly Thr Val Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu  
85 90 95  
Asp Val Asp Lys Gln Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe  
100 105 110  
Val Leu Pro Cys Ala Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro  
115 120 125  
Asp Leu Asp Glu Leu Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala  
130 135 140  
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145 150 155 160  
Leu Thr Ile Tyr Arg Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala  
165 170 175  
Gly Pro Asn Thr Gln Leu Ile Ala Val Pro Val Ile Asp Arg His Asp  
180 185 190  
Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp  
195 200 205  
Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val  
210 215 220  
Gly Gln Met Ala Gly Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu  
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acc gat gag cac ggt ttc aaa gct tta gaa aac gat gat cgt gcc cta			739
Thr Asp Glu His Gly Phe Lys Ala Leu Glu Asn Asp Asp Arg Ala Leu			
200	205	210	
acc gtc aag gtt ggc gaa gga gac act gca gcc aaa acc cgc gtc gac			787
Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala Lys Thr Arg Val Asp			
215	220	225	
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Asp Val Asp Asn Val Gly Ile Phe Leu Glu Lys Leu Ala Tyr His Arg			
230	235	240	245
atg cag tat gcg gaa agc gtg cga ttg ggg att taagagagcc taaacgcacg			888
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Gln Gln Ala Asp Thr Asp Val Val Ile Leu Ser Gly Arg His Leu Glu			
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Gly Leu Lys Thr Val Leu Asp Leu Gly Gln Tyr Asp Ile Thr Met Val			
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Gly Ser His Gly Ser Glu Asp Ser Ser Arg Pro Arg Thr Leu Thr Pro			
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Glu Glu Val Ala Arg Leu Ala Lys Ile Glu Ala Asp Leu Glu Lys Ile			
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Val Asp Gly Ile Glu Gly Ala Phe Val Glu Ile Lys Pro Phe His Arg			
115	120	125	
Val Leu His Phe Ile Arg Val Ser Asp Lys Asp Lys Val Gln Gly Ile			
130	135	140	
Leu Ala Gln Ala Ala His Val Asp Ser Ser Gly Leu Lys Val Thr Asn			
145	150	155	160



Gly Lys Ser Ile Ile Glu Tyr Ser Ile Ser Ser Thr Thr Lys Gly Thr  
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Trp Leu Lys Glu Tyr Val Asp Arg Thr Glu Pro Thr Gly Val Ile Phe  
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Leu Gly Asp Asp Thr Thr Asp Glu His Gly Phe Lys Ala Leu Glu Asn  
 195 200 205

Asp Asp Arg Ala Leu Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala  
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Lys Thr Arg Val Asp Asp Val Asp Asn Val Gly Ile Phe Leu Glu Lys  
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 Met Ala Arg Pro Ile  
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tcc gca acg tac agg ctt caa atg cga gga cct caa gca gat agc gcc 163  
 Ser Ala Thr Tyr Arg Leu Gln Met Arg Gly Pro Gln Ala Asp Ser Ala  
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ggg cgt tca ttt ggt ttt gcg cag gcc aaa gcc cag ctt ccc tat ctg 211  
 Gly Arg Ser Phe Gly Phe Ala Gln Ala Lys Ala Gln Leu Pro Tyr Leu  
 25 30 35

aag aag cta ggc atc agc cac ctg tac ctc tcc cct att ttt acg gcc 259  
 Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser Pro Ile Phe Thr Ala  
 40 45 50

atg cca gat tcc aat cat ggc tac gat gtc att gat ccc acc acc atc 307  
 Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile Asp Pro Thr Thr Ile  
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aat gaa gag ctc ggt ggc atg gag ggt ctt cga gat ctt gcc gca gct 355  
 Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg Asp Leu Ala Ala Ala  
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aca cac gag ttg ggc atg ggc atc atc att gat att gtt ccc aac cat 403  
 Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp Ile Val Pro Asn His

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Leu	Gly	Val	Ala	Val	Pro	His	Leu	Asn	Pro	Trp	Trp	Trp	Asp	Val	Leu		
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aaa	aac	ggc	aaa	gat	tcc	gct	ttt	gag	ttc	tat	ttc	gat	att	gac	tgg	499	
Lys	Asn	Gly	Lys	Asp	Ser	Ala	Phe	Glu	Phe	Tyr	Phe	Asp	Ile	Asp	Trp		
120								125				130					
cac	gaa	gac	aac	ggt	tct	ggt	ggc	aag	ctg	ggc	atg	ccg	att	ctg	ggt	547	
His	Glu	Asp	Asn	Gly	Ser	Gly	Gly	Lys	Leu	Gly	Met	Pro	Ile	Leu	Gly		
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gct	gaa	ggc	gat	gaa	gac	aag	ctg	gaa	ttc	gcg	gag	ctt	gat	gga	gag	595	
Ala	Glu	Gly	Asp	Glu	Asp	Lys	Leu	Glu	Phe	Ala	Glu	Leu	Asp	Gly	Glu		
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Lys	Val	Leu	Lys	Tyr	Phe	Asp	His	Leu	Phe	Pro	Ile	Ala	Pro	Gly	Thr		
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Glu	Glu	Gly	Thr	Pro	Gln	Glu	Val	Tyr	Lys	Arg	Gln	His	Tyr	Arg	Leu		
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Gln	Phe	Trp	Arg	Asp	Gly	Val	Ile	Asn	Phe	Arg	Arg	Phe	Phe	Ser	Val		
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Asn	Thr	Leu	Ala	Gly	Ile	Arg	Gln	Glu	Asp	Pro	Leu	Val	Phe	Glu	His		
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act	cat	cgt	ctg	ctg	cgc	gaa	ttg	gtg	gcg	gaa	gac	ctc	att	gac	ggc	835	
Thr	His	Arg	Leu	Leu	Arg	Glu	Leu	Val	Ala	Glu	Asp	Leu	Ile	Asp	Gly		
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gtg	cgc	gtc	gat	cac	ccc	gac	ggg	ctt	tcc	gat	cct	ttt	gga	tat	ctg	883	
Val	Arg	Val	Asp	His	Pro	Asp	Gly	Leu	Ser	Asp	Pro	Phe	Gly	Tyr	Leu		
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cac	aga	ctc	cgc	gac	ctc	att	gga	cct	gac	cgc	tgg	ctg	atc	atc	gaa	931	
His	Arg	Leu	Arg	Asp	Leu	Ile	Gly	Pro	Asp	Arg	Trp	Leu	Ile	Ile	Glu		
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aag	atc	ttg	agc	ggt	gat	gaa	cca	ctc	gat	ccc	cgc	ctg	gcc	ggt	gat	979	
Lys	Ile	Leu	Ser	Val	Asp	Glu	Pro	Leu	Asp	Pro	Arg	Leu	Ala	Val	Asp		
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ggc	acc	act	ggc	tac	gac	gcc	ctc	cgt	gaa	ctc	gac	ggc	gtg	ttt	atc	1027	
Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Arg	Glu	Leu	Asp	Gly	Val	Phe	Ile		
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Ser	Arg	Glu	Ser	Glu	Asp	Lys	Phe	Ser	Met	Leu	Ala	Leu	Thr	His	Ser		
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1123

Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser Thr Glu Glu Ser Leu  
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1171

Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala Glu Ile Leu Arg Leu  
345 350 355

gcc cgc gcc atg cgc cgc gat aac ttc tcc acc gca ggc acc aac gtc  
1219

Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr Ala Gly Thr Asn Val  
360 365 370

acc gaa gac aaa ctt agc gaa acc atc atc gaa tta gtc gcc gcc atg  
1267

Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu Leu Val Ala Ala Met  
375 380 385

ccc gtc tac cgc gcc gac tac atc tcc ctc tca cgc acc acc gcc acc  
1315

Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser Arg Thr Thr Ala Thr  
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gtc atc gcg gag atg tcc aaa cgc ttc ccc tcc cgg cgt gac gca ctc  
1363

Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser Arg Arg Asp Ala Leu  
410 415 420

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1411

Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly Glu Ala Lys Ile Arg  
425 430 435

ttc gct caa gtc tgc ggc gcc gtc atg gct aaa ggt gtg gaa gac acc  
1459

Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys Gly Val Glu Asp Thr  
440 445 450

acc ttc tac cgc gca tct agg ctc gtt gca ttg caa gaa gtc ggt ggc  
1507

Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu Gln Glu Val Gly Gly  
455 460 465

gcg ccg ggg aga ttc ggc gtc tcc gct gca gaa ttc cac ttg ctg cag  
1555

Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu Phe His Leu Leu Gln  
470 475 480 485

gaa gaa cgc agc ctg ctg tgg cca cgc acc atg acc acc ttg tcc acg  
1603

Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met Thr Thr Leu Ser Thr  
490 495 500

cat gac acc aaa cgt ggc gaa gat acc cgc gcc cgc atc atc tcc ctg  
1651

His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala Arg Ile Ile Ser Leu  
505 510 515

tct gaa gtc ccc gat atg tac tcc gag ctg gtc aat cgt gtt ttc gcg  
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 1747  
 Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser Phe Leu Leu Gln Asn  
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ctg ctg ggc gta tgg ccc gcc gac ggc gtg atc acc gat gcg ctg cgc  
 1795  
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gat cga ttc agg gaa tac gcc cta aaa gct atc cgc gaa gca tcc aca  
 1843  
 Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile Arg Glu Ala Ser Thr  
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 1891  
 Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe Glu Ala Ala Val Cys  
 585 590 595

gat tgg gtg gaa gcg ctt ttc gac gga ccc tcc acc tca cta atc acc  
 1939  
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 Glu Phe Val Ser His Ile Asn Arg Gly Ser Val Gln Ile Ser Leu Gly  
 615 620 625

agg aaa ctg ctg caa atg gtg ggc gct gga atc ccc gac act tac caa  
 2035  
 Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile Pro Asp Thr Tyr Gln  
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 2131  
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 680 685 690

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 2227  
 Asp Ile Ala Lys Met Ala Val Val His Lys Ser Leu Glu Leu Arg Ala  
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2275

Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His Gln Ala Val Phe Gly  
710 715 720 725

gaa ggt cgc gca gaa tcc cac atc atg ggc atc gcc cgc ggt aca gac  
2323

Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile Ala Arg Gly Thr Asp  
730 735 740

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2371

Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr Arg Arg Pro Leu Ile  
745 750 755

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2419

Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr Val Thr Leu Pro Gly  
760 765 770

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2467

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775 780 785

cca gcc acc gat ttg ttc tca cat cta ccc gta tct ttg ttg gtt tta  
2515

Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val Ser Leu Leu Val Leu  
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Val Pro Asp Ser Glu Phe  
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<212> PRT

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<400> 1142

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35 40 45

Pro Ile Phe Thr Ala Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile  
50 55 60

Asp Pro Thr Thr Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg  
65 70 75 80

Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp  
85 90 95

Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp

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Phe Asp Ile Asp Trp His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly 130 135 140		
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Glu Leu Asp Gly Glu Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro 165 170 175		
Ile Ala Pro Gly Thr Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg 180 185 190		
Gln His Tyr Arg Leu Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg 195 200 205		
Arg Phe Phe Ser Val Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro 210 215 220		
Leu Val Phe Glu His Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu 225 230 235 240		
Asp Leu Ile Asp Gly Val Arg Val Asp His Pro Asp Gly Leu Ser Asp 245 250 255		
Pro Phe Gly Tyr Leu His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg 260 265 270		
Trp Leu Ile Ile Glu Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro 275 280 285		
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Asp Gly Val Phe Ile Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu 305 310 315 320		
Ala Leu Thr His Ser Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser 325 330 335		
Thr Glu Glu Ser Leu Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala 340 345 350		
Glu Ile Leu Arg Leu Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr 355 360 365		
Ala Gly Thr Asn Val Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu 370 375 380		
Leu Val Ala Ala Met Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser 385 390 395 400		
Arg Thr Thr Ala Thr Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser 405 410 415		
Arg Arg Asp Ala Leu Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly 420 425 430		

Glu Ala Lys Ile Arg Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys  
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 Gly Val Glu Asp Thr Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu  
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 Gln Glu Val Gly Gly Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu  
 465 470 475 480  
 Phe His Leu Leu Gln Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met  
 485 490 495  
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala  
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 Arg Ile Ile Ser Leu Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val  
 515 520 525  
 Asn Arg Val Phe Ala Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser  
 530 535 540  
 Phe Leu Leu Gln Asn Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile  
 545 550 555 560  
 Thr Asp Ala Leu Arg Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile  
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 Arg Glu Ala Ser Thr Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe  
 580 585 590  
 Glu Ala Ala Val Cys Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser  
 595 600 605  
 Thr Ser Leu Ile Thr Glu Phe Val Ser His Ile Asn Arg Gly Ser Val  
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 625 630 635 640  
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 645 650 655  
 Pro Asp Asn Arg Arg Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu  
 660 665 670  
 Glu Arg Leu Gln Thr Trp Ala Trp Thr Gln Val Asn Ser Val Glu Asp  
 675 680 685  
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 690 695 700  
 Leu Glu Leu Arg Ala Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His  
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 Gln Ala Val Phe Gly Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile  
 725 730 735  
 Ala Arg Gly Thr Asp Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr  
 740 745 750

Arg Arg Pro Leu Ile Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr  
 755 760 765

Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg  
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Phe Ser Gly Val Val Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val  
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<211> 2556

<212> DNA

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<221> CDS

<222> (101)..(2533)

<223> FRXA01239

<400> 1143

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 Met Ala Arg Pro Ile  
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tcc gca acg tac agg ctt caa atg cga gga cct caa gca gat agc gcc 163  
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 Gly Arg Ser Phe Gly Phe Ala Gln Ala Lys Ala Gln Leu Pro Tyr Leu  
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aag aag cta ggc atc agc cac ctg tac ctc tcc cct att ttt acg gcc 259  
 Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser Pro Ile Phe Thr Ala  
 40 45 50

atg cca gat tcc aat cat ggc tac gat gtc att gat ccc acc acc atc 307  
 Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile Asp Pro Thr Thr Ile  
 55 60 65

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 Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg Asp Leu Ala Ala Ala  
 70 75 80 85

aca cac gag ttg ggc atg ggc atc atc att gat att gtt ccc aac cat 403  
 Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp Ile Val Pro Asn His  
 90 95 100

tta ggt gtt gcc gtt cca cat ttg aat cct tgg tgg tgg gat gtt cta 451  
 Leu Gly Val Ala Val Pro His Leu Asn Pro Trp Trp Trp Asp Val Leu  
 105 110 115

aaa aac ggc aaa gat tcc gct ttt gag ttc tat ttc gat att gac tgg 499  
 Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr Phe Asp Ile Asp Trp  
 120 125 130



cac gaa gac aac ggt tct ggt ggc aag ctg ggc atg ccg att ctg ggt 547  
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 135 140 145

gct gaa ggc gat gaa gac aag ctg gaa ttc gcg gag ctt gat gga gag 595  
 Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala Glu Leu Asp Gly Glu  
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aaa gtg ctc aaa tat ttt gac cac ctc ttc cca atc gcg cct ggt acc 643  
 Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro Ile Ala Pro Gly Thr  
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gaa gaa ggg aca ccg caa gaa gtc tac aag cgc cag cat tac cgc ctg 691  
 Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg Gln His Tyr Arg Leu  
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cag ttc tgg cgc gat ggc gtg atc aac ttc cgt cgc ttc ttt tcc gtg 739  
 Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg Arg Phe Phe Ser Val  
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aat acg ttg gct ggc atc agg caa gaa gat ccc tta gtg ttt gaa cat 787  
 Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro Leu Val Phe Glu His  
 215 220 225

act cat cgt ctg ctg cgc gaa ttg gtg gcg gaa gac ctc att gac ggc 835  
 Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu Asp Leu Ile Asp Gly  
 230 235 240 245

gtg cgc gtc gat cac ccc gac ggg ctt tcc gat cct ttt gga tat ctg 883  
 Val Arg Val Asp His Pro Asp Gly Leu Ser Asp Pro Phe Gly Tyr Leu  
 250 255 260

cac aga ctc cgc gac ctc att gga cct gac cgc tgg ctg atc atc gaa 931  
 His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg Trp Leu Ile Ile Glu  
 265 270 275

aag atc ttg agc gtt gat gaa cca ctc gat ccc cgc ctg gcc gtt gat 979  
 Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro Arg Leu Ala Val Asp  
 280 285 290

ggc acc act ggc tac gac gcc ctc cgt gaa ctc gac ggc gtg ttt atc  
 1027  
 Gly Thr Thr Gly Tyr Asp Ala Leu Arg Glu Leu Asp Gly Val Phe Ile  
 295 300 305

tcc cga gaa tct gag gac aaa ttc tcc atg ctg gcg ctg acc cac agt  
 1075  
 Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu Ala Leu Thr His Ser  
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 Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser Thr Glu Glu Ser Leu  
 330 335 340

aaa cga gtc gtc gcc caa caa gaa ctc gca gcc gaa atc tta agg ctc  
 1171  
 Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala Glu Ile Leu Arg Leu  
 345 350 355

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 Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr Ala Gly Thr Asn Val  
 360 365 370

acc gaa gac aaa ctt agc gaa acc atc atc gaa tta gtc gcc gcc atg  
 1267  
 Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu Leu Val Ala Ala Met  
 375 380 385

ccc gtc tac cgc gcc gac tac atc tcc ctc tca cgc acc acc gcc acc  
 1315  
 Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser Arg Thr Thr Ala Thr  
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gtc atc gcg gag atg tcc aaa cgc ttc ccc tcc cgg cgt gac gca ctc  
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 Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser Arg Arg Asp Ala Leu  
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 Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu Gln Glu Val Gly Gly  
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gcg ccg ggg aga ttc ggc gtc tcc gct gca gaa ttc cac ttg ctg cag  
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 Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu Phe His Leu Leu Gln  
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 490 495 500

cat gac acc aaa cgt ggc gaa gat acc cgc gcc cgc atc atc tcc ctg  
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 His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala Arg Ile Ile Ser Leu  
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 Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser Ph Leu Leu Gln Asn  
 535 540 545

ctg ctg ggc gta tgg ccc gcc gac ggc gtg atc acc gat gcg ctg cgc  
 1795  
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 Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile Arg Glu Ala Ser Thr  
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 1891  
 Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe Glu Ala Ala Val Cys  
 585 590 595

gat tgg gtg gaa gcg ctt ttc gac gga ccc tcc acc tca cta atc acc  
 1939  
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 600 605 610

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 1987  
 Glu Phe Val Ser His Ile Asn Arg Gly Ser Val Gln Ile Ser Leu Gly  
 615 620 625

agg aaa ctg ctg caa atg gtg ggc gct gga atc ccc gac act tac caa  
 2035  
 Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile Pro Asp Thr Tyr Gln  
 630 635 640 645

gga act gag ttt tta gaa gac tcc ctg gta gat ccc gat aac cga cgc  
 2083  
 Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp Pro Asp Asn Arg Arg  
 650 655 660

ttt gtt gat tac acc gcc aga gaa caa gtc ctg gag cgc ctg caa acc  
 2131  
 Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu Glu Arg Leu Gln Thr  
 665 670 675

tgg gat tgg acg cag gtt aat tcg gta gaa gac ttg gtg gat aac gcc  
 2179  
 Trp Asp Trp Thr Gln Val Asn Ser Val Glu Asp Leu Val Asp Asn Ala  
 680 685 690

gac atc gcc aaa atg gcc gtg gtc cat aaa tcc ctc gag ttg cgt gct  
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 Asp Ile Ala Lys Met Ala Val Val His Lys Ser Leu Glu Leu Arg Ala  
 695 700 705

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 2275  
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gaa ggt cgc gca gaa tcc cac atc atg ggc atc gcc cgc ggt aca gac  
 2323  
 Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile Ala Arg Gly Thr Asp  
 730 735 740

cga aac cac ctc aac atc att gct ctt gct acc cgt cga cca ctg atc  
2371

Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr Arg Arg Pro Leu Ile  
745 750 755

ttg gaa gac cgt ggc gga tgg tat gac acc acc gtc acg ctt cct ggt  
2419

Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr Val Thr Leu Pro Gly  
760 765 770

gga caa tgg gaa gac agg ctc acc ggg caa cgc ttc agt ggt gtt gtc  
2467

Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg Phe Ser Gly Val Val  
775 780 785

cca gcc acc gat ttg ttc tca cat cta ccc gta tct ttg ttg gtt tta  
2515

Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val Ser Leu Leu Val Leu  
790 795 800 805

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2556

Val Pro Asp Ser Glu Phe  
810

<210> 1144

<211> 811

<212> PRT

<213> Corynebacterium glutamicum

<400> 1144

Met Ala Arg Pro Ile Ser Ala Thr Tyr Arg Leu Gln Met Arg Gly Pro  
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Gln Leu Pro Tyr Leu Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser  
35 40 45

Pro Ile Phe Thr Ala Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile  
50 55 60

Asp Pro Thr Thr Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg  
65 70 75 80

Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp  
85 90 95

Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp  
100 105 110

Trp Trp Asp Val Leu Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr  
115 120 125

Phe Asp Ile Asp Trp His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly  
130 135 140

Met Pro Ile Leu Gly Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala  
145 150 155 160

Glu Leu Asp Gly Glu Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro  
 165 170 175  
 Ile Ala Pro Gly Thr Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg  
 180 185 190  
 Gln His Tyr Arg Leu Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg  
 195 200 205  
 Arg Phe Phe Ser Val Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro  
 210 215 220  
 Leu Val Phe Glu His Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu  
 225 230 235 240  
 Asp Leu Ile Asp Gly Val Arg Val Asp His Pro Asp Gly Leu Ser Asp  
 245 250 255  
 Pro Phe Gly Tyr Leu His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg  
 260 265 270  
 Trp Leu Ile Ile Glu Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro  
 275 280 285  
 Arg Leu Ala Val Asp Gly Thr Thr Gly Tyr Asp Ala Leu Arg Glu Leu  
 290 295 300  
 Asp Gly Val Phe Ile Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu  
 305 310 315 320  
 Ala Leu Thr His Ser Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser  
 325 330 335  
 Thr Glu Glu Ser Leu Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala  
 340 345 350  
 Glu Ile Leu Arg Leu Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr  
 355 360 365  
 Ala Gly Thr Asn Val Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu  
 370 375 380  
 Leu Val Ala Ala Met Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser  
 385 390 395 400  
 Arg Thr Thr Ala Thr Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser  
 405 410 415  
 Arg Arg Asp Ala Leu Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly  
 420 425 430  
 Glu Ala Lys Ile Arg Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys  
 435 440 445  
 Gly Val Glu Asp Thr Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu  
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 Gln Glu Val Gly Gly Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu  
 465 470 475 480

Phe His Leu Leu Gln Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met  
 485 490 495  
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala  
 500 505 510  
 Arg Ile Ile Ser Leu Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val  
 515 520 525  
 Asn Arg Val Phe Ala Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser  
 530 535 540  
 Phe Leu Leu Gln Asn Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile  
 545 550 555 560  
 Thr Asp Ala Leu Arg Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile  
 565 570 575  
 Arg Glu Ala Ser Thr Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe  
 580 585 590  
 Glu Ala Ala Val Cys Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser  
 595 600 605  
 Thr Ser Leu Ile Thr Glu Phe Val Ser His Ile Asn Arg Gly Ser Val  
 610 615 620  
 Gln Ile Ser Leu Gly Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile  
 625 630 635 640  
 Pro Asp Thr Tyr Gln Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp  
 645 650 655  
 Pro Asp Asn Arg Arg Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu  
 660 665 670  
 Glu Arg Leu Gln Thr Trp Asp Trp Thr Gln Val Asn Ser Val Glu Asp  
 675 680 685  
 Leu Val Asp Asn Ala Asp Ile Ala Lys Met Ala Val Val His Lys Ser  
 690 695 700  
 Leu Glu Leu Arg Ala Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His  
 705 710 715 720  
 Gln Ala Val Phe Gly Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile  
 725 730 735  
 Ala Arg Gly Thr Asp Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr  
 740 745 750  
 Arg Arg Pro Leu Ile Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr  
 755 760 765  
 Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg  
 770 775 780  
 Phe Ser Gly Val Val Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val  
 785 790 795 800  
 Ser Leu Leu Val Leu Val Pro Asp Ser Glu Phe

810

gatacagctc cttgatggag tgaataaatt cgcgagcctg ctcctgatct tgcacacgcg															60
tgatataggt cagaaatcgc gagcgcttga tctctagttc atg ctc aaa gac ttg															115
Met Leu Lys Asp Leu															
1 5															
acc ggc ctg agg gag ttg gta ttg cgt gag atg tgc cat agc atc tca															163
Thr Gly Leu Arg Glu Leu Val Leu Arg Glu Met Cys His Ser Ile Ser															
10 15 20															
cat ctt agc tcg cca acc ggc agc att ttc act agc ctg gtg gcc atg															211
His Leu Ser Ser Pro Thr Gly Ser Ile Phe Thr Ser Leu Val Ala Met															
25 30 35															
ttg acc tcg caa agc ttt tca gtg tgg gct cca ctt ccc cac gat gta															259
Leu Thr Ser Gln Ser Phe Ser Val Trp Ala Pro Leu Pro His Asp Val															
40 45 50															
cat ctg atc ctc aac ggc gaa acc ctc ccc atg cac aaa acg gag ggc															307
His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met His Lys Thr Glu Gly															
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Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala Gly Asp Arg Tyr Gly															
70 75 80 85															
ttt tcg ctt ttc gac ggc tcc tcc tgg tca aaa acc ctc ccc gat ccc															403
Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys Thr Leu Pro Asp Pro															
90 95 100															
cgc tcc aca tct caa cca gac ggg gtt cat ggt tta agt gaa gtc tcc															451
Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly Leu Ser Glu Val Ser															
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Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp Thr Gly Arg Ile Leu															
120 125 130															
cct ggc tcg gtg tta tat gag ctg cat gtg ggc acc ttt agt gaa gat															547
Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly Thr Phe Ser Glu Asp															
135 140 145															
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Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro Tyr Leu Arg Asp Leu															
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Gly Val Thr Ala Ile Glu Leu Leu Pro Val Gln Pro Phe Gly Gly Asn  
 170 175 180

cgc aat tgg ggc tac gac ggg gtg ctg tgg cac gcc gtc cat gca ggc 691  
 Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His Ala Val His Ala Gly  
 185 190 195

tac ggc ggt ccg gcg ggc ttg aaa aag ctt atc gac gcc tcc cac cag 739  
 Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile Asp Ala Ser His Gln  
 200 205 210

gcc ggc atc gcc gtc tac tta gac gtc gtg tac aac cac ttc ggc ccc 787  
 Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr Asn His Phe Gly Pro  
 215 220 225

gac ggc aac tac aac ggg caa ttt ggc ccc tac acc tct ggc ggc agc 835  
 Asp Gly Asn Tyr Asn Gly Gln Phe Gly Pro Tyr Thr Ser Gly Gly Ser  
 230 235 240 245

acc ggc tgg ggc gac gtg gtc aac atc aac ggc cat gat tca gat gaa 883  
 Thr Gly Trp Gly Asp Val Val Asn Ile Asn Gly His Asp Ser Asp Glu  
 250 255 260

gtc cgc aat tat att ctc gac gcc gca cgc cag tgg ttc gaa gat ttt 931  
 Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln Trp Phe Glu Asp Phe  
 265 270 275

cac gtt gat ggg ctc cgc ctc gat gcg gtg cat tct ctc gat gat cgc 979  
 His Val Asp Gly Leu Arg Leu Asp Ala Val His Ser Leu Asp Asp Arg  
 280 285 290

ggc gcc tat tcc cta ctt gcg cag ctg acc atg gtg gcc gag gat gtc  
 1027  
 Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met Val Ala Glu Asp Val  
 295 300 305

tcc gca caa aca ggc atc cca cgc tca ttg att gca gaa tct gaa ctc  
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 1123  
 Asn Asp Pro Lys Phe Val Thr Ser Arg Glu Ala Gly Gly Phe Gly Leu  
 330 335 340

gat gca cag tgg gtt gac gat atc cac cac gcc ctc cat gcc ctc gtt  
 1171  
 Asp Ala Gln Trp Val Asp Asp Ile His His Ala Leu His Ala Leu Val  
 345 350 355

tct ggc gaa cgc aat ggt tat tac agc gat ttc gga tct gtc gac aca  
 1219  
 Ser Gly Glu Arg Asn Gly Tyr Tyr Ser Asp Phe Gly Ser Val Asp Thr  
 360 365 370

tta gcc aaa acc ctg cgt gaa gta ttt gaa cac acc gga aac tac tcc  
 1267  
 Leu Ala Lys Thr Leu Arg Glu Val Phe Glu His Thr Gly Asn Tyr Ser  
 375 380 385



gag ctg att tac agc ttc act tcc ccc acc gtc acc gac acc tcc aca  
1891

Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val Thr Asp Thr Ser Thr  
585 590 595

acc ctt cag ccg tgg ggc ttt gcg atc ctg acc cga aac tagaaaaagg  
1940

Thr Leu Gln Pro Trp Gly Phe Ala Ile Leu Thr Arg Asn  
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1953

<210> 1146

<211> 610

<212> PRT

<213> Corynebacterium glutamicum

<400> 1146

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Ser Leu Val Ala Met Leu Thr Ser Gln Ser Phe Ser Val Trp Ala Pro  
35 40 45

Leu Pro His Asp Val His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met  
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His Lys Thr Glu Gly Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala  
65 70 75 80

Gly Asp Arg Tyr Gly Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys  
85 90 95

Thr Leu Pro Asp Pro Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly  
100 105 110

Leu Ser Glu Val Ser Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp  
115 120 125

Thr Gly Arg Ile Leu Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly  
130 135 140

Thr Phe Ser Glu Asp Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro  
145 150 155 160

Tyr Leu Arg Asp Leu Gly Val Thr Ala Ile Glu Leu Leu Pro Val Gln  
165 170 175

Pro Phe Gly Gly Asn Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His  
180 185 190

Ala Val His Ala Gly Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile  
195 200 205

Asp Ala Ser His Gln Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr  
210 215 220

acg tac cgc gga cgc aac cac ggc cgc cct gtg cac ccc gat atc acc  
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 Thr Tyr Arg Gly Arg Asn His Gly Arg Pro Val His Pro Asp Ile Thr  
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 1363  
 Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr Thr His Asp Gln Thr Gly  
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 490 495 500  
  
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 1651  
 Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys Leu Asp Trp Glu Phe  
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 1699  
 Thr Ala Glu Gln Arg Arg Ile Asn Asp Ala Tyr Lys Gln Leu Leu His  
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 1747  
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 1795  
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 Ile Leu Ala Asn Phe Ser Asp Asp Thr Ile Thr Val Pro Leu Gly Gly  
 570 575 580

Asn His Phe Gly Pro Asp Gly Asn Tyr Asn Gly Gln Phe Gly Pro Tyr  
 225 230 235 240  
 Thr Ser Gly Gly Ser Thr Gly Trp Gly Asp Val Val Asn Ile Asn Gly  
 245 250 255  
 His Asp Ser Asp Glu Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln  
 260 265 270  
 Trp Phe Glu Asp Phe His Val Asp Gly Leu Arg Leu Asp Ala Val His  
 275 280 285  
 Ser Leu Asp Asp Arg Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met  
 290 295 300  
 Val Ala Glu Asp Val Ser Ala Gln Thr Gly Ile Pro Arg Ser Leu Ile  
 305 310 315 320  
 Ala Glu Ser Glu Leu Asn Asp Pro Lys Phe Val Thr Ser Arg Glu Ala  
 325 330 335  
 Gly Gly Phe Gly Leu Asp Ala Gln Trp Val Asp Asp Ile His His Ala  
 340 345 350  
 Leu His Ala Leu Val Ser Gly Glu Arg Asn Gly Tyr Tyr Ser Asp Phe  
 355 360 365  
 Gly Ser Val Asp Thr Leu Ala Lys Thr Leu Arg Glu Val Phe Glu His  
 370 375 380  
 Thr Gly Asn Tyr Ser Thr Tyr Arg Gly Arg Asn His Gly Arg Pro Val  
 385 390 395 400  
 His Pro Asp Ile Thr Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr Thr  
 405 410 415  
 His Asp Gln Thr Gly Asn Arg Ala Ile Gly Asp Arg Pro Ser Thr Thr  
 420 425 430  
 Leu Thr Pro Glu Gln Gln Val Leu Lys Ala Ala Ile Ile Tyr Ser Ser  
 435 440 445  
 Pro Tyr Thr Pro Met Leu Phe Met Gly Glu Glu Phe Gly Ala Thr Thr  
 450 455 460  
 Pro Phe Ala Phe Phe Cys Ser His Thr Asp Pro Glu Leu Asn Arg Leu  
 465 470 475 480  
 Thr Ser Glu Gly Arg Lys Arg Glu Phe Ala Arg Leu Gly Trp Asn Ala  
 485 490 495  
 Asp Asp Ile Pro Ser Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys  
 500 505 510  
 Leu Asp Trp Glu Phe Thr Ala Glu Gln Arg Arg Ile Asn Asp Ala Tyr  
 515 520 525  
 Lys Gln Leu Leu His Leu Arg His Thr Leu Gly Phe Ser Gln Pro Asn  
 530 535 540

Leu Leu Thr Leu Glu Val Glu His Gly Glu Asn Trp Leu Ser Met Ala  
 545 550 555 560

Asn Gly Arg Gly Arg Ile Leu Ala Asn Phe Ser Asp Asp Thr Ile Thr  
 565 570 575

Val Pro Leu Gly Gly Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val  
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Arg Asn  
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<210> 1147

<211> 832

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(832)

<223> RXN02355

<400> 1147

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 Met Ser Ser Ile Ser  
 1 5

cgc aag acc ggc gcg tca ctt gca gcc acc aca ctg ttg gca gcg atc 163  
 Arg Lys Thr Gly Ala Ser Leu Ala Ala Thr Thr Leu Leu Ala Ala Ile  
 10 15 20

gca ctg gcc ggt tgt agt tca gac tca agc tcc gac tcc aca gat tcc 211  
 Ala Leu Ala Gly Cys Ser Ser Asp Ser Ser Ser Asp Ser Thr Asp Ser  
 25 30 35

acc gct agc gaa ggc gca gac agc cgc ggc ccc atc acc ttt gcg atg 259  
 Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro Ile Thr Phe Ala Met  
 40 45 50

ggc aaa aac gac acc gac aaa gtc att ccg atc atc gac cgc tgg aac 307  
 Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile Ile Asp Arg Trp Asn  
 55 60 65

gaa gcc cac ccc gat gag cag gta acg ctc aac gaa ctc gcc ggt gaa 355  
 Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn Glu Leu Ala Gly Glu  
 70 75 80 85

gcc gac gcg cag cgc gaa acc ctc gtg caa tcc ctg cag gcc ggc aac 403  
 Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser Leu Gln Ala Gly Asn  
 90 95 100

tct gac tac gac gtc atg gcg ctc gac gtc atc tgg acc gca gac ttc 451  
 Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile Trp Thr Ala Asp Phe  
 105 110 115

gcg gca aac caa tgg ctc gca cca ctt gaa ggc gac ctc gag gta gac 499  
 Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly Asp Leu Glu Val Asp  
           120                                  125                                  130

acc tcc gga ctg ctg caa tcc acc gtg gat tcc gca acc tac aac ggc 547  
 Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser Ala Thr Tyr Asn Gly  
           135                                  140                                  145

acc ctc tac gca ctg cca cag aac acc aac ggc cag cta ctg ttc cgc 595  
 Thr Leu Tyr Ala Leu Pro Gln Asn Thr Asn Gly Gln Leu Leu Phe Arg  
 150                                  155                                  160                                  165

aac acc gaa atc atc cca gaa gca cca gca aac tgg gct gac ctc gtg 643  
 Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn Trp Ala Asp Leu Val  
                                   170                                  175                                  180

gaa tcc tgc acg ctt gct gaa gaa gca ggc gtt gat tgc ctg acc act 691  
 Glu Ser Cys Thr Leu Ala Glu Glu Ala Gly Val Asp Cys Leu Thr Thr  
                                   185                                  190                                  195

cag ctc aag cag tac gaa ggc ctt tca gtg aac acc atc ggc ttc atc 739  
 Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn Thr Ile Gly Phe Ile  
                                   200                                  205                                  210

gaa ggt tgg gga ggc agc gtc cta gac gat gac ggc aaa cgt cac cgt 787  
 Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp Gly Lys Arg His Arg  
           215                                  220                                  225

aga cag cac gac ggc aag gca ggc ctt caa gcg ctt gtc gac ggc 832  
 Arg Gln His Asp Gly Lys Ala Gly Leu Gln Ala Leu Val Asp Gly  
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<210> 1148

<211> 244

<212> PRT

<213> Corynebacterium glutamicum

<400> 1148

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                                   20                                  25                                  30

Asp Ser Thr Asp Ser Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro  
           35                                  40                                  45

Ile Thr Phe Ala Met Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile  
           50                                  55                                  60

Ile Asp Arg Trp Asn Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn  
   65                                  70                                  75                                  80

Glu Leu Ala Gly Glu Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser  
                                   85                                  90                                  95

Leu Gln Ala Gly Asn Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile  
                                   100                                  105                                  110

Trp Thr Ala Asp Phe Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly

115	120	125
Asp Leu Glu Val Asp Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser 130	135	140
Ala Thr Tyr Asn Gly Thr Leu Tyr Ala Leu Pro Gln Asn Thr Asn Gly 145	150	155 160
Gln Leu Leu Phe Arg Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn 165	170	175
Trp Ala Asp Leu Val Glu Ser Cys Thr Leu Ala Glu Glu Ala Gly Val 180	185	190
Asp Cys Leu Thr Thr Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn 195	200	205
Thr Ile Gly Phe Ile Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp 210	215	220
Gly Lys Arg His Arg Arg Gln His Asp Gly Lys Ala Gly Leu Gln Ala 225	230	235 240
Leu Val Asp Gly		

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(586)  
 <223> RXN02909

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 Met Asn Arg Ala Arg  
 1 5  
 atc gcg acc ata ggc gtt ctt ccg ctt gct tta ctg ctg gcg tcc tgt 163  
 Ile Ala Thr Ile Gly Val Leu Pro Leu Ala Leu Leu Leu Ala Ser Cys  
 10 15 20  
 ggt tca gac acc gtg gaa atg aca gat tcc acc tgg ttg gtg acc aat 211  
 Gly Ser Asp Thr Val Glu Met Thr Asp Ser Thr Trp Leu Val Thr Asn  
 25 30 35  
 att tac acc gat cca gat gag tcg aat tcg atc agt aat ctt gtc att 259  
 Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile Ser Asn Leu Val Ile  
 40 45 50  
 tcc cag ccc agc tta gat ttt ggc aat tct tcc ctg tct ggt ttc act 307  
 Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser Leu Ser Gly Phe Thr  
 55 60 65  
 ggc tgt gtg cct ttt acg ggg cgt gcg gaa ttc ttc caa aat ggt gag 355

Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe Phe Gln Asn Gly Glu  
 70 75 80 85  
 caa agc tct gtt ctg gat gcc gat tat gtg acc ttg tct tcc ctg gat 403  
 Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr Leu Ser Ser Leu Asp  
 90 95 100  
 ttc gat aaa ctt ccc gat gat tgc caa gga caa gaa ctc aaa gtt cat 451  
 Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln Glu Leu Lys Val His  
 105 110 115  
 aac gag ctg gtt gat ctt ctg cct ggt tct ttt gaa atc tcc agg act 499  
 Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe Glu Ile Ser Arg Thr  
 120 125 130  
 tct ggt tca gaa atc ttg ctg act agc gat gtc gat gaa ctc gat cgg 547  
 Ser Gly Ser Glu Ile Leu Leu Thr Ser Asp Val Asp Glu Leu Asp Arg  
 135 140 145  
 cca gca atc cgc ttg gtg tcc tgg atc gcg ccg aca tct taagggtgcca 596  
 Pro Ala Ile Arg Leu Val Ser Trp Ile Ala Pro Thr Ser  
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 gggctttaaa gtg 609  
  
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 20 25 30  
 Trp Leu Val Thr Asn Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile  
 35 40 45  
 Ser Asn Leu Val Ile Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser  
 50 55 60  
 Leu Ser Gly Phe Thr Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe  
 65 70 75 80  
 Phe Gln Asn Gly Glu Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr  
 85 90 95  
 Leu Ser Ser Leu Asp Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln  
 100 105 110  
 Glu Leu Lys Val His Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe  
 115 120 125  
 Glu Ile Ser Arg Thr Ser Gly Ser Glu Ile Leu Leu Thr Ser Asp Val  
 130 135 140  
 Asp Glu Leu Asp Arg Pro Ala Ile Arg Leu Val Ser Trp Ile Ala Pro  
 145 150 155 160

Thr Ser

&lt;210&gt; 1151

&lt;211&gt; 1590

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1567)

&lt;223&gt; RXS00349

&lt;400&gt; 1151

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gtgattggac tcttttttctt tgcaaaatgt tttccagcgg atg ttg agt ttt gcg      115
                                   Met Leu Ser Phe Ala
                                   1                               5

acc ctt cgt ggc cgc att tca aca gtt gac gct gca aaa gcc gca cct      163
Thr Leu Arg Gly Arg Ile Ser Thr Val Asp Ala Ala Lys Ala Ala Pro
                                   10                               15                               20

ccg cca tcg cca cta gcc ccg att gat ctc act gac cat agt caa gtg      211
Pro Pro Ser Pro Leu Ala Pro Ile Asp Leu Thr Asp His Ser Gln Val
                                   25                               30                               35

gcc ggt gtg atg aat ttg gct gcg aga att ggc gat att ttg ctt tct      259
Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly Asp Ile Leu Leu Ser
                                   40                               45                               50

tca ggt acg tca aat agt gac acc aag gta caa gtt cga gca gtg acc      307
Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln Val Arg Ala Val Thr
                                   55                               60                               65

tct gcg tac ggt ttg tac tac acg cac gtg gat atc acg ttg aat acg      355
Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp Ile Thr Leu Asn Thr
                                   70                               75                               80                               85

atc acc atc ttc acc aac atc ggt gtg gag agg aag atg ccg gtc aac      403
Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg Lys Met Pro Val Asn
                                   90                               95                               100

gtg ttt cat gtt gta ggc aag ttg gac acc aac ttc tcc aaa ctg tct      451
Val Phe His Val Val Gly Lys Leu Asp Thr Asn Phe Ser Lys Leu Ser
                                   105                               110                               115

gag gtt gac cgt ttg atc cgt tcc att cag gct ggt gcg acc ccg cct      499
Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala Gly Ala Thr Pro Pro
                                   120                               125                               130

gag gtt gcc gag aaa atc ctg gac gag ttg gag caa tcc cct gcg tct      547
Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu Gln Ser Pro Ala Ser
                                   135                               140                               145

tat ggt ttc cct gtt gcg ttg ctt ggc tgg gca atg atg ggt ggt gct      595
Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala Met Met Gly Gly Ala
                                   150                               155                               160                               165

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gtt gct gtg ctg ttg ggt ggt gga tgg cag gtt tcc cta att gct ttt 643  
 Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val Ser Leu Ile Ala Phe  
 170 175 180

att acc gcg ttc acg atc att gcc acg acg tca ttt ttg gga aag aag 691  
 Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys  
 185 190 195

ggt ttg cct act ttc ttc caa aat gtt gtt ggt ggt ttt att gcc acg 739  
 Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr  
 200 205 210

ctg cct gca tcg att gct tat tct ttg gcg ttg caa ttt ggt ctt gag 787  
 Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu  
 215 220 225

atc aaa ccg agc cag atc atc gca tct gga att gtt gtg ctg ttg gca 835  
 Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala  
 230 235 240 245

ggt ttg aca ctc gtg caa tct ctg cag gac ggc atc acg ggc gct ccg 883  
 Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro  
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gtg aca gca agt gca cga ttt ttc gaa aca ctc ctg ttt acc ggc ggc 931  
 Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly  
 265 270 275

att gtt gct ggc gtg ggt ttg ggc att cag ctt tct gaa atc ttg cat 979  
 Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu Ser Glu Ile Leu His  
 280 285 290

gtc atg ttg cct gcc atg gag tcc gct gca gca cct aat tat tcg tct  
 1027  
 Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala Pro Asn Tyr Ser Ser  
 295 300 305

aca ttc gcc cgc att atc gct ggt ggc gtc acc gca gcg gcc ttc gca  
 1075  
 Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr Ala Ala Ala Phe Ala  
 310 315 320 325

gtg ggt tgt tac gcg gag tgg tcc tcg gtg att att gcg ggg ctt act  
 1123  
 Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile Ile Ala Gly Leu Thr  
 330 335 340

gcg ctg atg ggt tct gcg ttt tat tac ctc ttc gtt gtt tat tta ggc  
 1171  
 Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly  
 345 350 355

ccc gtc tct gcc gct gcg att gct gca aca gca gtt ggt ttc act ggt  
 1219  
 Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly  
 360 365 370

ggt ttg ctt gcc cgt cga ttc ttg att cca ccg ttg att gtg gcg att  
 1267  
 Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile

375                                      380                                      385  
 gcc ggc atc aca cca atg ctt cca ggt cta gca att tac cgc gga atg  
 1315  
 Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met  
 390                                      395                                      400                                      405  
 tac gcc acc ctg aat gat caa aca ctc atg ggt ttc acc aac att gcg  
 1363  
 Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala  
 410                                      415                                      420  
 gtt gct tta gcc act gct tca tca ctt gcc gct ggc gtg gtt ttg ggt  
 1411  
 Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly  
 425                                      430                                      435  
 gag tgg att gcc cgc agg cta cgt cgt cca cca cgc ttc aac cca tac  
 1459  
 Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr  
 440                                      445                                      450  
 cgt gca ttt acc aag gcg aat gag ttc tcc ttc cag gag gaa gct gag  
 1507  
 Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu  
 455                                      460                                      465  
 cag aat cag cgc cgg cag aga aaa cgt cca aag act aat cag aga ttc  
 1555  
 Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe  
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 <211> 489  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1152  
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 20                                      25                                      30  
 Asp His Ser Gln Val Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly  
 35                                      40                                      45  
 Asp Ile Leu Leu Ser Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln  
 50                                      55                                      60  
 Val Arg Ala Val Thr Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp  
 65                                      70                                      75                                      80  
 Ile Thr Leu Asn Thr Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg  
 85                                      90                                      95

Lys Met Pro Val Asn Val Phe His Val Val Gly Lys Leu Asp Thr Asn  
 100 105 110  
 Phe Ser Lys Leu Ser Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala  
 115 120 125  
 Gly Ala Thr Pro Pro Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu  
 130 135 140  
 Gln Ser Pro Ala Ser Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala  
 145 150 155 160  
 Met Met Gly Gly Ala Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val  
 165 170 175  
 Ser Leu Ile Ala Phe Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser  
 180 185 190  
 Phe Leu Gly Lys Lys Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly  
 195 200 205  
 Gly Phe Ile Ala Thr Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu  
 210 215 220  
 Gln Phe Gly Leu Glu Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile  
 225 230 235 240  
 Val Val Leu Leu Ala Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly  
 245 250 255  
 Ile Thr Gly Ala Pro Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu  
 260 265 270  
 Leu Phe Thr Gly Gly Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu  
 275 280 285  
 Ser Glu Ile Leu His Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala  
 290 295 300  
 Pro Asn Tyr Ser Ser Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr  
 305 310 315 320  
 Ala Ala Ala Phe Ala Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile  
 325 330 335  
 Ile Ala Gly Leu Thr Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe  
 340 345 350  
 Val Val Tyr Leu Gly Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala  
 355 360 365  
 Val Gly Phe Thr Gly Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro  
 370 375 380  
 Leu Ile Val Ala Ile Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala  
 385 390 395 400  
 Ile Tyr Arg Gly Met Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly  
 405 410 415

Phe Thr Asn Ile Ala Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala  
 420 425 430

Gly Val Val Leu Gly Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro  
 435 440 445

Arg Phe Asn Pro Tyr Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe  
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Gln Glu Glu Ala Glu Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys  
 465 470 475 480

Thr Asn Gln Arg Phe Gly Asn Lys Arg  
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(417)

<223> RXS03183

<400> 1153

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aaa gac ggc gtc ggc gta tcc acc ctt ggt ggc tac aac aac ggc atc 96  
 Lys Asp Gly Val Gly Val Ser Thr Leu Gly Gly Tyr Asn Asn Gly Ile  
 20 25 30

aac gtc aac tcc gaa aac aag gca acc gcc cgc gac ttc atc gaa ttc 144  
 Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe  
 35 40 45

atc atc aac gaa gag aac caa acc tgg ttc gcg gac aac tcc ttc cca 192  
 Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro  
 50 55 60

cca gtt ctg gca tcc atc tac gat gat gag tcc ctt gtt gag cag tac 240  
 Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr  
 65 70 75 80

cca tac ctg cca gca ctg aag gaa tcc ctg gaa aac gca gca cca cgc 288  
 Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg  
 85 90 95

cca gtg tct cct ttc tac cca gcc atc tcc aag gca atc cag gac aac 336  
 Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn  
 100 105 110

gcc tac gca gcg ctt aac ggc aac gtc gac gtt gac cag gca acc acc 384  
 Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr  
 115 120 125

gat atg aag gca gcg atc gaa aac gct tcc agc tagttcggta atttagttca 437  
 Asp Met Lys Ala Ala Ile Glu Asn Ala Ser Ser

130

135

ttc

440

&lt;210&gt; 1154

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1154

Glu Ala Glu Ala Thr Ala Gly Lys Phe Glu Val Gln Pro Leu Val Gly  
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Lys Asp Gly Val Gly Val Ser Thr Leu Gly Gly Tyr Asn Asn Gly Ile  
 20 25 30

Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe  
 35 40 45

Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro  
 50 55 60

Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr  
 65 70 75 80

Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg  
 85 90 95

Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn  
 100 105 110

Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr  
 115 120 125

Asp Met Lys Ala Ala Ile Glu Asn Ala Ser Ser  
 130 135

&lt;210&gt; 1155

&lt;211&gt; 1212

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1189)

&lt;223&gt; RXC00874

&lt;400&gt; 1155

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 Met Ser Ile Gly Gln  
 1 5

cac atc atc acc gag cgt ttc tac ggc gcc aag tcc cac acc atc gac 163  
 His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys Ser His Thr Ile Asp  
 10 15 20

aac gta gat att gtg ttg tcc cgc gaa tgt ggc gag aac act ttg gct 211

Asn Val Asp Ile Val Leu Ser Arg Glu Cys Gly Glu Asn Thr Leu Ala	
25 30 35	
gta gtg cgc atc aac aat gcg ctg tat cag ttg ttg gtc aat gat gat	259
Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu Leu Val Asn Asp Asp	
40 45 50	
ggc aaa gat gtt ctc aac gac cac gta gaa gag gtc ggt gcg agt ttc	307
Gly Lys Asp Val Leu Asn Asp His Val Glu Glu Val Gly Ala Ser Phe	
55 60 65	
gga gca tgg act ggc agc tct gct ttt ccc att ggc cct ttc act cca	355
Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile Gly Pro Phe Thr Pro	
70 75 80 85	
ctc ggc aca gaa caa tcc aat agc tct ttc atc acc gcc gac aat aaa	403
Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile Thr Ala Asp Asn Lys	
90 95 100	
gcg atc gtg aaa tac ttc cgc aaa tta gaa tcc ggg caa aac ccc gat	451
Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser Gly Gln Asn Pro Asp	
105 110 115	
gtg gag cta att tct aaa att tcc tcc tgc ccc aac atc gcg ccc atc	499
Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro Asn Ile Ala Pro Ile	
120 125 130	
ctg ggt ttt tcc tcc gct gag atc tcc ggg gct aac tac acc ctg gtc	547
Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala Asn Tyr Thr Leu Val	
135 140 145	
atg gcg cag cag tac gtt cca ggt ttg gat ggc tgg tca cac gcg ctg	595
Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly Trp Ser His Ala Leu	
150 155 160 165	
act act acc tct ggc agc ttt gca gag gat gca gaa aag atc ggc gaa	643
Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala Glu Lys Ile Gly Glu	
170 175 180	
gcc acc cgc aat gtt cac act gct ctt gca tcg gcc ttc cct act cgg	691
Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser Ala Phe Pro Thr Arg	
185 190 195	
gta gtt ccc gta gaa gca ctc gcc gat gcg ctc act acc cgc ctt aat	739
Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu Thr Thr Arg Leu Asn	
200 205 210	
gaa cta atc tcc caa gca ccc gaa atc gcc cgc ttc aaa gaa gca gcc	787
Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg Phe Lys Glu Ala Ala	
215 220 225	
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Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala His Ile Gln Arg Ile	
230 235 240 245	
cac ggt gac ctc cac ttg ggg cag ctc atc aaa acc ccc gaa cgc tac	883
His Gly Asp Leu His Leu Gly Gln Leu Ile Lys Thr Pro Glu Arg Tyr	
250 255 260	
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Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg Pro Leu Asn Gln Arg	

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 Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala Gly Il Ile Arg Ser  
 280 285 290  
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 1027  
 Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His Thr Gln Trp Ala Asn  
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 1123  
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 Glu Asn Thr Leu Ala Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu  
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 Leu Val Asn Asp Asp Gly Lys Asp Val Leu Asn Asp His Val Glu Glu  
 50 55 60  
 Val Gly Ala Ser Phe Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile  
 65 70 75 80  
 Gly Pro Phe Thr Pro Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile  
 85 90 95  
 Thr Ala Asp Asn Lys Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser  
 100 105 110  
 Gly Gln Asn Pro Asp Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro  
 115 120 125

Asn Ile Ala Pro Ile Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala  
 130 135 140  
 Asn Tyr Thr Leu Val Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly  
 145 150 155 160  
 Trp Ser His Ala Leu Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala  
 165 170 175  
 Glu Lys Ile Gly Glu Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser  
 180 185 190  
 Ala Phe Pro Thr Arg Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu  
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 Thr Thr Arg Leu Asn Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg  
 210 215 220  
 Phe Lys Glu Ala Ala Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala  
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 His Ile Gln Arg Ile His Gly Asp Leu His Leu Gly Gln Leu Ile Lys  
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 Thr Pro Glu Arg Tyr Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg  
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 Pro Leu Asn Gln Arg Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala  
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 Gly Ile Ile Arg Ser Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His  
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 Thr Gln Trp Ala Asn Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly  
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